```
R version 3.2.4 (2016-03-10) -- "Very Secure Dishes"
Copyright (C) 2016 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin13.4.0 (64-bit)

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  Natural language support but running in an English locale

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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

During startup - Warning messages:
1: Setting LC_CTYPE failed, using "C"
2: Setting LC_COLLATE failed, using "C"
3: Setting LC_TIME failed, using "C"
4: Setting LC_MESSAGES failed, using "C"
5: Setting LC_MONETARY failed, using "C"
[R.app GUI 1.67 (7152) x86_64-apple-darwin13.4.0]

WARNING: You're using a non-UTF8 locale, therefore only ASCII characters will
work.
Please read R for Mac OS X FAQ (see Help) section 9 and adjust your system
preferences accordingly.
[Workspace restored from /Users/OwainThomas/Dropbox/RESEARCH/EPI/Statistik EPI
2014/.RData]
[History restored from /Users/OwainThomas/Dropbox/RESEARCH/EPI/Statistik EPI
2014/.Rapp.history]

2016-07-06 14:02:50.954 R[5666:3360988] *** WARNING: Method
convertPointFromBase: in class NSView is deprecated on 10.7 and later. It
should not be used in new applications.
> epi<-read.table(file="epiresultat.txt", header=TRUE,dec=",")
> epi$preopHEPTEMminusINTEMmcf<-epi$Prov1heptemMCF-epi$Prov1intemMCF
> epi$postopHEPTEMminusINTEMmcf<-epi$Prov2heptemMCF-epi$Prov2intemMCF
> mean(epi$PatAge)
[1] 70.23684
> sd(epi$PatAge)
[1] 6.94548
> min(epi$PatAge)
[1] 57
> max(epi$PatAge)
[1] 82
>
> sum(epi$PatSex)
[1] 27
> #MCF
> boxplot(epi$Prov1extemMCF,epi$Prov2extemMCF,-100, epi$Prov1fibtemMCF,epi
$Prov2fibtemMCF,-100, epi$Prov1intemMCF,epi$Prov2intemMCF,-100, epi
```

```
$Prov1heptemMCF,epi$Prov2heptemMCF,-100,epi$preopHEPTEMminusINTEMmcf,epi
$postopHEPTEMminusINTEMmcf, horizontal=FALSE, na.rm=TRUE, axes=TRUE, main="Pre-
and postoperative ROTEM MCF Values",cex.main=1.65,
ylim=c(-5,95),cex.axis=1.5,cex.lab=1.45, ylab="Maximum clot firmness (MCF) in
mm", boxwex=1, col=c(24,0,0,24,0,0,24,0,0,24,0,0,24,0), lty=1)
>  text(x=1.5,y=90, "EXTEM", pos=3, cex=1.2)
>  text(x=4.5,y=90, "FIBTEM", pos=3, cex=1.2)
>  text(x=7.5,y=90, "INTEM", pos=3, cex=1.2)
>  text(x=10.5,y=90, "HEPTEM", pos=3, cex=1.2)
>  text(x=13.5,y=90, "HEPTEM -", pos=3, cex=1.2)
>  text(x=13.5,y=85, "INTEM", pos=3, cex=1.2)
>  legend(0.7,7, c("Preoperative","Postoperative"), cex= 1,fill=c(24,0))
>  legend(5.7,5,lty=3,lwd=2,c("Reference range"))
>  arrows(0.4,50,,72,code=0,lwd=2,lty=3)
>  arrows(3.4,9,,25,code=0,lwd=2,lty=3)
>  arrows(6.4,50,,72,code=0,lwd=2,lty=3)
>  arrows(9.4,50,,72,code=0,lwd=2,lty=3)
>
> #hist(epi$Prov1extemMCF)
> #hist(epi$Prov2extemMCF)
> mean(epi$Prov1extemMCF, na.rm=TRUE)
[1] 64.05263
> sd(epi$Prov1extemMCF, na.rm=TRUE)
[1] 7.897818
> mean(epi$Prov2extemMCF, na.rm=TRUE)
[1] 71.66667
> sd(epi$Prov2extemMCF, na.rm=TRUE)
[1] 6.111806
>
> t.test(epi$Prov1extemMCF,epi$Prov2extemMCF,alternative =
c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$Prov1extemMCF and epi$Prov2extemMCF
t = -5.0837, df = 32, p-value = 1.558e-05
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -11.247908  -4.812698
sample estimates:
mean of the differences
              -8.030303

> wilcox.test(epi$Prov1extemMCF,epi$Prov2extemMCF,alternative =
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1extemMCF and epi$Prov2extemMCF
V = 40, p-value = 7.779e-05
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1extemMCF, epi$Prov2extemMCF, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
```

```
2: In wilcox.test.default(epi$Prov1extemMCF, epi$Prov2extemMCF, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
> x<-1
> y<-85
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-3,"**",pos=3, cex=1.4)
>
> #hist(epi$Prov1fibtemMCF)
> #hist(epi$Prov2fibtemMCF)
> mean(epi$Prov1fibtemMCF, na.rm=TRUE)
[1] 20.08108
> sd(epi$Prov1fibtemMCF, na.rm=TRUE)
[1] 7.166195
> mean(epi$Prov2fibtemMCF, na.rm=TRUE)
[1] 33.72727
> sd(epi$Prov2fibtemMCF, na.rm=TRUE)
[1] 9.155848
> t.test(epi$Prov1fibtemMCF,epi$Prov2fibtemMCF,alternative =
c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$Prov1fibtemMCF and epi$Prov2fibtemMCF
t = -6.8746, df = 31, p-value = 1.048e-07
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -17.788756  -9.648744
sample estimates:
mean of the differences
              -13.71875

> wilcox.test(epi$Prov1fibtemMCF,epi$Prov2fibtemMCF,alternative =
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1fibtemMCF and epi$Prov2fibtemMCF
V = 21, p-value = 5.753e-06
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$Prov1fibtemMCF, epi$Prov2fibtemMCF, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
> x<-4
> y<-85
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-3,"**",pos=3, cex=1.4)
>
> #hist(epi$Prov1intemMCF)
> #hist(epi$Prov2intemMCF)
> mean(epi$Prov1intemMCF, na.rm=TRUE)
[1] 63.28947
```

```
> sd(epi$Prov1intemMCF, na.rm=TRUE)
[1] 5.862883
> mean(epi$Prov2intemMCF, na.rm=TRUE)
[1] 69.54545
> sd(epi$Prov2intemMCF, na.rm=TRUE)
[1] 8.551648
> t.test(epi$Prov1intemMCF,epi$Prov2intemMCF,alternative =
c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$Prov1intemMCF and epi$Prov2intemMCF
t = -3.8044, df = 32, p-value = 0.0006047
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -9.956928 -3.012769
sample estimates:
mean of the differences
              -6.484848

> wilcox.test(epi$Prov1intemMCF,epi$Prov2intemMCF,alternative =
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1intemMCF and epi$Prov2intemMCF
V = 60.5, p-value = 0.0002462
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1intemMCF, epi$Prov2intemMCF, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1intemMCF, epi$Prov2intemMCF, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
> x<-7
> y<-85
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-3,"**",pos=3, cex=1.4)
>
> #hist(epi$Prov1heptemMCF)
> #hist(epi$Prov2heptemMCF)
> mean(epi$Prov1heptemMCF, na.rm=TRUE)
[1] 62.18421
> sd(epi$Prov1heptemMCF, na.rm=TRUE)
[1] 5.834915
> mean(epi$Prov2heptemMCF, na.rm=TRUE)
[1] 69.40625
> sd(epi$Prov2heptemMCF, na.rm=TRUE)
[1] 6.399896
> t.test(epi$Prov1heptemMCF,epi$Prov2heptemMCF,alternative =
c("two.sided"),paired = TRUE)

	Paired t-test
```

```
data:  epi$Prov1heptemMCF and epi$Prov2heptemMCF
t = -6.3687, df = 31, p-value = 4.317e-07
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -9.365446 -4.822054
sample estimates:
mean of the differences 
               -7.09375 

> wilcox.test(epi$Prov1heptemMCF,epi$Prov2heptemMCF,alternative =
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1heptemMCF and epi$Prov2heptemMCF
V = 21.5, p-value = 2.327e-05
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1heptemMCF, epi$Prov2heptemMCF, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1heptemMCF, epi$Prov2heptemMCF, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
> x<-10
> y<-85
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-3,"**",pos=3, cex=1.4)
> 
> mean(epi$preopHEPTEMminusINTEMmcf, na.rm=TRUE)
[1] -1.105263
> sd(epi$preopHEPTEMminusINTEMmcf, na.rm=TRUE)
[1] 1.752056
> mean(epi$postopHEPTEMminusINTEMmcf, na.rm=TRUE)
[1] -0.15625
> sd(epi$postopHEPTEMminusINTEMmcf, na.rm=TRUE)
[1] 6.687057
> #hist(epi$preopHEPTEMminusINTEMmcf)
> epi$preopHEPTEMminusINTEMmcf
 [1]  0 -2 -3 -2  2 -2  0  1 -1 -4 -4  2 -1 -3 -3  1 -3 -2  1 -4  0  0  0 -1  0
[26]  0  1 -2 -4 -1  0 -1  1 -4 -1 -1 -2  0
> #hist(epi$postopHEPTEMminusINTEMmcf)
> 
> t.test(epi$preopHEPTEMminusINTEMmcf,epi$postopHEPTEMminusINTEMmcf,alternative
= c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$preopHEPTEMminusINTEMmcf and epi$postopHEPTEMminusINTEMmcf
t = -0.55375, df = 31, p-value = 0.5837
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -3.073271  1.760771
```

```
sample estimates:
mean of the differences
               -0.65625

> wilcox.test(epi$preopHEPTEMminusINTEMmcf,epi
$postopHEPTEMminusINTEMmcf,alternative = c("two.sided"),paired = TRUE)

    Wilcoxon signed rank test with continuity correction

data:  epi$preopHEPTEMminusINTEMmcf and epi$postopHEPTEMminusINTEMmcf
V = 156.5, p-value = 0.5819
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$preopHEPTEMminusINTEMmcf, epi
$postopHEPTEMminusINTEMmcf,  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$preopHEPTEMminusINTEMmcf, epi
$postopHEPTEMminusINTEMmcf,  :
  cannot compute exact p-value with zeroes
>
>
>
> #CT
> boxplot(epi$Prov1extemCT,epi$Prov2extemCT,-1000, epi$Prov1intemCT,epi
$Prov2intemCT,-1000, epi$Prov1heptemCT,epi$Prov2heptemCT,-1000,epi
$preopINTEMminusHEPTEMct,epi$postopINTEMminusHEPTEMct, horizontal=FALSE,
na.rm=TRUE, axes=TRUE, main="Pre- and postoperative ROTEM CT
Values",cex.main=1.65,cex.axis=1.5,cex.lab=1.45, ylab="Clotting time (CT) in
s", boxwex=1, col=c(24,0,0,24,0,0,24,0,0,24,0,0,24,0), ylim=c(-102,400),lty=1)
Warning messages:
1: In is.na(x) : is.na() applied to non-(list or vector) of type 'NULL'
2: In is.na(x) : is.na() applied to non-(list or vector) of type 'NULL'
3: In is.na(x) : is.na() applied to non-(list or vector) of type 'NULL'
4: In is.na(x) : is.na() applied to non-(list or vector) of type 'NULL'
5: In is.na(x) : is.na() applied to non-(list or vector) of type 'NULL'
6: In is.na(x) : is.na() applied to non-(list or vector) of type 'NULL'
> text(x=1.5,y=380, "EXTEM", pos=3, cex=1.2)
> text(x=4.5,y=380, "INTEM", pos=3, cex=1.2)
> text(x=7.5,y=380, "HEPTEM", pos=3, cex=1.2)
> text(x=10.5,y=380, "INTEM -", pos=3, cex=1.2)
> text(x=10.5,y=355, "HEPTEM", pos=3, cex=1.2)
> legend(0.7,-20, c("Preoperative","Postoperative"), cex= 1,fill=c(24,0))
>
> legend(4.7,-25,lty=3,lwd=2,c("Reference range"))
> arrows(0.4,38,,79,code=0,lwd=2,lty=3)
> arrows(3.4,100,,240,code=0,lwd=2,lty=3)
> arrows(6.4,100,,240,code=0,lwd=2,lty=3)
>
> mean(epi$Prov1extemCT, na.rm=TRUE)
[1] 47.52632
> sd(epi$Prov1extemCT, na.rm=TRUE)
[1] 13.90652
> mean(epi$Prov2extemCT, na.rm=TRUE)
[1] 48.12121
> sd(epi$Prov2extemCT, na.rm=TRUE)
```

```
[1] 12.19825
>
> mean(epi$Prov1intemCT, na.rm=TRUE)
[1] 175.9474
> sd(epi$Prov1intemCT, na.rm=TRUE)
[1] 46.48158
> mean(epi$Prov2intemCT, na.rm=TRUE)
[1] 165.0303
> sd(epi$Prov2intemCT, na.rm=TRUE)
[1] 42.96982
>
> mean(epi$Prov1heptemCT, na.rm=TRUE)
[1] 187.7632
> sd(epi$Prov1heptemCT, na.rm=TRUE)
[1] 49.63675
> mean(epi$Prov2heptemCT, na.rm=TRUE)
[1] 181.7273
> sd(epi$Prov2heptemCT, na.rm=TRUE)
[1] 45.23016
>
> t.test(epi$Prov1extemCT,epi$Prov2extemCT,alternative = c("two.sided"),paired
= TRUE)

    Paired t-test

data:  epi$Prov1extemCT and epi$Prov2extemCT
t = -0.71131, df = 32, p-value = 0.482
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -7.376024  3.557842
sample estimates:
mean of the differences
              -1.909091

> wilcox.test(epi$Prov1extemCT,epi$Prov2extemCT,alternative =
c("two.sided"),paired = TRUE)

    Wilcoxon signed rank test with continuity correction

data:  epi$Prov1extemCT and epi$Prov2extemCT
V = 178.5, p-value = 0.1117
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1extemCT, epi$Prov2extemCT, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1extemCT, epi$Prov2extemCT, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
> mean(epi$Prov1extemCT, na.rm=TRUE)
[1] 47.52632
> sd(epi$Prov1intemCT, na.rm=TRUE)
[1] 46.48158
>
> t.test(epi$Prov1intemCT,epi$Prov2intemCT,alternative = c("two.sided"),paired
```

```
= TRUE)

	Paired t-test

data:  epi$Prov1intemCT and epi$Prov2intemCT
t = 1.462, df = 32, p-value = 0.1535
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -6.07791 36.98700
sample estimates:
mean of the differences 
               15.45455 

> wilcox.test(epi$Prov1intemCT,epi$Prov2intemCT,alternative = 
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1intemCT and epi$Prov2intemCT
V = 371.5, p-value = 0.1058
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$Prov1intemCT, epi$Prov2intemCT, alternative = 
c("two.sided"),  :
  cannot compute exact p-value with ties
> mean(epi$Prov1extemCT, na.rm=TRUE)
[1] 47.52632
> 
> t.test(epi$Prov1heptemCT,epi$Prov2heptemCT,alternative = 
c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$Prov1heptemCT and epi$Prov2heptemCT
t = 0.69247, df = 32, p-value = 0.4936
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -17.23871  34.99629
sample estimates:
mean of the differences 
               8.878788 

> wilcox.test(epi$Prov1heptemCT,epi$Prov2heptemCT,alternative = 
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1heptemCT and epi$Prov2heptemCT
V = 334.5, p-value = 0.3391
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$Prov1heptemCT, epi$Prov2heptemCT, alternative = 
c("two.sided"),  :
  cannot compute exact p-value with ties
```

```
>
>
> t.test(epi$Prov1CT,epi$Prov2fibtemCT,alternative = c("two.sided"),paired =
TRUE)
Error in t.test.default(epi$Prov1CT, epi$Prov2fibtemCT, alternative =
c("two.sided"),  :
  not enough 'x' observations
> wilcox.test(epi$Prov1fibtemCT,epi$Prov2fibtemCT,alternative =
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1fibtemCT and epi$Prov2fibtemCT
V = 165, p-value = 0.1055
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1fibtemCT, epi$Prov2fibtemCT, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1fibtemCT, epi$Prov2fibtemCT, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
>
>
>
> t.test(epi$Prov1intemCT,epi$Prov2intemCT,alternative = c("two.sided"),paired
= TRUE)

	Paired t-test

data:  epi$Prov1intemCT and epi$Prov2intemCT
t = 1.462, df = 32, p-value = 0.1535
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -6.07791 36.98700
sample estimates:
mean of the differences
               15.45455

> wilcox.test(epi$Prov1intemCT,epi$Prov2intemCT,alternative =
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1intemCT and epi$Prov2intemCT
V = 371.5, p-value = 0.1058
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$Prov1intemCT, epi$Prov2intemCT, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
>
>
>
```

```
> t.test(epi$Prov1heptemCT,epi$Prov2heptemCT,alternative =
c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$Prov1heptemCT and epi$Prov2heptemCT
t = 0.69247, df = 32, p-value = 0.4936
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -17.23871  34.99629
sample estimates:
mean of the differences
               8.878788

> wilcox.test(epi$Prov1heptemCT,epi$Prov2heptemCT,alternative =
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1heptemCT and epi$Prov2heptemCT
V = 334.5, p-value = 0.3391
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$Prov1heptemCT, epi$Prov2heptemCT, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
>
>
> t.test(epi$preopINTEMminusHEPTEMct,epi$postopINTEMminusHEPTEMct,alternative =
c("two.sided"),paired = TRUE)
Error in t.test.default(epi$preopINTEMminusHEPTEMct, epi
$postopINTEMminusHEPTEMct,  :
  'y' is missing for paired test
> wilcox.test(epi$preopINTEMminusHEPTEMct,epi
$postopINTEMminusHEPTEMct,alternative = c("two.sided"),paired = TRUE)
Error in wilcox.test.default(epi$preopINTEMminusHEPTEMct, epi
$postopINTEMminusHEPTEMct,  :
  'x' must be numeric
>
>
>
> #MultiplateADP
> boxplot(epi$Prov1multiplateADP,epi$Prov2multiplateADP,-100, epi
$Prov1multiplateCOL,epi$Prov2multiplateCOL,-100, epi$Prov1multiplateTRAP,epi
$Prov2multiplateTRAP,-100, epi$Prov1multiplateASPI,epi$Prov2multiplateASPI,
horizontal=FALSE, na.rm=TRUE, axes=TRUE, main="Pre- and postoperative
Multiplate Values",cex.main=1.65, ylim=c(-20,180),cex.axis=1.5,cex.lab=1.45,
ylab="Area Under Curve (AUC)", boxwex=1,
col=c(24,0,0,24,0,0,24,0,0,24,0,0,24,0), lty=1)
> text(x=1.5,y=173, "ADP", pos=3, cex=1.2)
> text(x=4.5,y=173, "COL", pos=3, cex=1.2)
> text(x=7.5,y=173, "TRAP", pos=3, cex=1.2)
> text(x=10.5,y=173, "ASPI", pos=3, cex=1.2)
>
> legend(0.7,0, c("Preoperative","Postoperative"), cex= 1,fill=c(24,0))
```

```
> legend(5.7,0,lty=3,lwd=2,c("Reference range"))
> arrows(0.4,57,,113,code=0,lwd=2,lty=3)
> arrows(3.4,72,,125,code=0,lwd=2,lty=3)
> arrows(6.4,84,,128,code=0,lwd=2,lty=3)
> arrows(9.4,71,,115,code=0,lwd=2,lty=3)
>
> t.test(epi$Prov1multiplateADP,epi$Prov2multiplateADP,alternative =
c("two.sided"),paired = TRUE)

    Paired t-test

data:  epi$Prov1multiplateADP and epi$Prov2multiplateADP
t = -1.5086, df = 32, p-value = 0.1412
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -23.146033   3.449064
sample estimates:
mean of the differences
              -9.848485

> wilcox.test(epi$Prov1multiplateADP,epi$Prov2multiplateADP,alternative =
c("two.sided"),paired = TRUE)

    Wilcoxon signed rank test with continuity correction

data:  epi$Prov1multiplateADP and epi$Prov2multiplateADP
V = 200, p-value = 0.235
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1multiplateADP, epi$Prov2multiplateADP,  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1multiplateADP, epi$Prov2multiplateADP,  :
  cannot compute exact p-value with zeroes
>
> t.test(epi$Prov1multiplateCOL,epi$Prov2multiplateCOL,alternative =
c("two.sided"),paired = TRUE)

    Paired t-test

data:  epi$Prov1multiplateCOL and epi$Prov2multiplateCOL
t = -5.1807, df = 32, p-value = 1.175e-05
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -45.97478 -20.02522
sample estimates:
mean of the differences
                    -33

> wilcox.test(epi$Prov1multiplateCOL,epi$Prov2multiplateCOL,alternative =
c("two.sided"),paired = TRUE)

    Wilcoxon signed rank test with continuity correction

data:  epi$Prov1multiplateCOL and epi$Prov2multiplateCOL
V = 37.5, p-value = 2.372e-05
```

```
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1multiplateCOL, epi$Prov2multiplateCOL,  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1multiplateCOL, epi$Prov2multiplateCOL,  :
  cannot compute exact p-value with zeroes
> 
> x<-4
> y<-170
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-6,"**",pos=3, cex=1.4)
> 
> t.test(epi$Prov1multiplateTRAP,epi$Prov2multiplateTRAP,alternative = 
c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$Prov1multiplateTRAP and epi$Prov2multiplateTRAP
t = -1.0839, df = 32, p-value = 0.2865
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -24.430100   7.460403
sample estimates:
mean of the differences 
              -8.484848 

> wilcox.test(epi$Prov1multiplateTRAP,epi$Prov2multiplateTRAP,alternative = 
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1multiplateTRAP and epi$Prov2multiplateTRAP
V = 231.5, p-value = 0.3861
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$Prov1multiplateTRAP, epi$Prov2multiplateTRAP,  :
  cannot compute exact p-value with ties
> 
> t.test(epi$Prov1multiplateASPI,epi$Prov2multiplateASPI,alternative = 
c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$Prov1multiplateASPI and epi$Prov2multiplateASPI
t = -3.1759, df = 32, p-value = 0.003298
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -37.801125  -8.259481
sample estimates:
mean of the differences 
               -23.0303 

> wilcox.test(epi$Prov1multiplateASPI,epi$Prov2multiplateASPI,alternative = 
```

```
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1multiplateASPI and epi$Prov2multiplateASPI
V = 124.5, p-value = 0.005454
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$Prov1multiplateASPI, epi$Prov2multiplateASPI,  :
  cannot compute exact p-value with ties
> x<-10
> y<-170
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-6,"**",pos=3, cex=1.4)
> 
> mean(epi$Prov1multiplateADP, na.rm=TRUE)
[1] 68.10526
> sd(epi$Prov1multiplateADP, na.rm=TRUE)
[1] 21.04023
> mean(epi$Prov2multiplateADP, na.rm=TRUE)
[1] 77.39394
> sd(epi$Prov2multiplateADP, na.rm=TRUE)
[1] 27.00456
> 
> mean(epi$Prov1multiplateCOL, na.rm=TRUE)
[1] 62.26316
> sd(epi$Prov1multiplateCOL, na.rm=TRUE)
[1] 21.94918
> mean(epi$Prov2multiplateCOL, na.rm=TRUE)
[1] 94.30303
> sd(epi$Prov2multiplateCOL, na.rm=TRUE)
[1] 30.3526
> 
> mean(epi$Prov1multiplateTRAP, na.rm=TRUE)
[1] 102.8684
> sd(epi$Prov1multiplateTRAP, na.rm=TRUE)
[1] 31.77979
> mean(epi$Prov2multiplateTRAP, na.rm=TRUE)
[1] 108.9697
> sd(epi$Prov2multiplateTRAP, na.rm=TRUE)
[1] 32.84194
> 
> mean(epi$Prov1multiplateASPI, na.rm=TRUE)
[1] 72.10526
> sd(epi$Prov1multiplateASPI, na.rm=TRUE)
[1] 23.98174
> mean(epi$Prov2multiplateASPI, na.rm=TRUE)
[1] 94.09091
> sd(epi$Prov2multiplateASPI, na.rm=TRUE)
[1] 38.98186
> 
> hist(epi$Prov1multiplateADP)
> hist(epi$Prov1multiplateCOL)
> hist(epi$Prov1multiplateTRAP)
```

```
> hist(epi$Prov1multiplateASPI)
> 
> t.test(epi$Prov1multiplateTRAP,epi$Prov2multiplateTRAP,alternative = 
c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$Prov1multiplateTRAP and epi$Prov2multiplateTRAP
t = -1.0839, df = 32, p-value = 0.2865
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -24.430100   7.460403
sample estimates:
mean of the differences 
              -8.484848 

> wilcox.test(epi$Prov1multiplateTRAP,epi$Prov2multiplateTRAP,alternative = 
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1multiplateTRAP and epi$Prov2multiplateTRAP
V = 231.5, p-value = 0.3861
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$Prov1multiplateTRAP, epi$Prov2multiplateTRAP,  :
  cannot compute exact p-value with ties
> 
> t.test(epi$Prov1multiplateASPI,epi$Prov2multiplateASPI,alternative = 
c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$Prov1multiplateASPI and epi$Prov2multiplateASPI
t = -3.1759, df = 32, p-value = 0.003298
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -37.801125  -8.259481
sample estimates:
mean of the differences 
               -23.0303 

> wilcox.test(epi$Prov1multiplateASPI,epi$Prov2multiplateASPI,alternative = 
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1multiplateASPI and epi$Prov2multiplateASPI
V = 124.5, p-value = 0.005454
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$Prov1multiplateASPI, epi$Prov2multiplateASPI,  :
  cannot compute exact p-value with ties
> x<-10
```

```
> y<-170
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-6,"**",pos=3, cex=1.4)
>
> mean(epi$Prov1multiplateADP, na.rm=TRUE)
[1] 68.10526
> sd(epi$Prov1multiplateADP, na.rm=TRUE)
[1] 21.04023
> mean(epi$Prov2multiplateADP, na.rm=TRUE)
[1] 77.39394
> sd(epi$Prov2multiplateADP, na.rm=TRUE)
[1] 27.00456
>
> mean(epi$Prov1multiplateCOL, na.rm=TRUE)
[1] 62.26316
> sd(epi$Prov1multiplateCOL, na.rm=TRUE)
[1] 21.94918
> mean(epi$Prov2multiplateCOL, na.rm=TRUE)
[1] 94.30303
> sd(epi$Prov2multiplateCOL, na.rm=TRUE)
[1] 30.3526
>
> mean(epi$Prov1multiplateTRAP, na.rm=TRUE)
[1] 102.8684
> sd(epi$Prov1multiplateTRAP, na.rm=TRUE)
[1] 31.77979
> mean(epi$Prov2multiplateTRAP, na.rm=TRUE)
[1] 108.9697
> sd(epi$Prov2multiplateTRAP, na.rm=TRUE)
[1] 32.84194
>
> mean(epi$Prov1multiplateASPI, na.rm=TRUE)
[1] 72.10526
> sd(epi$Prov1multiplateASPI, na.rm=TRUE)
[1] 23.98174
> mean(epi$Prov2multiplateASPI, na.rm=TRUE)
[1] 94.09091
> sd(epi$Prov2multiplateASPI, na.rm=TRUE)
[1] 38.98186
>
> hist(epi$Prov1multiplateADP)
> hist(epi$Prov1multiplateCOL)
> hist(epi$Prov1multiplateTRAP)
> hist(epi$Prov1multiplateASPI)
>
>
>
>
> #rutinPK
> dev.new(width=3)
> boxplot(epi$Prov1rutinPK,epi$Prov2rutinPK, horizontal=FALSE, na.rm=TRUE,
axes=TRUE, main="PT-INR",cex.main=1.65,
ylim=c(0.8,1.8),cex.axis=1.5,cex.lab=1.45, xlim=c(0,2.5),ylab="PT-INR",
boxwex=1, col=c(24,0), lty=1)
> #legend(0.1,1.8, c("Preoperative","Postoperative"), cex= 1,fill=c(24,0))
```

```
> arrows(0.25,0.9,,1.2,code=0,lwd=2,lty=3)
>
> t.test(epi$Prov1rutinPK,epi$Prov2rutinPK,alternative = c("two.sided"),paired
= TRUE)

	Paired t-test

data:  epi$Prov1rutinPK and epi$Prov2rutinPK
t = -5.6176, df = 30, p-value = 4.077e-06
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.20673186 -0.09649394
sample estimates:
mean of the differences
             -0.1516129

> wilcox.test(epi$Prov1rutinPK,epi$Prov2rutinPK,alternative =
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1rutinPK and epi$Prov2rutinPK
V = 0, p-value = 3.92e-05
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1rutinPK, epi$Prov2rutinPK, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1rutinPK, epi$Prov2rutinPK, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
> x<-1
> y<-0.83
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,0.8,"**",pos=3, cex=1.4)
>
>
>
> #rutinAPTT
> dev.new(width=3)
> boxplot(epi$Prov1rutinAPTT,epi$Prov2rutinAPTT, horizontal=FALSE, na.rm=TRUE,
axes=TRUE, main="aPTT",cex.main=1.65, ylim=c(19,max(epi$Prov1rutinAPTT,epi
$Prov2rutinAPTT,na.rm=TRUE)),cex.axis=1.5,cex.lab=1.45,
xlim=c(0,2.5),ylab="aPTT (s)", boxwex=1, col=c(24,0), lty=1)
> arrows(0.25,26,,33,code=0,lwd=2,lty=3)
>
> t.test(epi$Prov1rutinAPTT,epi$Prov2rutinAPTT,alternative =
c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$Prov1rutinAPTT and epi$Prov2rutinAPTT
t = -2.8253, df = 29, p-value = 0.008461
alternative hypothesis: true difference in means is not equal to 0
```

```
95 percent confidence interval:
 -4.3671924 -0.6994742
sample estimates:
mean of the differences
              -2.533333

> wilcox.test(epi$Prov1rutinAPTT,epi$Prov2rutinAPTT,alternative =
c("two.sided"),paired = TRUE)

    Wilcoxon signed rank test with continuity correction

data:  epi$Prov1rutinAPTT and epi$Prov2rutinAPTT
V = 89.5, p-value = 0.005653
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1rutinAPTT, epi$Prov2rutinAPTT, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1rutinAPTT, epi$Prov2rutinAPTT, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
> x<-1
> y<-20.5
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-0.7,"**",pos=3, cex=1.4)
>
> #rutinCRP
> dev.new(width=3)
> boxplot(epi$Prov1rutinCRP,epi$Prov2rutinCRP, horizontal=FALSE, na.rm=TRUE,
axes=TRUE, main="CRP",cex.main=1.65,cex.axis=1.5,cex.lab=1.45,
xlim=c(0,2.5),ylab="CRP (mg/L)", boxwex=1, col=c(24,0), lty=1)
> arrows(0.25,0,,3,code=0,lwd=2,lty=3)
> t.test(epi$Prov1rutinCRP,epi$Prov2rutinCRP,alternative =
c("two.sided"),paired = TRUE)

    Paired t-test

data:  epi$Prov1rutinCRP and epi$Prov2rutinCRP
t = -7.5742, df = 29, p-value = 2.38e-08
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -107.688  -61.896
sample estimates:
mean of the differences
                -84.792

> wilcox.test(epi$Prov1rutinCRP,epi$Prov2rutinCRP,alternative =
c("two.sided"),paired = TRUE)

    Wilcoxon signed rank test

data:  epi$Prov1rutinCRP and epi$Prov2rutinCRP
V = 0, p-value = 1.863e-09
alternative hypothesis: true location shift is not equal to 0
```

```
> x<-1
> y<-250
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-1,"**",pos=3, cex=1.4)
>
>
>
> #rutinTPK
> dev.new(width=3)
> boxplot(epi$Prov1rutinTPK,epi$Prov2rutinTPK, horizontal=FALSE, na.rm=TRUE,
axes=TRUE, main="Plc",cex.main=1.65, ylim=c(-50,max(epi$Prov1rutinTPK,epi
$Prov2rutinTPK,na.rm=TRUE)),cex.axis=1.5,cex.lab=1.45, xlim=c(0,2.5),ylab="Plc
(millions/mL)", boxwex=1, col=c(24,0), lty=1)
> arrows(0.25,145,,387,code=0,lwd=2,lty=3)
>
> t.test(epi$Prov1rutinTPK,epi$Prov2rutinTPK,alternative =
c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$Prov1rutinTPK and epi$Prov2rutinTPK
t = -3.0816, df = 30, p-value = 0.004385
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -122.2372  -24.7951
sample estimates:
mean of the differences
              -73.51613

> wilcox.test(epi$Prov1rutinTPK,epi$Prov2rutinTPK,alternative =
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1rutinTPK and epi$Prov2rutinTPK
V = 80.5, p-value = 0.001065
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$Prov1rutinTPK, epi$Prov2rutinTPK, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
> x<-1
> y<--40
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-30,"**",pos=3, cex=1.4)
>
> #Boxplot PIVKA
> hist(epi$PIVKAMpreop)
> hist(epi$PIVKAMpostop)
> dev.new(width=3)
> boxplot(epi$PIVKAMpreop,epi$PIVKAMpostop, horizontal=FALSE, na.rm=TRUE,
axes=TRUE, main="PIVKA",cex.main=1.65, ylim=c(0,89),cex.axis=1.5,cex.lab=1.45,
```

```
xlim=c(0,2.5),ylab="PIVKA (mg/L)", boxwex=1, col=c(24,0), lty=1)
> arrows(0.25,0,,0.2,code=0,lwd=2,lty=3)
>
> t.test(epi$PIVKAMpreop,epi$PIVKAMpostop,alternative = c("two.sided"),paired =
TRUE)

	Paired t-test

data:  epi$PIVKAMpreop and epi$PIVKAMpostop
t = -1.8204, df = 30, p-value = 0.07868
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -49.134869   2.821966
sample estimates:
mean of the differences
              -23.15645

> wilcox.test(epi$PIVKAMpreop,epi$PIVKAMpostop,alternative =
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test

data:  epi$PIVKAMpreop and epi$PIVKAMpostop
V = 25, p-value = 8.419e-07
alternative hypothesis: true location shift is not equal to 0

> x<-1
> y<-70
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-3,"**",pos=3, cex=1.4)
> legend(0.1,90, c("Preoperative","Postoperative"), cex= 1,fill=c(24,0))
>
> #Boxplot DDimer
> mean(epi$DDpreop, na.rm=TRUE)
[1] 0.2471081
> sd(epi$DDpreop, na.rm=TRUE)
[1] 0.224601
> mean(epi$DDpostop, na.rm=TRUE)
[1] 1.733645
> sd(epi$DDpostop, na.rm=TRUE)
[1] 1.04771
>
> hist(epi$DDpreop)
> hist(epi$DDpostop)
> dev.new(width=3)
> boxplot(epi$DDpreop,epi$DDpostop, horizontal=FALSE, na.rm=TRUE, axes=TRUE,
main="D-dimer",cex.main=1.65, ylim=c(0,6),cex.axis=1.5,cex.lab=1.45,
xlim=c(0,2.5),ylab="D-Dimer (mg/L)", boxwex=1, col=c(24,0), lty=1,plot=TRUE)
> arrows(0.25,0,,0.25,code=0,lwd=2,lty=3)
>
> t.test(epi$DDpreop,epi$DDpostop,alternative = c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$DDpreop and epi$DDpostop
```

```
t = -8.1538, df = 30, p-value = 4.213e-09
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.841091 -1.103554
sample estimates:
mean of the differences
              -1.472323

> wilcox.test(epi$DDpreop,epi$DDpostop,alternative = c("two.sided"),paired =
TRUE)

	Wilcoxon signed rank test

data:  epi$DDpreop and epi$DDpostop
V = 0, p-value = 9.313e-10
alternative hypothesis: true location shift is not equal to 0

> x<-1
> y<-5
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-0.2,"**",pos=3, cex=1.4)
> #legend(0.1,90, c("Preoperative","Postoperative"), cex= 1,fill=c(24,0))
>
>
>
>
> ###Before and after diagrams
> #Before and after diagrams for EXTEM-MCF
> preop<-epi$Prov1extemMCF
> postop<-epi$Prov2extemMCF
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
         [,1]      [,2]      [,3]      [,4] [,5]     [,6]      [,7]      [,8]
[1,] 11.13194  6.118056  8.145833  3.107639  3.1 10.07292  7.104167  6.100694
[2,] 56.00000 63.000000 73.000000 75.000000 66.0 67.00000 42.000000 63.000000
[3,] 71.00000 76.000000 74.000000 75.000000 77.0 73.00000 73.000000 73.000000
          [,9]     [,10]     [,11]    [,12]     [,13]     [,14] [,15]
[1,]  2.201389  5.145833  5.069444 14.09722  5.131944  6.180556    NA
[2,] 75.000000 61.000000 63.000000 57.00000 65.000000 69.000000    55
[3,] 75.000000 68.000000 77.000000 74.00000 66.000000 70.000000    NA
         [,16]     [,17]    [,18]     [,19] [,20]     [,21]     [,22]
[1,]  2.121528  5.194444 15.15278  5.909722    NA  5.111111  4.958333
[2,] 47.000000 59.000000 61.00000 54.000000    64 60.000000 64.000000
[3,] 63.000000 69.000000 80.00000 68.000000    NA 71.000000 64.000000
         [,23]     [,24]     [,25] [,26]     [,27]     [,28] [,29] [,30]
[1,]  5.145833  2.097222  2.180556    NA  5.059028  3.138889    NA    NA
[2,] 69.000000 58.000000 66.000000    74 79.000000 58.000000    67    74
[3,] 72.000000 65.000000 63.000000    NA 60.000000 54.000000    NA    NA
        [,31]     [,32]     [,33]     [,34]     [,35]     [,36]     [,37]
[1,] 11.17361  6.222222  6.180556  7.104167  6.291667  5.027778  7.076389
```

```
[2,] 59.00000 67.000000 61.000000 62.000000 71.000000 63.000000 72.000000
[3,] 80.00000 76.000000 77.000000 75.000000 77.000000 73.000000 79.000000
         [,38]
[1,]  6.097222
[2,] 75.000000
[3,] 77.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative ROTEM-EXTEM-MCF",ylab="Maximum clot
firmness (mm)",  cex.main=1.3, cex.lab=1.4,lwd=1)
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> lines(c(-.4,-.4), c(50,72), type="l", lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1extemMCF, na.rm=TRUE)
> postopmean<-mean(epi$Prov2extemMCF, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(8,78,"P<0.01", cex=2)
>
>
>
> #Before and after diagrams for EXTEM-CT
> preop<-epi$Prov1extemCT
> postop<-epi$Prov2extemCT
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
         [,1]      [,2]      [,3]      [,4] [,5]     [,6]       [,7]      [,8]
[1,] 11.13194  6.118056  8.145833  3.107639  3.1 10.07292   7.104167  6.100694
[2,] 46.00000 46.000000 44.000000 51.000000 47.0 41.00000 108.000000 25.000000
[3,] 23.00000 43.000000 40.000000 43.000000 37.0 40.00000  51.000000 42.000000
          [,9]     [,10]     [,11]    [,12]     [,13]     [,14] [,15]
[1,]  2.201389  5.145833  5.069444 14.09722  5.131944  6.180556    NA
[2,] 36.000000 33.000000 49.000000 32.00000 42.000000 44.000000    36
[3,] 38.000000 43.000000 31.000000 44.00000 42.000000 42.000000    NA
         [,16]     [,17]    [,18]     [,19] [,20]     [,21]     [,22]
[1,]  2.121528  5.194444 15.15278  5.909722    NA  5.111111  4.958333
[2,] 45.000000 38.000000 41.00000 44.000000    44 42.000000 38.000000
[3,] 57.000000 42.000000 47.00000 41.000000    NA 41.000000 48.000000
         [,23]     [,24]     [,25] [,26]     [,27]     [,28] [,29] [,30]
[1,]  5.145833  2.097222  2.180556    NA  5.059028  3.138889    NA    NA
```

```
[2,] 52.000000 52.000000 43.000000    70 57.000000 54.000000    68    63
[3,] 59.000000 44.000000 51.000000    NA 61.000000 63.000000    NA    NA
        [,31]     [,32]     [,33]     [,34]     [,35]     [,36]     [,37]
[1,] 11.17361  6.222222  6.180556  7.104167  6.291667  5.027778  7.076389
[2,] 40.00000 39.000000 47.000000 42.000000 41.000000 47.000000 56.000000
[3,] 46.00000 53.000000 44.000000 48.000000 80.000000 55.000000 72.000000
         [,38]
[1,]  6.097222
[2,] 63.000000
[3,] 77.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative ROTEM-EXTEM-CT",ylab="Clotting time
(s)",  cex.main=1.3, cex.lab=1.4,lwd=1)
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> lines(c(-.4,-.4), c(38,79), type="l", lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1extemCT, na.rm=TRUE)
> postopmean<-mean(epi$Prov2extemCT, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(8,60,"N/S", cex=2)
>
>
> #Before and after diagrams for INTEM-MCF
> preop<-epi$Prov1intemMCF
> postop<-epi$Prov2intemMCF
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
         [,1]      [,2]      [,3]      [,4] [,5]     [,6]      [,7]      [,8]
[1,] 11.13194  6.118056  8.145833  3.107639  3.1 10.07292  7.104167  6.100694
[2,] 60.00000 61.000000 75.000000 77.000000 62.0 65.00000 56.000000 61.000000
[3,] 74.00000 75.000000 79.000000 74.000000 69.0 77.00000 73.000000 73.000000
          [,9]     [,10]     [,11]    [,12]     [,13]     [,14] [,15]
[1,]  2.201389  5.145833  5.069444 14.09722  5.131944  6.180556    NA
[2,] 74.000000 61.000000 63.000000 59.00000 64.000000 71.000000    56
[3,] 73.000000 69.000000 73.000000 76.00000 64.000000 68.000000    NA
         [,16]     [,17]    [,18]     [,19] [,20]     [,21]     [,22]
[1,]  2.121528  5.194444 15.15278  5.909722    NA  5.111111  4.958333
[2,] 60.000000 57.000000 61.00000 54.000000    65 60.000000 63.000000
```

```
[3,] 61.000000 68.000000 77.00000 69.000000        NA 71.000000 71.000000
         [,23]     [,24]     [,25] [,26]     [,27]     [,28] [,29] [,30]
[1,]  5.145833  2.097222  2.180556    NA  5.059028  3.138889    NA    NA
[2,] 68.000000 59.000000 62.000000    70 58.000000 57.000000    64    69
[3,] 71.000000 64.000000 62.000000    NA 56.000000 48.000000    NA    NA
        [,31]     [,32]     [,33]     [,34]     [,35]     [,36]     [,37]
[1,] 11.17361  6.222222  6.180556  7.104167  6.291667  5.027778  7.076389
[2,] 58.00000 66.000000 62.000000 56.000000 70.000000 59.000000 71.000000
[3,] 76.00000 74.000000 73.000000 72.000000 77.000000 72.000000 77.000000
         [,38]
[1,]  6.097222
[2,] 71.000000
[3,] 39.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative ROTEM-INTEM-MCF",ylab="Maximum clot
firmness (mm)",  cex.main=1.3, cex.lab=1.4,lwd=1)
>
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> lines(c(-.4,-.4), c(50,72), type="l", lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1intemMCF, na.rm=TRUE)
> postopmean<-mean(epi$Prov2intemMCF, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(8,65,"P<0.01", cex=2)
>
>
>
> #Before and after diagrams for INTEM-CT
> preop<-epi$Prov1intemCT
> postop<-epi$Prov2intemCT
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
          [,1]       [,2]       [,3]       [,4]  [,5]      [,6]       [,7]
[1,]  11.13194   6.118056   8.145833   3.107639   3.1  10.07292   7.104167
[2,] 161.00000 290.000000 171.000000 145.000000 357.0 211.00000 188.000000
[3,] 178.00000 159.000000 153.000000 142.000000 173.0 147.00000 110.000000
            [,8]       [,9]      [,10]      [,11]     [,12]      [,13]
[1,]   6.100694   2.201389   5.145833   5.069444  14.09722   5.131944
```

```
[2,] 175.000000 157.000000 177.000000 161.000000 137.00000 152.000000
[3,] 134.000000 152.000000 131.000000 164.000000 205.00000 171.000000
          [,14] [,15]      [,16]      [,17]     [,18]      [,19] [,20]
[1,]   6.180556    NA   2.121528   5.194444  15.15278   5.909722    NA
[2,] 195.000000   144 227.000000 202.000000 193.00000 229.000000   141
[3,] 227.000000    NA 156.000000 161.000000 212.00000 182.000000    NA
          [,21]      [,22]      [,23]      [,24]      [,25] [,26]      [,27]
[1,]   5.111111   4.958333   5.145833   2.097222   2.180556    NA   5.059028
[2,] 134.000000 147.000000 121.000000 199.000000 198.000000   170 158.000000
[3,] 200.000000 122.000000 167.000000 132.000000 223.000000    NA 168.000000
          [,28] [,29] [,30]     [,31]      [,32]      [,33]      [,34]
[1,]   3.138889    NA    NA  11.17361   6.222222   6.180556   7.104167
[2,] 159.000000   125   150 184.00000 181.000000 177.000000 133.000000
[3,] 147.000000    NA    NA 147.00000 150.000000 337.000000 148.000000
          [,35]      [,36]      [,37]      [,38]
[1,]   6.291667   5.027778   7.076389   6.097222
[2,] 204.000000 185.000000 148.000000 100.000000
[3,] 165.000000 133.000000 156.000000  94.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative ROTEM-INTEM-CT",ylab="Clotting time
(s)",  cex.main=1.3, cex.lab=1.4,lwd=1)
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
> 
> #normal range - enter manually!
> lines(c(-.4,-.4), c(100,240), type="l", lwd=6, lty=3)
> 
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1intemCT, na.rm=TRUE)
> postopmean<-mean(epi$Prov2intemCT, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
> 
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(8,220,"N/S", cex=2)
> 
> 
> 
> #Before and after diagrams for HEPTEM-MCF
> preop<-epi$Prov1heptemMCF
> postop<-epi$Prov2heptemMCF
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
         [,1]      [,2]      [,3]      [,4] [,5]     [,6]      [,7]      [,8]
[1,] 11.13194  6.118056  8.145833  3.107639  3.1 10.07292  7.104167  6.100694
```

```
[2,] 60.00000 59.000000 72.000000 75.000000 64.0 63.00000 56.000000 62.000000
[3,] 71.00000 69.000000 75.000000 75.000000 70.0 75.00000 70.000000 70.000000
          [,9]     [,10]     [,11]    [,12]     [,13]     [,14] [,15]
[1,]  2.201389  5.145833  5.069444 14.09722  5.131944  6.180556    NA
[2,] 73.000000 57.000000 59.000000 61.00000 63.000000 68.000000    53
[3,] 75.000000        NA 73.000000 74.00000 63.000000 67.000000    NA
         [,16]     [,17]    [,18]     [,19] [,20]     [,21]     [,22]
[1,]  2.121528  5.194444 15.15278  5.909722    NA  5.111111  4.958333
[2,] 61.000000 54.000000 59.00000 55.000000    61 60.000000 63.000000
[3,] 57.000000 66.000000 76.00000 67.000000    NA 71.000000 70.000000
         [,23]     [,24]     [,25] [,26]     [,27]     [,28] [,29] [,30]
[1,]  5.145833  2.097222  2.180556    NA  5.059028  3.138889    NA    NA
[2,] 68.000000 58.000000 62.000000    70 59.000000 55.000000    60    68
[3,] 71.000000 63.000000 62.000000    NA 58.000000 48.000000    NA    NA
        [,31]     [,32]     [,33]     [,34]     [,35]     [,36]     [,37]
[1,] 11.17361  6.222222  6.180556  7.104167  6.291667  5.027778  7.076389
[2,] 58.00000 65.000000 63.000000 52.000000 69.000000 58.000000 69.000000
[3,] 71.00000 72.000000 74.000000 70.000000 76.000000 71.000000 77.000000
         [,38]
[1,]  6.097222
[2,] 71.000000
[3,] 74.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative ROTEM-HEPTEM-MCF",ylab="Maximum clot
firmness (mm)",  cex.main=1.3, cex.lab=1.4,lwd=1)
> 
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
> 
> #normal range - enter manually!
> lines(c(-.4,-.4), c(50,72), type="l", lwd=6, lty=3)
> 
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1heptemMCF, na.rm=TRUE)
> postopmean<-mean(epi$Prov2heptemMCF, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
> 
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(8,64,"P<0.01", cex=2)
> 
> 
> 
> #Before and after diagrams for HEPTEM-CT
> preop<-epi$Prov1heptemCT
> postop<-epi$Prov2heptemCT
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
```

```
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
          [,1]       [,2]       [,3]       [,4]  [,5]      [,6]       [,7]
[1,]  11.13194   6.118056   8.145833   3.107639   3.1  10.07292   7.104167
[2,] 188.00000 357.000000 223.000000 225.000000 139.0 252.00000 197.000000
[3,] 184.00000 166.000000 162.000000 151.000000 211.0 169.00000 127.000000
           [,8]       [,9]      [,10]      [,11]     [,12]      [,13]
[1,]   6.100694   2.201389   5.145833   5.069444  14.09722   5.131944
[2,] 199.000000 174.000000 178.000000 220.000000 169.00000 185.000000
[3,] 145.000000 133.000000  61.000000 207.000000 241.00000 205.000000
          [,14] [,15]      [,16]      [,17]     [,18]      [,19] [,20]
[1,]   6.180556    NA   2.121528   5.194444  15.15278   5.909722    NA
[2,] 125.000000   177 132.000000 287.000000 298.00000 135.000000   190
[3,] 261.000000    NA 184.000000 223.000000 212.00000 228.000000    NA
          [,21]      [,22]      [,23]      [,24]      [,25] [,26]      [,27]
[1,]   5.111111   4.958333   5.145833   2.097222   2.180556    NA   5.059028
[2,] 183.000000 153.000000 182.000000 150.000000 219.000000   155 157.000000
[3,] 229.000000 130.000000 216.000000 163.000000 250.000000    NA 159.000000
          [,28] [,29] [,30]     [,31]      [,32]      [,33]      [,34]
[1,]   3.138889    NA    NA  11.17361   6.222222   6.180556   7.104167
[2,] 199.000000   143   180 183.00000 162.000000 100.000000 182.000000
[3,] 160.000000    NA    NA 147.00000 199.000000 278.000000 158.000000
          [,35]      [,36]      [,37]      [,38]
[1,]   6.291667   5.027778   7.076389   6.097222
[2,] 219.000000 205.000000 159.000000 154.000000
[3,] 165.000000 146.000000 154.000000 173.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative ROTEM-HEPTEM-CT",ylab="Clotting time
(s)",  cex.main=1.3, cex.lab=1.4,lwd=1)
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> lines(c(-.4,-.4), c(100,240), type="l", lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1heptemCT, na.rm=TRUE)
> postopmean<-mean(epi$Prov2heptemCT, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(7,220,"N/S", cex=2)
>
>
> #Before and after diagrams for FIBTEM-MCF
> preop<-epi$Prov1fibtemMCF
> postop<-epi$Prov2fibtemMCF
> preopdata<-t(matrix(preop))
```

```
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
         [,1]      [,2]      [,3]      [,4] [,5]     [,6]      [,7]      [,8]
[1,] 11.13194  6.118056  8.145833  3.107639  3.1 10.07292  7.104167  6.100694
[2,] 11.00000 20.000000 35.000000 26.000000 22.0 19.00000 12.000000 15.000000
[3,] 43.00000 37.000000 40.000000 39.000000 37.0 40.00000 52.000000 34.000000
          [,9]     [,10]     [,11]    [,12]     [,13]     [,14] [,15]
[1,]  2.201389  5.145833  5.069444 14.09722  5.131944  6.180556    NA
[2,] 34.000000 25.000000 21.000000 13.00000 22.000000 26.000000    17
[3,] 35.000000 31.000000 41.000000 40.00000 31.000000 24.000000    NA
         [,16]     [,17]    [,18]     [,19] [,20]     [,21]     [,22]
[1,]  2.121528  5.194444 15.15278  5.909722    NA  5.111111  4.958333
[2,] 13.000000 13.000000 17.00000 11.000000    19 19.000000 13.000000
[3,] 15.000000 25.000000 48.00000 31.000000    NA 29.000000 26.000000
         [,23]     [,24]     [,25] [,26]     [,27]     [,28] [,29] [,30]
[1,]  5.145833  2.097222  2.180556    NA  5.059028  3.138889    NA    NA
[2,] 28.000000 11.000000 16.000000    29 30.000000 13.000000    17    26
[3,] 31.000000 22.000000 24.000000    NA 16.000000 20.000000    NA    NA
        [,31]     [,32]     [,33]     [,34]     [,35]     [,36]     [,37]
[1,] 11.17361  6.222222  6.180556  7.104167  6.291667  5.027778  7.076389
[2,] 16.00000        NA 18.000000 13.000000 32.000000 20.000000 17.000000
[3,] 49.00000 39.000000 42.000000 27.000000 38.000000 31.000000 34.000000
         [,38]
[1,]  6.097222
[2,] 34.000000
[3,] 42.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative ROTEM-INTEM-MCF",ylab="Maximum clot
firmness (mm)",  cex.main=1.3, cex.lab=1.4,lwd=1)
>
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> lines(c(-.4,-.4), c(9,25), type="l", lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1fibtemMCF, na.rm=TRUE)
> postopmean<-mean(epi$Prov2fibtemMCF, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(8,64,"P<0.01", cex=2)
>
>
```

```
> #Before and after diagrams for HEPTEM-INTEM-MCF
> preop<-epi$preopHEPTEMminusINTEMmcf
> postop<-epi$postopHEPTEMminusINTEMmcf
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
         [,1]      [,2]      [,3]      [,4] [,5]     [,6]      [,7]      [,8]
[1,] 11.13194  6.118056  8.145833  3.107639  3.1 10.07292  7.104167  6.100694
[2,]  0.00000 -2.000000 -3.000000 -2.000000  2.0 -2.00000  0.000000  1.000000
[3,] -3.00000 -6.000000 -4.000000  1.000000  1.0 -2.00000 -3.000000 -3.000000
          [,9]     [,10]     [,11]    [,12]     [,13]     [,14] [,15]
[1,]  2.201389  5.145833  5.069444 14.09722  5.131944  6.180556    NA
[2,] -1.000000 -4.000000 -4.000000  2.00000 -1.000000 -3.000000    -3
[3,]  2.000000        NA  0.000000 -2.00000 -1.000000 -1.000000    NA
         [,16]     [,17]    [,18]     [,19] [,20]    [,21]     [,22]    [,23]
[1,]  2.121528  5.194444 15.15278  5.909722    NA 5.111111  4.958333 5.145833
[2,]  1.000000 -3.000000 -2.00000  1.000000    -4 0.000000  0.000000 0.000000
[3,] -4.000000 -2.000000 -1.00000 -2.000000    NA 0.000000 -1.000000 0.000000
         [,24]    [,25] [,26]    [,27]     [,28] [,29] [,30]    [,31]
[1,]  2.097222 2.180556    NA 5.059028  3.138889    NA    NA 11.17361
[2,] -1.000000 0.000000     0 1.000000 -2.000000    -4    -1  0.00000
[3,] -1.000000 0.000000    NA 2.000000  0.000000    NA    NA -5.00000
         [,32]    [,33]     [,34]     [,35]     [,36]     [,37]     [,38]
[1,]  6.222222 6.180556  7.104167  6.291667  5.027778  7.076389  6.097222
[2,] -1.000000 1.000000 -4.000000 -1.000000 -1.000000 -2.000000  0.000000
[3,] -2.000000 1.000000 -2.000000 -1.000000 -1.000000  0.000000 35.000000
> ylimits<-c(1.1*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative ROTEM-HEPTEM-INTEM-MCF",ylab="Maximum
clot firmness (mm)",  cex.main=1.3, cex.lab=1.4,lwd=1)
>
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> #there are no normal ranges for HEPTEM-INTEM. lines(c(-.4,-.4), c(50,72),
type="l", lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$preopHEPTEMminusINTEMmcf, na.rm=TRUE)
> postopmean<-mean(epi$postopHEPTEMminusINTEMmcf, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(8,3,"N/S", cex=2)
>
```

```
>
>
> #Before and after diagrams for INTEM-HEPTEM-CT
> preop<-epi$preopINTEMminusHEPTEMct
> postop<-epi$postopINTEMminusHEPTEMct
> preopdata<-t(matrix(preop))
Error in matrix(preop) : 'data' must be of a vector type, was 'NULL'
> postopdata<-t(matrix(postop))
Error in matrix(postop) : 'data' must be of a vector type, was 'NULL'
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> ylimits<-c(1.1*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
Warning messages:
1: In min(preop, postop, na.rm = TRUE) :
  no non-missing arguments to min; returning Inf
2: In max(preop, postop, na.rm = TRUE) :
  no non-missing arguments to max; returning -Inf
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative ROTEM-INTEM-HEPTEM-CT",ylab="Clotting
time (s)",  cex.main=1.3, cex.lab=1.4,lwd=1)
Error in plot.window(...) : need finite 'ylim' values
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> ## there are no normal values here. lines(c(-.4,-.4), c(100,240), type="l",
lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$preopINTEMminusHEPTEMct, na.rm=TRUE)
Warning message:
In mean.default(epi$preopINTEMminusHEPTEMct, na.rm = TRUE) :
  argument is not numeric or logical: returning NA
> postopmean<-mean(epi$postopINTEMminusHEPTEMct, na.rm=TRUE)
Warning message:
In mean.default(epi$postopINTEMminusHEPTEMct, na.rm = TRUE) :
  argument is not numeric or logical: returning NA
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(7,13,"N/S", cex=2)
>
>
>
>
>
> ##Multiplate before and after diagrams
> #Before and after diagrams for multiplateADP
```

```
> preop<-epi$Prov1multiplateADP
> postop<-epi$Prov2multiplateADP
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
          [,1]      [,2]      [,3]      [,4] [,5]     [,6]       [,7]
[1,]  11.13194  6.118056  8.145833  3.107639  3.1 10.07292   7.104167
[2,]  63.00000 63.000000 63.000000 81.000000 89.0 67.00000  13.000000
[3,] 114.00000 84.000000 16.000000 94.000000 57.0 61.00000 134.000000
          [,8]      [,9]     [,10]     [,11]    [,12]     [,13]     [,14]
[1,]  6.100694  2.201389  5.145833  5.069444 14.09722  5.131944  6.180556
[2,] 79.000000 76.000000 48.000000 94.000000 26.00000 41.000000 82.000000
[3,] 94.000000 57.000000 65.000000 66.000000 85.00000 59.000000 82.000000
     [,15]     [,16]     [,17]     [,18]     [,19] [,20]     [,21]     [,22]
[1,]    NA  2.121528  5.194444  15.15278  5.909722    NA  5.111111  4.958333
[2,]    46 60.000000 54.000000  67.00000 72.000000    62 62.000000 86.000000
[3,]    NA 47.000000 64.000000 143.00000 98.000000    NA 95.000000 72.000000
         [,23]     [,24]     [,25] [,26]     [,27]     [,28] [,29] [,30]
[1,]  5.145833  2.097222  2.180556    NA  5.059028  3.138889    NA    NA
[2,] 69.000000 95.000000 89.000000    82 77.000000 60.000000    81    88
[3,] 72.000000 50.000000 54.000000    NA 59.000000 29.000000    NA    NA
         [,31]     [,32]      [,33]     [,34]     [,35]     [,36]     [,37]
[1,]  11.17361  6.222222   6.180556  7.104167  6.291667  5.027778  7.076389
[2,]  38.00000 86.000000  95.000000 51.000000 86.000000 29.000000 63.000000
[3,] 102.00000 87.000000 115.000000 86.000000 78.000000 69.000000 91.000000
          [,38]
[1,]   6.097222
[2,] 105.000000
[3,]  75.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative Multiplate ADP",ylab="Area under curve
(AUC)",  cex.main=1.3, cex.lab=1.4,lwd=1)
>
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> lines(c(-.4,-.4), c(57,113), type="l", lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1multiplateADP, na.rm=TRUE)
> postopmean<-mean(epi$Prov2multiplateADP, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
```

```
> text(8,72,"N/S", cex=2)
>
>
>
> #Before and after diagrams for multiplateCOL
> preop<-epi$Prov1multiplateCOL
> postop<-epi$Prov2multiplateCOL
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
          [,1]      [,2]      [,3]       [,4] [,5]      [,6]       [,7]
[1,]  11.13194  6.118056  8.145833   3.107639  3.1  10.07292   7.104167
[2,]  66.00000 64.000000 40.000000 100.000000 66.0  67.00000  11.000000
[3,] 131.00000 96.000000 81.000000 132.000000 76.0 153.00000 152.000000
           [,8]       [,9]     [,10]     [,11]     [,12]     [,13]     [,14]
[1,]   6.100694   2.201389  5.145833  5.069444  14.09722  5.131944  6.180556
[2,]  94.000000 100.000000 60.000000 70.000000  42.00000 45.000000 72.000000
[3,] 101.000000 113.000000 71.000000 70.000000 118.00000 64.000000 76.000000
     [,15]     [,16]     [,17]     [,18]     [,19] [,20]     [,21]     [,22]
[1,]    NA  2.121528  5.194444  15.15278  5.909722    NA  5.111111  4.958333
[2,]    40 61.000000 25.000000  41.00000 56.000000    64 54.000000 75.000000
[3,]    NA 53.000000 64.000000 159.00000 93.000000    NA 98.000000 73.000000
         [,23]     [,24]     [,25] [,26]     [,27]     [,28] [,29] [,30]
[1,]  5.145833  2.097222  2.180556    NA  5.059028  3.138889    NA    NA
[2,] 42.000000 76.000000 69.000000    86 57.000000 46.000000    67    86
[3,] 74.000000 75.000000 75.000000    NA 52.000000 35.000000    NA    NA
         [,31]      [,32]     [,33]      [,34]      [,35]     [,36]      [,37]
[1,]  11.17361   6.222222  6.180556   7.104167   6.291667  5.027778   7.076389
[2,]  46.00000  52.000000 88.000000  35.000000  98.000000 38.000000  65.000000
[3,] 106.00000 108.000000 98.000000 104.000000 129.000000 79.000000 115.000000
          [,38]
[1,]   6.097222
[2,] 102.000000
[3,]  88.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative Multiplate COL",ylab="Area under curve
(AUC)",  cex.main=1.3, cex.lab=1.4,lwd=1)
>
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> lines(c(-.4,-.4), c(72,125), type="l", lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1multiplateCOL, na.rm=TRUE)
```

```
> postopmean<-mean(epi$Prov2multiplateCOL, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(9,72,"P<0.01", cex=2)
>
>
> #Before and after diagrams for multiplateTRAP
> preop<-epi$Prov1multiplateTRAP
> postop<-epi$Prov2multiplateTRAP
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
          [,1]       [,2]       [,3]       [,4]  [,5]      [,6]       [,7]
[1,]  11.13194   6.118056   8.145833   3.107639   3.1  10.07292   7.104167
[2,] 112.00000 115.000000 102.000000 129.000000 119.0 101.00000  22.000000
[3,] 150.00000 138.000000 135.000000 152.000000  97.0 153.00000 150.000000
           [,8]       [,9]     [,10]      [,11]     [,12]     [,13]      [,14]
[1,]   6.100694   2.201389  5.145833   5.069444  14.09722  5.131944   6.180556
[2,] 128.000000 126.000000 96.000000 124.000000  79.00000 80.000000  83.000000
[3,] 120.000000 102.000000 79.000000  93.000000 104.00000 89.000000 143.000000
     [,15]     [,16]     [,17]     [,18]      [,19] [,20]      [,21]
[1,]    NA  2.121528  5.194444  15.15278   5.909722    NA   5.111111
[2,]    75 92.000000 38.000000  79.00000  99.000000   101 113.000000
[3,]    NA 24.000000 82.000000 154.00000 114.000000    NA 108.000000
          [,22]     [,23]      [,24]      [,25] [,26]     [,27]      [,28]
[1,]   4.958333  5.145833   2.097222   2.180556    NA  5.059028   3.138889
[2,] 132.000000 71.000000 130.000000 105.000000   163 91.000000 113.000000
[3,] 103.000000 76.000000  71.000000  73.000000    NA 78.000000  41.000000
     [,29] [,30]     [,31]      [,32]      [,33]      [,34]      [,35]
[1,]    NA    NA  11.17361   6.222222   6.180556   7.104167   6.291667
[2,]   117   137  85.00000 138.000000 129.000000  62.000000 126.000000
[3,]    NA    NA 109.00000 145.000000 119.000000 124.000000 139.000000
          [,36]      [,37]      [,38]
[1,]   5.027778   7.076389   6.097222
[2,]  31.000000 106.000000 160.000000
[3,] 121.000000  87.000000 123.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative Multiplate TRAP",ylab="Area under curve
(AUC)",  cex.main=1.3, cex.lab=1.4,lwd=1)
>
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
```

```
> lines(c(-.4,-.4), c(84,128), type="l", lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1multiplateTRAP, na.rm=TRUE)
> postopmean<-mean(epi$Prov2multiplateTRAP, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(9,110,"N/S", cex=2)
>
>
>
>
> #Before and after diagrams for multiplateASPI
> preop<-epi$Prov1multiplateASPI
> postop<-epi$Prov2multiplateASPI
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
          [,1]      [,2]       [,3]       [,4] [,5]      [,6]       [,7]
[1,]  11.13194  6.118056   8.145833   3.107639  3.1  10.07292   7.104167
[2,]  82.00000 81.000000  79.000000 103.000000 68.0  75.00000  48.000000
[3,] 130.00000 97.000000 123.000000 129.000000 85.0 144.00000 148.000000
          [,8]      [,9]     [,10]     [,11]     [,12]     [,13]      [,14]
[1,]  6.100694  2.201389  5.145833  5.069444  14.09722  5.131944   6.180556
[2,] 90.000000 58.000000 74.000000 83.000000  63.00000 68.000000  84.000000
[3,] 99.000000 55.000000 57.000000 87.000000 123.00000 81.000000 106.000000
     [,15]     [,16]     [,17]     [,18]     [,19] [,20]     [,21]      [,22]
[1,]    NA  2.121528  5.194444  15.15278  5.909722    NA  5.111111   4.958333
[2,]    52 66.000000 24.000000  35.00000 71.000000    76 70.000000  99.000000
[3,]    NA 21.000000  6.000000 163.00000 77.000000    NA 95.000000 107.000000
         [,23]     [,24]     [,25] [,26]     [,27]     [,28] [,29] [,30]
[1,]  5.145833  2.097222  2.180556    NA  5.059028  3.138889    NA    NA
[2,] 21.000000 88.000000 91.000000   135 64.000000 73.000000    77    55
[3,] 63.000000 78.000000 75.000000    NA 18.000000 27.000000    NA    NA
         [,31]      [,32]      [,33]     [,34]      [,35]      [,36]
[1,]  11.17361   6.222222   6.180556  7.104167   6.291667   5.027778
[2,]  93.00000  34.000000  99.000000 56.000000  75.000000  39.000000
[3,] 120.00000 125.000000 115.000000 83.000000 143.000000 109.000000
          [,37]      [,38]
[1,]   7.076389   6.097222
[2,]  72.000000 119.000000
[3,] 120.000000  96.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative Multiplate ASPI",ylab="Area under curve
(AUC)",  cex.main=1.3, cex.lab=1.4,lwd=1)
```

```
>
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> lines(c(-.4,-.4), c(71,115), type="l", lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1multiplateASPI, na.rm=TRUE)
> postopmean<-mean(epi$Prov2multiplateASPI, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(9,90,"P<0.01", cex=2)
>
>
>
>
>
> #Before and after diagrams for PK
> preop<-epi$Prov1rutinPK
> postop<-epi$Prov2rutinPK
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
         [,1]     [,2]     [,3]     [,4] [,5]     [,6]     [,7]     [,8]
[1,] 11.13194 6.118056 8.145833 3.107639  3.1 10.07292 7.104167 6.100694
[2,]  1.00000       NA 1.100000 1.100000  1.1  1.00000 1.300000 1.100000
[3,]  1.20000 1.100000 1.100000 1.200000  1.3  1.20000 1.300000 1.300000
         [,9]    [,10]    [,11]    [,12]    [,13]    [,14] [,15]    [,16]
[1,] 2.201389 5.145833 5.069444 14.09722 5.131944 6.180556    NA 2.121528
[2,] 0.900000 0.900000 1.000000  1.00000 1.000000 1.100000   0.9 1.000000
[3,] 1.000000 1.200000 1.200000  1.40000 1.100000 1.100000    NA 1.600000
        [,17]    [,18]    [,19] [,20]    [,21]    [,22]    [,23]    [,24]
[1,] 5.194444 15.15278 5.909722    NA 5.111111 4.958333 5.145833 2.097222
[2,] 1.100000  1.00000 1.000000     1 1.000000 1.000000 1.100000 0.900000
[3,] 1.100000  1.20000 1.100000    NA 1.100000 1.100000 1.200000 1.300000
        [,25] [,26]    [,27]    [,28] [,29] [,30]    [,31]    [,32]    [,33]
[1,] 2.180556    NA 5.059028 3.138889    NA    NA 11.17361 6.222222 6.180556
[2,]       NA   0.9 1.000000 1.100000    NA   1.1  1.00000 1.000000 1.100000
[3,] 1.000000   0.9 1.100000 1.500000   1.1    NA  1.00000 1.000000 1.100000
        [,34]    [,35]    [,36]    [,37]    [,38]
[1,] 7.104167 6.291667 5.027778 7.076389 6.097222
[2,]       NA 1.100000 1.100000 1.100000 0.900000
[3,] 1.000000 1.300000 1.100000 1.400000 1.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
```

```
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative PT-INR",ylab="PT-INR",  cex.main=1.3,
cex.lab=1.4,lwd=1)
>
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> lines(c(-.4,-.4), c(0.9,1.2), type="l", lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1rutinPK, na.rm=TRUE)
> postopmean<-mean(epi$Prov2rutinPK, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> t.test(epi$Prov1rutinPK,epi$Prov2rutinPK, alternative =
c("two.sided"),paired=TRUE)

    Paired t-test

data:  epi$Prov1rutinPK and epi$Prov2rutinPK
t = -5.6176, df = 30, p-value = 4.077e-06
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.20673186 -0.09649394
sample estimates:
mean of the differences
             -0.1516129

> wilcox.test(epi$Prov1rutinPK,epi$Prov2rutinPK, alternative =
c("two.sided"),paired=TRUE)

    Wilcoxon signed rank test with continuity correction

data:  epi$Prov1rutinPK and epi$Prov2rutinPK
V = 0, p-value = 3.92e-05
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1rutinPK, epi$Prov2rutinPK, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1rutinPK, epi$Prov2rutinPK, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(8,1.45,"P<0.01", cex=2)
>
>
>
>
>
> #Before and after diagrams for APTT
```

```
> preop<-epi$Prov1rutinAPTT
> postop<-epi$Prov2rutinAPTT
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
         [,1]      [,2]      [,3]      [,4] [,5]     [,6]      [,7]      [,8]
[1,] 11.13194  6.118056  8.145833  3.107639  3.1 10.07292  7.104167  6.100694
[2,] 26.00000        NA 34.000000 34.000000 29.0       NA 26.000000 26.000000
[3,] 30.00000 29.000000 33.000000 29.000000 35.0 32.00000 26.000000 34.000000
          [,9]     [,10]     [,11]    [,12]     [,13]     [,14] [,15]
[1,]  2.201389  5.145833  5.069444 14.09722  5.131944  6.180556    NA
[2,] 24.000000 26.000000 27.000000 24.00000 31.000000 26.000000    26
[3,] 25.000000 25.000000 35.000000 28.00000 30.000000 28.000000    NA
         [,16]     [,17]    [,18]     [,19] [,20]     [,21]     [,22]
[1,]  2.121528  5.194444 15.15278  5.909722    NA  5.111111  4.958333
[2,] 26.000000 30.000000 27.00000 31.000000    25 26.000000 27.000000
[3,] 43.000000 29.000000 26.00000 25.000000    NA 27.000000 30.000000
         [,23]     [,24]     [,25] [,26]     [,27]     [,28] [,29] [,30]
[1,]  5.145833  2.097222  2.180556    NA  5.059028  3.138889    NA    NA
[2,] 25.000000 25.000000        NA    29 24.000000 27.000000    NA    27
[3,] 27.000000 29.000000 28.000000    28 27.000000 32.000000    33    NA
        [,31]     [,32]     [,33]     [,34]     [,35]     [,36]     [,37]
[1,] 11.17361  6.222222  6.180556  7.104167  6.291667  5.027778  7.076389
[2,] 32.00000 22.000000 24.000000        NA 27.000000 24.000000 28.000000
[3,] 29.00000 24.000000 26.000000 25.000000 30.000000 26.000000 43.000000
         [,38]
[1,]  6.097222
[2,] 26.000000
[3,] 30.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative aPTT",ylab="aPTT (s)",  cex.main=1.3,
cex.lab=1.4,lwd=1)
>
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> lines(c(-.4,-.4), c(28,36), type="l", lwd=6, lty=3)
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1rutinAPTT, na.rm=TRUE)
> postopmean<-mean(epi$Prov2rutinAPTT, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> t.test(epi$Prov1rutinAPTT,epi$Prov2rutinAPTT, alternative =
```

```
c("two.sided"),paired=TRUE)

	Paired t-test

data:  epi$Prov1rutinAPTT and epi$Prov2rutinAPTT
t = -2.8253, df = 29, p-value = 0.008461
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -4.3671924 -0.6994742
sample estimates:
mean of the differences
              -2.533333

> wilcox.test(epi$Prov1rutinAPTT,epi$Prov2rutinAPTT, alternative =
c("two.sided"),paired=TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1rutinAPTT and epi$Prov2rutinAPTT
V = 89.5, p-value = 0.005653
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1rutinAPTT, epi$Prov2rutinAPTT, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1rutinAPTT, epi$Prov2rutinAPTT, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
> 
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(8,35,"P<0.01", cex=2)
> 
> 
> 
> 
> 
> #Before and after diagrams for TPK
> dev.new(width=5)
> preop<-epi$Prov1rutinTPK
> postop<-epi$Prov2rutinTPK
> preopdata<-t(matrix(preop))
> postopdata<-t(matrix(postop))
> withdrawaltime<-t(matrix(epi$withdrawaltime))
> meanwithdrawaltime<-mean(epi$withdrawaltime, na.rm=TRUE)
> y<-rbind(preop, postop)
> beforeandafterdata<-rbind(withdrawaltime, preopdata, postopdata)
> beforeandafterdata
          [,1]       [,2]       [,3]       [,4]  [,5]      [,6]       [,7]
[1,]  11.13194   6.118056   8.145833   3.107639   3.1  10.07292   7.104167
[2,] 229.00000 224.000000 205.000000 477.000000 105.0 202.00000 131.000000
[3,]        NA 286.000000 312.000000 657.000000 131.0        NA 325.000000
           [,8]       [,9]      [,10]      [,11]     [,12]      [,13]
[1,]   6.100694   2.201389   5.145833   5.069444  14.09722   5.131944
[2,] 189.000000 305.000000 145.000000 221.000000 170.00000 169.000000
[3,] 262.000000 310.000000 162.000000 244.000000 351.00000 142.000000
```

```
          [,14] [,15]      [,16]      [,17]     [,18]      [,19] [,20]
[1,]   6.180556    NA   2.121528   5.194444  15.15278   5.909722    NA
[2,] 240.000000   132 269.000000 212.000000 224.00000 142.000000   159
[3,] 273.000000    NA 221.000000 309.000000 864.00000 216.000000    NA
          [,21]      [,22]      [,23]      [,24]      [,25] [,26]      [,27]
[1,]   5.111111   4.958333   5.145833   2.097222   2.180556    NA   5.059028
[2,] 153.000000 221.000000 171.000000 238.000000 237.000000   336 119.000000
[3,] 282.000000 248.000000 177.000000 140.000000 200.000000    NA 134.000000
          [,28] [,29] [,30]     [,31]      [,32]      [,33]      [,34]
[1,]   3.138889    NA    NA  11.17361   6.222222   6.180556   7.104167
[2,] 175.000000   251   293 179.00000 274.000000 194.000000 129.000000
[3,]  35.000000    NA    NA 337.00000 303.000000 280.000000 210.000000
          [,35]      [,36]      [,37]      [,38]
[1,]   6.291667   5.027778   7.076389   6.097222
[2,] 189.000000 196.000000 277.000000 316.000000
[3,] 286.000000 389.000000 370.000000 319.000000
> ylimits<-c(0.9*(min(preop,postop,na.rm=TRUE)),max(preop,postop, na.rm=TRUE))
> xlimits<-c(0,max(epi$withdrawaltime, na.rm=TRUE))
> xlabel<-"Days after surgery"
> plot(c(0,beforeandafterdata[1,1]),c(beforeandafterdata[2,1],
beforeandafterdata[3,1]),
type="l",col="black",xlim=xlimits,ylim=ylimits,ann=TRUE,axes=TRUE,xlab=xlabel,
main="Individual pre- and postoperative Plc",ylab="Plc (millions/ml)",
cex.main=1.3, cex.lab=1.4,lwd=1)
>
> for (x in 2:38) {lines(c(0,beforeandafterdata[1,x]),
c(beforeandafterdata[2,x], beforeandafterdata[3,x]), type="l", col="black",
lwd=1)}
>
> #normal range - enter manually!
> lines(c(-.4,-.4), c(145,280), type="l", code=0,lwd=2,lty=3)
Warning message:
In plot.xy(xy.coords(x, y), type = type, ...) :
  "code" is not a graphical parameter
>
> #Average pre and postoperative values at t=0 and t=mean withdrawal time
> preopmean<-mean(epi$Prov1rutinTPK, na.rm=TRUE)
> postopmean<-mean(epi$Prov2rutinTPK, na.rm=TRUE)
> lines(c(0, meanwithdrawaltime), c(preopmean, postopmean), type="l", lwd=6,
lty=4)
>
> t.test(epi$Prov1rutinTPK,epi$Prov2rutinTPK, alternative =
c("two.sided"),paired=TRUE)

	Paired t-test

data:  epi$Prov1rutinTPK and epi$Prov2rutinTPK
t = -3.0816, df = 30, p-value = 0.004385
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -122.2372  -24.7951
sample estimates:
mean of the differences
              -73.51613

> wilcox.test(epi$Prov1rutinTPK,epi$Prov2rutinTPK, alternative =
```

```
c("two.sided"),paired=TRUE)

    Wilcoxon signed rank test with continuity correction

data:  epi$Prov1rutinTPK and epi$Prov2rutinTPK
V = 80.5, p-value = 0.001065
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$Prov1rutinTPK, epi$Prov2rutinTPK, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
>
> #Significance value for pre- to postop change - see t.test or Wilcoxon's.
> text(8,400,"P<0.01", cex=2)
>
>
> ###Some means and SD's from the data
> mean(epi$Alb, na.rm=TRUE)
[1] 36.60714
> sd(epi$Alb, na.rm=TRUE)
[1] 3.715227
>
> mean(epi$withdrawaltime, na.rm=TRUE)
[1] 6.180324
> sd(epi$withdrawaltime, na.rm=TRUE)
[1] 3.152811
>
> mean(epi$oplangd, na.rm=TRUE)
[1] 10.34211
> sd(epi$oplangd, na.rm=TRUE)
[1] 11.75719
>
> mean(epi$PEROPbloedning, na.rm=TRUE)
[1] 661.1111
> sd(epi$PEROPbloedning, na.rm=TRUE)
[1] 784.5027
>
> mean(epi$Prov1rutinBIL, na.rm=TRUE)
[1] 14.05263
> sd(epi$Prov1rutinBIL, na.rm=TRUE)
[1] 21.78016
> mean(epi$Prov2rutinBIL, na.rm=TRUE)
[1] 10.51613
> sd(epi$Prov2rutinBIL, na.rm=TRUE)
[1] 16.47801
> t.test(epi$Prov1rutinBIL, epi$Prov2rutinBIL, alternative =
c("two.sided"),paired=TRUE)

    Paired t-test

data:  epi$Prov1rutinBIL and epi$Prov2rutinBIL
t = 2.5067, df = 30, p-value = 0.01783
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.6634288 6.4978615
```

```
sample estimates:
mean of the differences 
               3.580645 

> wilcox.test(epi$Prov1rutinBIL, epi$Prov2rutinBIL, alternative =
c("two.sided"),paired=TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1rutinBIL and epi$Prov2rutinBIL
V = 258.5, p-value = 0.009943
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1rutinBIL, epi$Prov2rutinBIL, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1rutinBIL, epi$Prov2rutinBIL, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
> 
> mean(epi$Prov1rutinGT, na.rm=TRUE)
[1] 1.306757
> sd(epi$Prov1rutinGT, na.rm=TRUE)
[1] 1.997771
> mean(epi$Prov2rutinGT, na.rm=TRUE)
[1] 2.11
> sd(epi$Prov2rutinGT, na.rm=TRUE)
[1] 1.872609
> t.test(epi$Prov1rutinGT, epi$Prov2rutinGT, alternative =
c("two.sided"),paired=TRUE)

	Paired t-test

data:  epi$Prov1rutinGT and epi$Prov2rutinGT
t = -2.4204, df = 30, p-value = 0.02177
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.6427357 -0.1391998
sample estimates:
mean of the differences 
             -0.8909677 

> wilcox.test(epi$Prov1rutinGT, epi$Prov2rutinGT, alternative =
c("two.sided"),paired=TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1rutinGT and epi$Prov2rutinGT
V = 95, p-value = 0.004833
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1rutinGT, epi$Prov2rutinGT, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
```

```
2: In wilcox.test.default(epi$Prov1rutinGT, epi$Prov2rutinGT, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
>
> mean(epi$Prov1rutinCRP, na.rm=TRUE)
[1] 6.784211
> sd(epi$Prov1rutinCRP, na.rm=TRUE)
[1] 9.436312
> mean(epi$Prov2rutinCRP, na.rm=TRUE)
[1] 91.96667
> sd(epi$Prov2rutinCRP, na.rm=TRUE)
[1] 59.82762
> t.test(epi$Prov1rutinCRP, epi$Prov2rutinCRP, alternative =
c("two.sided"),paired=TRUE)

	Paired t-test

data:  epi$Prov1rutinCRP and epi$Prov2rutinCRP
t = -7.5742, df = 29, p-value = 2.38e-08
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -107.688  -61.896
sample estimates:
mean of the differences
                -84.792

> wilcox.test(epi$Prov1rutinCRP, epi$Prov2rutinCRP, alternative =
c("two.sided"),paired=TRUE)

	Wilcoxon signed rank test

data:  epi$Prov1rutinCRP and epi$Prov2rutinCRP
V = 0, p-value = 1.863e-09
alternative hypothesis: true location shift is not equal to 0

>
> mean(epi$Prov1rutinKREA, na.rm=TRUE)
[1] 73.37838
> sd(epi$Prov1rutinKREA, na.rm=TRUE)
[1] 19.00928
> mean(epi$Prov2rutinKREA, na.rm=TRUE)
[1] 65.22581
> sd(epi$Prov2rutinKREA, na.rm=TRUE)
[1] 18.27149
> t.test(epi$Prov1rutinKREA, epi$Prov2rutinKREA, alternative =
c("two.sided"),paired=TRUE)

	Paired t-test

data:  epi$Prov1rutinKREA and epi$Prov2rutinKREA
t = 3.0497, df = 29, p-value = 0.004856
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 1.602930 8.130403
sample estimates:
mean of the differences
```

```
               4.866667

> wilcox.test(epi$Prov1rutinKREA, epi$Prov2rutinKREA, alternative =
c("two.sided"),paired=TRUE)

    Wilcoxon signed rank test with continuity correction

data:  epi$Prov1rutinKREA and epi$Prov2rutinKREA
V = 318, p-value = 0.009062
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1rutinKREA, epi$Prov2rutinKREA, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1rutinKREA, epi$Prov2rutinKREA, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
> 
> mean(epi$PEROPbloedning, na.rm=TRUE)
[1] 661.1111
> sd(epi$PEROPbloedning, na.rm=TRUE)
[1] 784.5027
> 
> mean(epi$DRAENmaengd, na.rm=TRUE)
[1] 430.2273
> sd(epi$DRAENmaengd, na.rm=TRUE)
[1] 355.2178
> 
> ####Hb
> mean(epi$Prov1rutinHB, na.rm=TRUE)
[1] 119.5
> sd(epi$Prov1rutinHB, na.rm=TRUE)
[1] 16.14922
> 
> mean(epi$Prov2rutinHB, na.rm=TRUE)
[1] 112.7576
> sd(epi$Prov2rutinHB, na.rm=TRUE)
[1] 11.9714
> min(epi$Prov2rutinHB, na.rm=TRUE)
[1] 87
> max(epi$Prov2rutinHB, na.rm=TRUE)
[1] 147
> 
> ###Correlations
> #Correlation between withdrawal time and EXTEM-MCF
> plot(epi$withdrawaltime, epi$Prov2extemMCF, xlab="Day of epidural
withdrawal", ylab = "EXTEM-MCF (mm)", abline(lm(epi$Prov2extemMCF~epi
$withdrawaltime)),cex.main=1.3, cex.lab=1.4, ylim=c(0,80))
> cor.test(epi$withdrawaltime, epi$Prov2extemMCF, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$Prov2extemMCF
t = 2.9901, df = 31, p-value = 0.005423
```

```
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1549956 0.7023547
sample estimates:
      cor
0.4731287

> cor.test(epi$withdrawaltime, epi$Prov2extemMCF, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$Prov2extemMCF
S = 2929, p-value = 0.0024
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.5105266

Warning message:
In cor.test.default(epi$withdrawaltime, epi$Prov2extemMCF, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=12, y=60, "P<0.01", pos=3, cex=2)
> text(x=12, y=55, "r=0.47", pos=3, cex=2)
>
> #Correlation between withdrawal time and FIBTEM-MCF
> plot(epi$withdrawaltime, epi$Prov2fibtemMCF, xlab="Day of epidural
withdrawal", ylab = "FIBTEM-MCF (mm)", abline(lm(epi$Prov2fibtemMCF~epi
$withdrawaltime)),cex.main=1.3, cex.lab=1.4, ylim=c(0,80))
> cor.test(epi$withdrawaltime, epi$Prov2fibtemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$Prov2fibtemMCF
t = 4.3392, df = 31, p-value = 0.0001412
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.3439931 0.7910728
sample estimates:
      cor
0.6147076

> cor.test(epi$withdrawaltime, epi$Prov2fibtemMCF, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$Prov2fibtemMCF
S = 2088.6, p-value = 4.093e-05
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.6509734
```

```
Warning message:
In cor.test.default(epi$withdrawaltime, epi$Prov2fibtemMCF, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=12, y=70, "P<0.01", pos=3, cex=2)
> text(x=12, y=65, "r=0.61", pos=3, cex=2)
>
> #Correlation between withdrawal time and INTEM-MCF
> plot(epi$withdrawaltime, epi$Prov2intemMCF, xlab="Day of epidural
withdrawal", ylab = "INTEM-MCF (mm)", abline(lm(epi$Prov2intemMCF~epi
$withdrawaltime)),cex.main=1.3, cex.lab=1.4, ylim=c(0,80))
> cor.test(epi$withdrawaltime, epi$Prov2intemMCF, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$Prov2intemMCF
t = 2.678, df = 31, p-value = 0.01174
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1058989 0.6761435
sample estimates:
      cor
0.4334494

> cor.test(epi$withdrawaltime, epi$Prov2intemMCF, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$Prov2intemMCF
S = 1875.2, p-value = 1.023e-05
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.6866393

Warning message:
In cor.test.default(epi$withdrawaltime, epi$Prov2intemMCF, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=12, y=60, "P<0.05", pos=3, cex=2)
> text(x=12, y=55, "r=0.43", pos=3, cex=2)
>
> #Correlation between withdrawal time and HEPTEM-MCF
> plot(epi$withdrawaltime, epi$Prov2heptemMCF, xlab="Day of epidural
withdrawal", ylab = "HEPTEM-MCF (mm)", abline(lm(epi$Prov2heptemMCF~epi
$withdrawaltime)),cex.main=1.3, cex.lab=1.4, ylim=c(0,80))
> cor.test(epi$withdrawaltime, epi$Prov2heptemMCF, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$Prov2heptemMCF
t = 2.8901, df = 30, p-value = 0.007092
alternative hypothesis: true correlation is not equal to 0
```

```
95 percent confidence interval:
 0.1409112 0.7012560
sample estimates:
      cor 
0.4666751 

> cor.test(epi$withdrawaltime, epi$Prov2heptemMCF, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$Prov2heptemMCF
S = 2716.7, p-value = 0.003411
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.5020796 

Warning message:
In cor.test.default(epi$withdrawaltime, epi$Prov2heptemMCF, use = 
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=15, y=70, "**", pos=3, cex=2)
> text(x=12, y=60, "P<0.01", pos=3, cex=2)
> text(x=12, y=55, "r=0.47", pos=3, cex=2)
> 
> #Correlation between withdrawal time and Prov2multiplateADP
> plot(epi$withdrawaltime, epi$Prov2multiplateADP, xlab="Day of epidural 
withdrawal", ylab = "Multiplate-ADP (Area under curve)", abline(lm(epi
$Prov2heptemMCF~epi$withdrawaltime)),cex.main=1.3, cex.lab=1.4,ylim=c(30,160))
> cor.test(epi$withdrawaltime, epi$Prov2multiplateADP, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$Prov2multiplateADP
t = 3.6191, df = 31, p-value = 0.00104
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.2481091 0.7482973
sample estimates:
      cor 
0.5449964 

> cor.test(epi$withdrawaltime, epi$Prov2multiplateADP, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$Prov2multiplateADP
S = 2357.4, p-value = 0.0001855
alternative hypothesis: true rho is not equal to 0
sample estimates:
     rho 
0.606053 
```

```
Warning message:
In cor.test.default(epi$withdrawaltime, epi$Prov2multiplateADP,  :
  Cannot compute exact p-value with ties
> text(x=13, y=60, "P<0.01", pos=3, cex=2)
> text(x=13, y=50, "r=0.54", pos=3, cex=2)
>
>
> #Correlation between withdrawal time and Prov2multiplateCOL
> plot(epi$withdrawaltime, epi$Prov2multiplateCOL, xlab="Day of epidural
withdrawal", ylab = "Multiplate-COL (Area under curve)", abline(lm(epi
$Prov2multiplateCOL~epi$withdrawaltime)),cex.main=1.3,
cex.lab=1.4,ylim=c(30,160))
> cor.test(epi$withdrawaltime, epi$Prov2multiplateCOL, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$Prov2multiplateCOL
t = 4.3567, df = 31, p-value = 0.0001344
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.3461759 0.7919982
sample estimates:
      cor 
0.6162468 

> cor.test(epi$withdrawaltime, epi$Prov2multiplateCOL, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$Prov2multiplateCOL
S = 2142.8, p-value = 5.659e-05
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.6419196 

Warning message:
In cor.test.default(epi$withdrawaltime, epi$Prov2multiplateCOL,  :
  Cannot compute exact p-value with ties
> text(x=13, y=60, "P<0.01", pos=3, cex=2)
> text(x=13, y=50, "r=0.61", pos=3, cex=2)
>
> #Correlation between withdrawal time and Prov2multiplateTRAP
> plot(epi$withdrawaltime, epi$Prov2multiplateCOL, xlab="Day of epidural
withdrawal", ylab = "Multiplate-TRAP (Area under curve)", abline(lm(epi
$Prov2multiplateTRAP~epi$withdrawaltime)),cex.main=1.3,
cex.lab=1.4,ylim=c(30,160))
> cor.test(epi$withdrawaltime, epi$Prov2multiplateTRAP, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$Prov2multiplateTRAP
t = 3.5038, df = 31, p-value = 0.001419
```

```
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.2316643 0.7405179
sample estimates:
      cor 
0.5326132 

> cor.test(epi$withdrawaltime, epi$Prov2multiplateTRAP, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$Prov2multiplateTRAP
S = 2114.2, p-value = 4.777e-05
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.6466901 

Warning message:
In cor.test.default(epi$withdrawaltime, epi$Prov2multiplateTRAP,  :
  Cannot compute exact p-value with ties
> text(x=13, y=60, "P<0.01", pos=3, cex=2)
> text(x=13, y=50, "r=0.53", pos=3, cex=2)
> 
> #Correlation between withdrawal time and Prov2multiplateASPI
> plot(epi$withdrawaltime, epi$Prov2multiplateCOL, xlab="Day of epidural 
withdrawal", ylab = "Multiplate-ASPI (Area under curve)", abline(lm(epi
$Prov2multiplateASPI~epi$withdrawaltime)),cex.main=1.3,
cex.lab=1.4,ylim=c(30,160))
> cor.test(epi$withdrawaltime, epi$Prov2multiplateASPI, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$Prov2multiplateASPI
t = 4.3702, df = 31, p-value = 0.0001293
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.3478537 0.7927082
sample estimates:
      cor 
0.6174285 

> cor.test(epi$withdrawaltime, epi$Prov2multiplateASPI, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$Prov2multiplateASPI
S = 1882.3, p-value = 1.075e-05
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.6854468 
```

```
Warning message:
In cor.test.default(epi$withdrawaltime, epi$Prov2multiplateASPI,  :
  Cannot compute exact p-value with ties
> text(x=13, y=60, "P<0.01", pos=3, cex=2)
> text(x=13, y=50, "r=0.61", pos=3, cex=2)
>
> #Correlation between Plc and multiplate ADP
> dev.new(width=5)
> plot(epi$Prov2rutinTPK, epi$Prov2multiplateADP,main="Multiplate ADP AUC vs
Plc", xlab="Platelet count (millions/mL)", ylab = "Multiplate-ADP (Area under
curve)", abline(lm(epi$Prov2multiplateADP~epi$Prov2rutinTPK)),cex.main=1.3,
cex.lab=1.4,ylim=c(30,160))
> cor.test(epi$Prov2rutinTPK, epi$Prov2multiplateADP, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinTPK and epi$Prov2multiplateADP
t = 4.0675, df = 29, p-value = 0.0003329
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.3158253 0.7886309
sample estimates:
      cor
0.6027158

> cor.test(epi$Prov2rutinTPK, epi$Prov2multiplateADP, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinTPK and epi$Prov2multiplateADP
S = 2328.7, p-value = 0.00214
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.5305094

Warning message:
In cor.test.default(epi$Prov2rutinTPK, epi$Prov2multiplateADP, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=700, y=80, "P<0.01", pos=3, cex=2)
> text(x=700, y=70, "r=0.60", pos=3, cex=2)
> arrows(50,57,,113,code=0,lwd=2,lty=3)
>
>
>
> #Correlation between Plc and multiplate COL
> plot(epi$Prov2rutinTPK, epi$Prov2multiplateCOL, xlab="Platelet count
(millions/mL)", ylab = "Multiplate-COL (Area under curve)", abline(lm(epi
$Prov2multiplateCOL~epi$Prov2rutinTPK)),cex.main=1.3,
cex.lab=1.4,ylim=c(30,160))
> cor.test(epi$Prov2rutinTPK, epi$Prov2multiplateCOL, use="complete.obs",
method="pearson")
```

```
    Pearson's product-moment correlation

data:  epi$Prov2rutinTPK and epi$Prov2multiplateCOL
t = 5.9174, df = 29, p-value = 1.998e-06
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.5220598 0.8667749
sample estimates:
      cor 
0.7395863 

> cor.test(epi$Prov2rutinTPK, epi$Prov2multiplateCOL, use="complete.obs", 
method="spearman")

    Spearman's rank correlation rho

data:  epi$Prov2rutinTPK and epi$Prov2multiplateCOL
S = 1362.2, p-value = 3.902e-06
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.7253656 

Warning message:
In cor.test.default(epi$Prov2rutinTPK, epi$Prov2multiplateCOL, use = 
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=700, y=100, "P<0.01", pos=3, cex=2)
> text(x=700, y=90, "r=0.74", pos=3, cex=2)
> 
> #Correlation between Plc and multiplate TRAP
> plot(epi$Prov2rutinTPK, epi$Prov2multiplateTRAP, xlab="Platelet count 
(millions/mL)", ylab = "Multiplate-TRAP (Area under curve)", abline(lm(epi
$Prov2multiplateTRAP~epi$Prov2rutinTPK)),cex.main=1.3, 
cex.lab=1.4,ylim=c(30,160))
> cor.test(epi$Prov2rutinTPK, epi$Prov2multiplateTRAP, use="complete.obs", 
method="pearson")

    Pearson's product-moment correlation

data:  epi$Prov2rutinTPK and epi$Prov2multiplateTRAP
t = 4.1616, df = 29, p-value = 0.0002575
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.3282701 0.7938231
sample estimates:
     cor 
0.611483 

> cor.test(epi$Prov2rutinTPK, epi$Prov2multiplateTRAP, use="complete.obs", 
method="spearman")

    Spearman's rank correlation rho

data:  epi$Prov2rutinTPK and epi$Prov2multiplateTRAP
S = 1792.7, p-value = 0.0001108
```

```
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.6385724 

Warning message:
In cor.test.default(epi$Prov2rutinTPK, epi$Prov2multiplateTRAP,  :
  Cannot compute exact p-value with ties
> text(x=700, y=100, "P<0.01", pos=3, cex=2)
> text(x=700, y=90, "r=0.61", pos=3, cex=2)
> 
> 
> #Correlation between Plc and multiplate ASPI
> plot(epi$Prov2rutinTPK, epi$Prov2multiplateASPI, xlab="Platelet count 
(millions/mL)", ylab = "Multiplate-ASPI (Area under curve)", abline(lm(epi
$Prov2multiplateASPI~epi$Prov2rutinTPK)),cex.main=1.3, 
cex.lab=1.4,ylim=c(30,160))
> cor.test(epi$Prov2rutinTPK, epi$Prov2multiplateASPI, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinTPK and epi$Prov2multiplateASPI
t = 4.2389, df = 29, p-value = 0.0002084
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.3383307 0.7979716
sample estimates:
      cor 
0.6185201 

> cor.test(epi$Prov2rutinTPK, epi$Prov2multiplateASPI, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinTPK and epi$Prov2multiplateASPI
S = 1444.9, p-value = 8.137e-06
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.7086821 

Warning message:
In cor.test.default(epi$Prov2rutinTPK, epi$Prov2multiplateASPI,  :
  Cannot compute exact p-value with ties
> text(x=700, y=100, "P<0.01", pos=3, cex=2)
> text(x=700, y=90, "r=0.62", pos=3, cex=2)
> 
> 
> #Correlation between d-dimer and FIBTEM-Li60
> plot(epi$DDpostop, epi$Prov2fibtemLI60, xlab="Postoperative d-dimer (mg/L)", 
ylab = "FIBTEM-Li60", abline(lm(epi$Prov2fibtemLI60 ~epi
$DDpostop)),cex.main=1.3, cex.lab=1.4)
> cor.test(epi$DDpostop, epi$Prov2fibtemLI60, use="complete.obs", 
method="pearson")
```

```
    Pearson's product-moment correlation

data:  epi$DDpostop and epi$Prov2fibtemLI60
t = -3.6528, df = 28, p-value = 0.001057
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.7706403 -0.2613083
sample estimates:
       cor 
-0.5680962 

> cor.test(epi$DDpostop, epi$Prov2fibtemLI60, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$DDpostop and epi$Prov2fibtemLI60
S = 6870.7, p-value = 0.002678
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.5285284 

Warning message:
In cor.test.default(epi$DDpostop, epi$Prov2fibtemLI60, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> 
> text(x=4.5, y=98, "P<0.01", pos=3, cex=2)
> text(x=4.5, y=97, "r=-0.56", pos=3, cex=2)
> 
> #Correlation between d-dimer and EXTEM-Li60
> plot(epi$DDpostop, epi$Prov2extemLI60, xlab="Postoperative d-dimer", ylab =
"EXTEM-Li60", abline(lm(epi$Prov2extemLI60 ~epi$DDpostop)),cex.main=1.3,
cex.lab=1.4)
> cor.test(epi$DDpostop, epi$Prov2extemLI60, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$DDpostop and epi$Prov2extemLI60
t = -1.8044, df = 29, p-value = 0.08157
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.60404504  0.04128158
sample estimates:
       cor 
-0.3177058 

> cor.test(epi$DDpostop, epi$Prov2extemLI60, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$DDpostop and epi$Prov2extemLI60
S = 5277.7, p-value = 0.7321
```

```
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho 
-0.06405276 

Warning message:
In cor.test.default(epi$DDpostop, epi$Prov2extemLI60, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=4.5, y=93, "N/S", pos=3, cex=2)
> 
> #Correlation between d-dimer and INTEM-Li60
> plot(epi$DDpostop, epi$Prov2intemLI60, xlab="Postoperative d-dimer", ylab = 
"INTEM-Li60", abline(lm(epi$Prov2intemLI60 ~epi$DDpostop)),cex.main=1.3, 
cex.lab=1.4)
> cor.test(epi$DDpostop, epi$Prov2intemLI60, use="complete.obs", 
method="pearson")

    Pearson's product-moment correlation

data:  epi$DDpostop and epi$Prov2intemLI60
t = 0.8787, df = 26, p-value = 0.3876
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.2170022  0.5105531
sample estimates:
      cor 
0.1698233 

> cor.test(epi$DDpostop, epi$Prov2intemLI60, use="complete.obs", 
method="spearman")

    Spearman's rank correlation rho

data:  epi$DDpostop and epi$Prov2intemLI60
S = 2773, p-value = 0.2165
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.2410964 

Warning message:
In cor.test.default(epi$DDpostop, epi$Prov2intemLI60, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=4.5, y=93, "N/S", pos=3, cex=2)
> 
> #Correlation between withdrawal time and D-Dimer
> plot(epi$withdrawaltime, epi$DDpostop, xlab="Day of epidural withdrawal", 
ylab = "D-dimer", abline(lm(epi$DDpostop~epi$withdrawaltime)),cex.main=1.3, 
cex.lab=1.4)
> cor.test(epi$withdrawaltime, epi$DDpostop, use="complete.obs", 
method="pearson")

    Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$DDpostop
t = 2.6428, df = 29, p-value = 0.01312
```

```
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1021768 0.6875695
sample estimates:
     cor
0.440566

> cor.test(epi$withdrawaltime, epi$DDpostop, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$DDpostop
S = 3224.5, p-value = 0.05365
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.3499042

Warning message:
In cor.test.default(epi$withdrawaltime, epi$DDpostop, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=13, y=5, "P=0.05", pos=3, cex=2)
> text(x=13, y=4.5, "rho=0.34", pos=3, cex=2)
>
> hist(epi$DDpostop)
> hist(epi$Prov2fibtemLI60)
>
> #Correlation between withdrawal time and Fibtem-Li60
> plot(epi$withdrawaltime, epi$Prov2fibtemLI60, xlab="Day of epidural
withdrawal", ylab = "FIBTEM-Li60", abline(lm(epi$Prov2fibtemLI60~epi
$withdrawaltime)),cex.main=1.3, cex.lab=1.4)
> cor.test(epi$withdrawaltime, epi$Prov2fibtemLI60, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$Prov2fibtemLI60
t = -4.9153, df = 30, p-value = 2.959e-05
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.8245592 -0.4161145
sample estimates:
       cor
-0.6678986

> cor.test(epi$withdrawaltime, epi$Prov2fibtemLI60, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$Prov2fibtemLI60
S = 9239.1, p-value = 1.085e-05
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
```

```
-0.6933778

Warning message:
In cor.test.default(epi$withdrawaltime, epi$Prov2fibtemLI60, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=13, y=5, "P<0.01", pos=3, cex=2)
> text(x=13, y=4.5, "r=-0.67", pos=3, cex=2)
>
>
> #Correlation between withdrawal time and CRP
> plot(epi$withdrawaltime, epi$Prov2rutinCRP, xlab="Day of epidural
withdrawal", ylab = "CRP", abline(lm(epi$Prov2rutinCRP~epi
$withdrawaltime)),cex.main=1.3, cex.lab=1.4)
> cor.test(epi$withdrawaltime, epi$Prov2rutinCRP, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$Prov2rutinCRP
t = -1.6047, df = 28, p-value = 0.1198
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.58890747  0.07823845
sample estimates:
       cor
-0.2902109

> cor.test(epi$withdrawaltime, epi$Prov2rutinCRP, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$Prov2rutinCRP
S = 5519.1, p-value = 0.226
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.2278242

Warning message:
In cor.test.default(epi$withdrawaltime, epi$Prov2rutinCRP, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=13, y=150, "N/S", pos=3, cex=2)
>
> #Correlation between DDimer and CRP
> plot(epi$Prov2rutinCRP, epi$DDpostop, xlab="CRP", ylab = "D-dimer",
abline(lm(epi$DDpostop~epi$Prov2rutinCRP)),cex.main=1.3, cex.lab=1.4,
xlim=c(0,200), ylim=c(0,4))
> cor.test(epi$DDpostop, epi$Prov2rutinCRP, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$DDpostop and epi$Prov2rutinCRP
```

```
t = 1.6004, df = 26, p-value = 0.1216
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.08287968  0.60494847
sample estimates:
      cor 
0.2994566 

> cor.test(epi$withdrawaltime, epi$Prov2rutinCRP, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$Prov2rutinCRP
S = 5519.1, p-value = 0.226
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.2278242 

Warning message:
In cor.test.default(epi$withdrawaltime, epi$Prov2rutinCRP, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=160, y=1.5, "N/S", pos=3, cex=2)
> 
> ##Calculation of liver tests
> boxplot(main="Bilirubin",epi$Prov1rutinBIL,epi$Prov2rutinBIL)
> mean(epi$Prov1rutinBIL, na.rm=TRUE)
[1] 14.05263
> sd(epi$Prov1rutinBIL, na.rm=TRUE)
[1] 21.78016
> mean(epi$Prov2rutinBIL, na.rm=TRUE)
[1] 10.51613
> sd(epi$Prov2rutinBIL, na.rm=TRUE)
[1] 16.47801
> t.test(epi$Prov1rutinBIL,epi$Prov2rutinBIL,alternative =
c("two.sided"),paired = TRUE)

    Paired t-test

data:  epi$Prov1rutinBIL and epi$Prov2rutinBIL
t = 2.5067, df = 30, p-value = 0.01783
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.6634288 6.4978615
sample estimates:
mean of the differences 
               3.580645 

> wilcox.test(epi$Prov1rutinBIL,epi$Prov2rutinBIL,alternative =
c("two.sided"),paired = TRUE)

    Wilcoxon signed rank test with continuity correction

data:  epi$Prov1rutinBIL and epi$Prov2rutinBIL
```

```
V = 258.5, p-value = 0.009943
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1rutinBIL, epi$Prov2rutinBIL, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1rutinBIL, epi$Prov2rutinBIL, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
> 
> boxplot(main="ALP",epi$Prov1rutinALP,epi$Prov2rutinALP)
> mean(epi$Prov1rutinALP, na.rm=TRUE)
[1] 1.64
> sd(epi$Prov1rutinALP, na.rm=TRUE)
[1] 1.045347
> mean(epi$Prov2rutinALP, na.rm=TRUE)
[1] 2.297813
> sd(epi$Prov2rutinALP, na.rm=TRUE)
[1] 1.302295
> t.test(epi$Prov1rutinALP,epi$Prov2rutinALP,alternative =
c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$Prov1rutinALP and epi$Prov2rutinALP
t = -2.6637, df = 31, p-value = 0.01215
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.1410564 -0.1514436
sample estimates:
mean of the differences 
               -0.64625 

> wilcox.test(epi$Prov1rutinALP,epi$Prov2rutinALP,alternative =
c("two.sided"),paired = TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$Prov1rutinALP and epi$Prov2rutinALP
V = 116, p-value = 0.009961
alternative hypothesis: true location shift is not equal to 0

Warning messages:
1: In wilcox.test.default(epi$Prov1rutinALP, epi$Prov2rutinALP, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
2: In wilcox.test.default(epi$Prov1rutinALP, epi$Prov2rutinALP, alternative =
c("two.sided"),  :
  cannot compute exact p-value with zeroes
> 
> 
> ###Diagrams for advanced tests 140520
> 
> 
> ###Boxplot coagulation factors
```

```
> dev.new(width=3)
> boxplot(main="Fibrinogen",epi$FIBpreop,epi$FIBpostop,horizontal=FALSE,
na.rm=TRUE, axes=TRUE,cex.main=1.65,cex.axis=1.5,cex.lab=1.45, ylab="Fibrinogen
concentration (g/L)", boxwex=1, col=c(24,0), lty=1,ylim=c(0,8), xlim=c(0,2.5))
> arrows(0.25,2,,4,code=0,lwd=2,lty=3)
> my.legend.size <-legend(0.2,1, c("Preoperative","Postoperative"), cex=
1,fill=c(24,0),plot=FALSE)
> my.legend.size
$rect
$rect$w
[1] 2.322804

$rect$h
[1] 1.004651

$rect$left
[1] 0.2

$rect$top
[1] 1


$text
$text$x
[1] 0.8443182 0.8443182

$text$y
[1] 0.6651163 0.3302326


> legend((2.5-my.legend.size$rect$w)/2,1, c("Preoperative","Postoperative"),
cex= 1,fill=c(24,0))
> mean(epi$FIBpreop, na.rm=TRUE)
[1] 3.159189
> sd(epi$FIBpreop, na.rm=TRUE)
[1] 0.941389
> mean(epi$FIBpostop, na.rm=TRUE)
[1] 5.84129
> sd(epi$FIBpostop, na.rm=TRUE)
[1] 1.08464
>
>
> #hist(epi$FIBpreop)
> #hist(epi$FIBpostop)
>
> t.test(epi$FIBpreop,epi$FIBpostop,alternative = c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$FIBpreop and epi$FIBpostop
t = -11.345, df = 30, p-value = 2.239e-12
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -3.081371 -2.141210
sample estimates:
mean of the differences
```

```
                -2.61129

> wilcox.test(epi$FIBpreop,epi$FIBpostop,alternative = c("two.sided"),paired =
TRUE)

    Wilcoxon signed rank test with continuity correction

data:  epi$FIBpreop and epi$FIBpostop
V = 3, p-value = 1.656e-06
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$FIBpreop, epi$FIBpostop, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
> x<-1
> y<-1.5
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-0.6,"**",pos=3, cex=1.4)
>
>
> boxplot(epi$F2preop,epi$F2postop,-100, epi$F7preop,epi$F7postop,-100, epi
$F9preop,epi$F9postop,-100, epi$F10preop,epi$F10postop,-100, epi$F11preop,epi
$F11postop,-100, epi$F12preop,epi$F12postop,-100, epi$F13preop,epi$F13postop,
horizontal=FALSE, na.rm=TRUE, axes=TRUE, main="Pre- and postoperative
concentrations of coagulation factors",cex.main=1.65,cex.axis=1.5,cex.lab=1.45,
ylab="Plasma concentration (kIE/L)", boxwex=1,
col=c(24,0,0,24,0,0,24,0,0,24,0,0,24,0,0,24,0,0,24,0,0,24,0,0),
lty=1,ylim=c(0.3,2.9),
names=c("F","2","","F","7","","F","9","","F","10","","F","11","","F","12","","F
","13"))
> legend(0,2.8, c("Preoperative","Postoperative"), cex= 1,fill=c(24,0))
> legend(5.7,5,lty=3,lwd=2,c("Reference range"))
> arrows(0.4,0.7,,1.5,code=0,lwd=2,lty=3)
> arrows(3.4,0.6,,1.6,code=0,lwd=2,lty=3)
> arrows(6.4,0.7,,1.3,code=0,lwd=2,lty=3)
> arrows(9.4,0.7,,1.52,code=0,lwd=2,lty=3)
> arrows(12.4,0.6,,1.3,code=0,lwd=2,lty=3)
> arrows(15.4,1.07,,1.5,code=0,lwd=2,lty=3)
> arrows(18.4,0.7,,1.4,code=0,lwd=2,lty=3)
>
>
>
> #hist(epi$F2preop)
> mean(epi$F2preop, na.rm=TRUE)
[1] 1.0395
> sd(epi$F2preop, na.rm=TRUE)
[1] 0.1941889
>
> #hist(epi$F2postop)
> mean(epi$F2postop, na.rm=TRUE)
[1] 1.038968
> sd(epi$F2postop, na.rm=TRUE)
[1] 0.2792906
>
```

```
> t.test(epi$F2preop, epi$F2postop,alternative = c("two.sided"),paired = TRUE)

    Paired t-test

data:  epi$F2preop and epi$F2postop
t = -0.57852, df = 30, p-value = 0.5672
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.13751286  0.07680318
sample estimates:
mean of the differences
            -0.03035484

> wilcox.test(epi$F2preop, epi$F2postop,alternative = c("two.sided"),paired =
TRUE)

    Wilcoxon signed rank test

data:  epi$F2preop and epi$F2postop
V = 224, p-value = 0.6496
alternative hypothesis: true location shift is not equal to 0

>
> hist(epi$F7preop)
> mean(epi$F7preop, na.rm=TRUE)
[1] 1.101763
> sd(epi$F7preop, na.rm=TRUE)
[1] 0.2338181
>
> #hist(epi$F7postop)
> mean(epi$F7postop, na.rm=TRUE)
[1] 1.003161
> sd(epi$F7postop, na.rm=TRUE)
[1] 0.2336632
>
> t.test(epi$F7preop, epi$F7postop,alternative = c("two.sided"),paired = TRUE)

    Paired t-test

data:  epi$F7preop and epi$F7postop
t = 1.8705, df = 30, p-value = 0.0712
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.00623686  0.14204331
sample estimates:
mean of the differences
             0.06790323

> wilcox.test(epi$F7preop, epi$F7postop,alternative = c("two.sided"),paired =
TRUE)

    Wilcoxon signed rank test

data:  epi$F7preop and epi$F7postop
V = 323, p-value = 0.1461
alternative hypothesis: true location shift is not equal to 0
```

```
> #N/S
> x<-1
> y<-85
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-3,"**",pos=3, cex=1.4)
> 
> #hist(epi$F9preop)
> mean(epi$F9preop, na.rm=TRUE)
[1] 1.075526
> sd(epi$F9preop, na.rm=TRUE)
[1] 0.258687
> 
> #hist(epi$F9postop)
> mean(epi$F9postop, na.rm=TRUE)
[1] 1.522516
> sd(epi$F9postop, na.rm=TRUE)
[1] 0.3873196
> 
> t.test(epi$F9preop, epi$F9postop,alternative = c("two.sided"),paired = TRUE)

	Paired t-test

data:  epi$F9preop and epi$F9postop
t = -6.5032, df = 30, p-value = 3.448e-07
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.6060707 -0.3163809
sample estimates:
mean of the differences 
             -0.4612258 

> wilcox.test(epi$F9preop, epi$F9postop,alternative = c("two.sided"),paired =
TRUE)

	Wilcoxon signed rank test

data:  epi$F9preop and epi$F9postop
V = 22, p-value = 4.992e-07
alternative hypothesis: true location shift is not equal to 0

> x<-7
> y<-2.7
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-0.1,"**",pos=3, cex=1.4)
> 
> #hist(epi$F10preop)
> mean(epi$F10preop, na.rm=TRUE)
[1] 0.8509737
> sd(epi$F10preop, na.rm=TRUE)
[1] 0.1776195
> 
> #hist(epi$F10postop)
> mean(epi$F10postop, na.rm=TRUE)
```

```
[1] 0.9247742
> sd(epi$F10postop, na.rm=TRUE)
[1] 0.2636621
>
> t.test(epi$F10preop, epi$F10postop,alternative = c("two.sided"),paired =
TRUE)

	Paired t-test

data:  epi$F10preop and epi$F10postop
t = -2.0785, df = 30, p-value = 0.04631
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.163017255 -0.001434358
sample estimates:
mean of the differences
            -0.08222581

> wilcox.test(epi$F10preop, epi$F10postop,alternative = c("two.sided"),paired =
TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$F10preop and epi$F10postop
V = 146, p-value = 0.04669
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$F10preop, epi$F10postop, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
> x<-10
> y<-2.7
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-0.1,"*",pos=3, cex=1.4)
>
> #hist(epi$F11preop)
> mean(epi$F11preop, na.rm=TRUE)
[1] 1.023395
> sd(epi$F11preop, na.rm=TRUE)
[1] 0.2127542
>
> #hist(epi$F11postop)
> mean(epi$F11postop, na.rm=TRUE)
[1] 1.063677
> sd(epi$F11postop, na.rm=TRUE)
[1] 0.3265792
>
> t.test(epi$F11preop, epi$F11postop,alternative = c("two.sided"),paired =
TRUE)

	Paired t-test

data:  epi$F11preop and epi$F11postop
t = -1.2461, df = 30, p-value = 0.2224
```

```
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.1531418  0.0370773
sample estimates:
mean of the differences
            -0.05803226

> wilcox.test(epi$F11preop, epi$F11postop,alternative = c("two.sided"),paired =
TRUE)

	Wilcoxon signed rank test with continuity correction

data:  epi$F11preop and epi$F11postop
V = 189.5, p-value = 0.2557
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$F11preop, epi$F11postop, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
> #N/S
> x<-10
> y<-2.7
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-0.1,"*",pos=3, cex=1.4)
>
>
> #hist(epi$F12preop)
> mean(epi$F12preop, na.rm=TRUE)
[1] 0.9438158
> sd(epi$F12preop, na.rm=TRUE)
[1] 0.2528337
>
> #hist(epi$F12postop)
> mean(epi$F12postop, na.rm=TRUE)
[1] 0.7950968
> sd(epi$F12postop, na.rm=TRUE)
[1] 0.3280546
>
> t.test(epi$F12preop, epi$F12postop,alternative = c("two.sided"),paired =
TRUE)

	Paired t-test

data:  epi$F12preop and epi$F12postop
t = 5.3943, df = 30, p-value = 7.652e-06
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.1001053 0.2220882
sample estimates:
mean of the differences
              0.1610968

> wilcox.test(epi$F12preop, epi$F12postop,alternative = c("two.sided"),paired =
TRUE)
```

```
    Wilcoxon signed rank test with continuity correction

data:  epi$F12preop and epi$F12postop
V = 454, p-value = 5.645e-05
alternative hypothesis: true location shift is not equal to 0

Warning message:
In wilcox.test.default(epi$F12preop, epi$F12postop, alternative =
c("two.sided"),  :
  cannot compute exact p-value with ties
> x<-16
> y<-2.7
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
> text(x+0.5,y-0.1,"**",pos=3, cex=1.4)
>
> #hist(epi$F13preop)
> mean(epi$F13preop, na.rm=TRUE)
[1] 1.203579
> sd(epi$F13preop, na.rm=TRUE)
[1] 0.3481401
>
> #hist(epi$F13postop)
> mean(epi$F13postop, na.rm=TRUE)
[1] 0.7787742
> sd(epi$F13postop, na.rm=TRUE)
[1] 0.2205076
>
> t.test(epi$F13preop, epi$F13postop,alternative = c("two.sided"),paired =
TRUE)

    Paired t-test

data:  epi$F13preop and epi$F13postop
t = 8.4888, df = 30, p-value = 1.794e-09
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.2953388 0.4824676
sample estimates:
mean of the differences
              0.3889032

> wilcox.test(epi$F13preop, epi$F13postop,alternative = c("two.sided"),paired =
TRUE)

    Wilcoxon signed rank test

data:  epi$F13preop and epi$F13postop
V = 496, p-value = 9.313e-10
alternative hypothesis: true location shift is not equal to 0

> x<-19
> y<-2.7
> arrows(x,y,x+1,y, length=0.05, angle=90, code=1)
> arrows(x,y,x+1,y, length=0.05, angle=90, code=2)
```

```
> text(x+0.5,y-0.1,"**",pos=3, cex=1.4)
>
>
> mean(epi$Prov2rutinCRP,na.rm=TRUE)
[1] 91.96667
> sd(epi$Prov2rutinCRP,na.rm=TRUE)
[1] 59.82762
> hist(epi$Prov2rutinCRP)
>
> mean(epi$Prov1rutinPK,na.rm=TRUE)
[1] 1.029412
> sd(epi$Prov1rutinPK,na.rm=TRUE)
[1] 0.08714117
> hist(epi$Prov1rutinPK)
>
> mean(epi$Prov2rutinPK,na.rm=TRUE)
[1] 1.168571
> sd(epi$Prov2rutinPK,na.rm=TRUE)
[1] 0.1529541
> hist(epi$Prov2rutinPK)
>
>
> mean(epi$Prov1rutinAPTT,na.rm=TRUE)
[1] 27
> sd(epi$Prov1rutinAPTT,na.rm=TRUE)
[1] 2.872281
> hist(epi$Prov1rutinAPTT)
>
> mean(epi$Prov2rutinAPTT,na.rm=TRUE)
[1] 29.6
> sd(epi$Prov2rutinAPTT,na.rm=TRUE)
[1] 4.447074
> hist(epi$Prov2rutinAPTT)
>
>
> mean(epi$Prov1rutinTPK,na.rm=TRUE)
[1] 213.1053
> sd(epi$Prov1rutinTPK,na.rm=TRUE)
[1] 72.11282
> hist(epi$Prov1rutinTPK)
>
> mean(epi$Prov2rutinTPK,na.rm=TRUE)
[1] 283.0645
> sd(epi$Prov2rutinTPK,na.rm=TRUE)
[1] 153.446
> hist(epi$Prov2rutinTPK)
>
>
> #Correlation between withdrawal time and TPK
> hist(epi$withdrawaltime)
>
> plot(epi$withdrawaltime, epi$Prov2rutinTPK, xlab="Day of epidural
withdrawal", ylab = "Platelet count (millions/mL)", abline(lm(epi
$Prov2rutinTPK~epi$withdrawaltime)),cex.main=1.3, cex.lab=1.4)
> cor.test(epi$withdrawaltime, epi$Prov2rutinTPK, use="complete.obs",
method="pearson")
```

```

	Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$Prov2rutinTPK
t = 3.6065, df = 29, p-value = 0.001151
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.2517544 0.7607874
sample estimates:
     cor 
0.556455 

> cor.test(epi$withdrawaltime, epi$Prov2rutinTPK, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$Prov2rutinTPK
S = 2363, p-value = 0.002504
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.5235982 

Warning message:
In cor.test.default(epi$withdrawaltime, epi$Prov2rutinTPK, use = 
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=13, y=700, "P<0.01", pos=3, cex=2)
> text(x=13, y=640, "r=0.56", pos=3, cex=2)
> 
> ####SMALL DIAGRAMS FOR COMPOSITE PLOT
> 
> #Standard plot
> cor.test(epi$XPARAM, epi$YPARAM, use="complete.obs", method="pearson")
Error in cor.test.default(epi$XPARAM, epi$YPARAM, use = "complete.obs",  : 
  'x' must be a numeric vector
> cor.test(epi$XPARAM, epi$YPARAM, use="complete.obs", method="spearman")
Error in cor.test.default(epi$XPARAM, epi$YPARAM, use = "complete.obs",  : 
  'x' must be a numeric vector
> #RESULT:
> plot(epi$XPARAM, epi$YPARAM, xlab="", ylab = "", cex.axis=3, cex=2.5, pch=19, 
axes=F)
Error in plot.window(...) : need finite 'xlim' values
In addition: Warning messages:
1: In min(x) : no non-missing arguments to min; returning Inf
2: In max(x) : no non-missing arguments to max; returning -Inf
3: In min(x) : no non-missing arguments to min; returning Inf
4: In max(x) : no non-missing arguments to max; returning -Inf
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #INR vs EXTEM-MCF
> cor.test(epi$Prov2rutinPK, epi$Prov2extemMCF, use="complete.obs", 
```

```
method="pearson")

    Pearson's product-moment correlation

data:  epi$Prov2rutinPK and epi$Prov2extemMCF
t = -1.4426, df = 31, p-value = 0.1592
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.5470235  0.1012061
sample estimates:
       cor 
-0.2508175 

> cor.test(epi$Prov2rutinPK, epi$Prov2extemMCF, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$Prov2rutinPK and epi$Prov2extemMCF
S = 6546.7, p-value = 0.6027
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho 
-0.09402775 

Warning message:
In cor.test.default(epi$Prov2rutinPK, epi$Prov2extemMCF, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinPK, epi$Prov2extemMCF, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #INR vs EXTEM-CT
> cor.test(epi$Prov2rutinPK, epi$Prov2extemCT, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$Prov2rutinPK and epi$Prov2extemCT
t = 1.1177, df = 31, p-value = 0.2723
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1571117  0.5059370
sample estimates:
      cor 
0.1968129 

> cor.test(epi$Prov2rutinPK, epi$Prov2extemCT, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho
```

```
data:  epi$Prov2rutinPK and epi$Prov2extemCT
S = 5462.4, p-value = 0.6296
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
0.08716727

Warning message:
In cor.test.default(epi$Prov2rutinPK, epi$Prov2extemCT, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinPK, epi$Prov2extemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #INR vs INTEM-CT
> cor.test(epi$Prov2rutinPK, epi$Prov2intemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinPK and epi$Prov2intemCT
t = -0.50255, df = 31, p-value = 0.6188
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4202349  0.2614838
sample estimates:
        cor
-0.08989508

> cor.test(epi$Prov2rutinPK, epi$Prov2intemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinPK and epi$Prov2intemCT
S = 6241.9, p-value = 0.8118
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho
-0.04309158

Warning message:
In cor.test.default(epi$Prov2rutinPK, epi$Prov2intemCT, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinPK, epi$Prov2intemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
```

```
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
> #INR vs FIBTEM-MCF
> cor.test(epi$Prov2rutinPK, epi$Prov2fibtemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinPK and epi$Prov2fibtemMCF
t = -0.99309, df = 31, p-value = 0.3284
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4893990  0.1784758
sample estimates:
       cor
-0.1755922

> cor.test(epi$Prov2rutinPK, epi$Prov2fibtemMCF, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinPK and epi$Prov2fibtemMCF
S = 6137.7, p-value = 0.8872
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho
-0.02568291

Warning message:
In cor.test.default(epi$Prov2rutinPK, epi$Prov2fibtemMCF, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinPK, epi$Prov2fibemMCF, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #aPTT vs INTEM-CT
> cor.test(epi$Prov2rutinAPTT, epi$Prov2intemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinAPTT and epi$Prov2intemCT
t = -0.89483, df = 31, p-value = 0.3778
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4760559  0.1952656
sample estimates:
       cor
```

```
-0.1586808

> cor.test(epi$Prov2rutinAPTT, epi$Prov2intemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinAPTT and epi$Prov2intemCT
S = 6583.8, p-value = 0.5789
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
-0.100237 

Warning message:
In cor.test.default(epi$Prov2rutinAPTT, epi$Prov2intemCT, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinAPTT, epi$Prov2intemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> 
> #aPTT vs EXTEM-MCF
> cor.test(epi$Prov2rutinAPTT, epi$Prov2extemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinAPTT and epi$Prov2extemMCF
t = -0.16956, df = 31, p-value = 0.8665
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3698837  0.3161730
sample estimates:
        cor 
-0.03044012 

> cor.test(epi$Prov2rutinAPTT, epi$Prov2extemMCF, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinAPTT and epi$Prov2extemMCF
S = 5841.2, p-value = 0.8951
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
0.02386784 

Warning message:
```

```
In cor.test.default(epi$Prov2rutinAPTT, epi$Prov2extemMCF, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinAPTT, epi$Prov2extemMCF, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #aPTT vs EXTEM-CT
> cor.test(epi$Prov2rutinAPTT, epi$Prov2extemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinAPTT and epi$Prov2extemCT
t = 0.96335, df = 31, p-value = 0.3428
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1835627  0.4853891
sample estimates:
      cor
0.1704904

> cor.test(epi$Prov2rutinAPTT, epi$Prov2extemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinAPTT and epi$Prov2extemCT
S = 6474.8, p-value = 0.65
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho
-0.08202175

Warning message:
In cor.test.default(epi$Prov2rutinAPTT, epi$Prov2extemCT, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinAPTT, epi$Prov2extemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #aPTT vs FIBTEM-MCF
> cor.test(epi$Prov2rutinAPTT, epi$Prov2fibtemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation
```

```
data:  epi$Prov2rutinAPTT and epi$Prov2fibtemMCF
t = -0.9046, df = 31, p-value = 0.3727
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4773939  0.1935995
sample estimates:
       cor 
-0.1603683 

> cor.test(epi$Prov2rutinAPTT, epi$Prov2fibtemMCF, use="complete.obs", 
method="spearman")

    Spearman's rank correlation rho

data:  epi$Prov2rutinAPTT and epi$Prov2fibtemMCF
S = 6003.7, p-value = 0.9855
alternative hypothesis: true rho is not equal to 0
sample estimates:
         rho 
-0.003286168 

Warning message:
In cor.test.default(epi$Prov2rutinAPTT, epi$Prov2fibtemMCF, use = 
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinAPTT, epi$Prov2fibtemMCF, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #aPTT vs FIBTEM-CT
> cor.test(epi$Prov2rutinAPTT, epi$Prov2fibtemCT, use="complete.obs", 
method="pearson")

    Pearson's product-moment correlation

data:  epi$Prov2rutinAPTT and epi$Prov2fibtemCT
t = 1.129, df = 31, p-value = 0.2676
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1551655  0.5074197
sample estimates:
      cor 
0.1987298 

> cor.test(epi$Prov2rutinAPTT, epi$Prov2fibtemCT, use="complete.obs", 
method="spearman")

    Spearman's rank correlation rho

data:  epi$Prov2rutinAPTT and epi$Prov2fibtemCT
S = 4797.7, p-value = 0.2687
alternative hypothesis: true rho is not equal to 0
```

```
sample estimates:
      rho 
0.1982488 

Warning message:
In cor.test.default(epi$Prov2rutinAPTT, epi$Prov2fibtemCT, use = 
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinAPTT, epi$Prov2fibtemCT, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #Plc vs EXTEM-MCF
> cor.test(epi$Prov2rutinTPK, epi$Prov2extemMCF, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinTPK and epi$Prov2extemMCF
t = 3.7841, df = 29, p-value = 0.0007166
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.2770366 0.7720028
sample estimates:
      cor 
0.5749378 

> cor.test(epi$Prov2rutinTPK, epi$Prov2extemMCF, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinTPK and epi$Prov2extemMCF
S = 1981.3, p-value = 0.0003543
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.6005494 

Warning message:
In cor.test.default(epi$Prov2rutinTPK, epi$Prov2extemMCF, use = 
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinTPK, epi$Prov2extemMCF, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2extemMCF~ epi$Prov2rutinTPK),lwd=3))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(500, 55 , "r=0.57 **", pos=3, cex=7)
> 
```

```
>
> #Plc vs EXTEM-CT
> cor.test(epi$Prov2rutinTPK, epi$Prov2extemCT, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$Prov2rutinTPK and epi$Prov2extemCT
t = -0.19277, df = 29, p-value = 0.8485
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3852304  0.3226567
sample estimates:
        cor
-0.03577342

> cor.test(epi$Prov2rutinTPK, epi$Prov2extemCT, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$Prov2rutinTPK and epi$Prov2extemCT
S = 4601.2, p-value = 0.699
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
0.07233799

Warning message:
In cor.test.default(epi$Prov2rutinTPK, epi$Prov2extemCT, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinTPK, epi$Prov2extemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #Plc vs INTEM-CT
> cor.test(epi$Prov2rutinTPK, epi$Prov2intemCT, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$Prov2rutinTPK and epi$Prov2intemCT
t = 0.4713, df = 29, p-value = 0.641
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.2756719  0.4282934
sample estimates:
       cor
0.08718459

> cor.test(epi$Prov2rutinTPK, epi$Prov2intemCT, use="complete.obs",
```

```
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinTPK and epi$Prov2intemCT
S = 5611.2, p-value = 0.4814
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.1312897

Warning message:
In cor.test.default(epi$Prov2rutinTPK, epi$Prov2intemCT, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinTPK, epi$Prov2intemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #Plc vs FIBTEM-MCF
> cor.test(epi$Prov2rutinTPK, epi$Prov2fibtemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinTPK and epi$Prov2fibtemMCF
t = 3.5516, df = 29, p-value = 0.001331
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.2437729 0.7571824
sample estimates:
      cor
0.5505567

> cor.test(epi$Prov2rutinTPK, epi$Prov2fibtemMCF, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinTPK and epi$Prov2fibtemMCF
S = 1826, p-value = 0.0001375
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.6318629

Warning message:
In cor.test.default(epi$Prov2rutinTPK, epi$Prov2fibtemMCF, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinTPK, epi$Prov2fibtemMCF, xlab="", ylab = "", cex.axis=3,
```

```
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2fibtemMCF~epi$Prov2rutinTPK),lwd=3))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(550, 20 , "r=0.55 **", cex=7)
>
>
> #DD vs EXTEM-MCF
> cor.test(epi$DDpostop, epi$Prov2extemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$DDpostop and epi$Prov2extemMCF
t = 1.1426, df = 29, p-value = 0.2626
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1584429  0.5233974
sample estimates:
      cor
0.2075496

> cor.test(epi$DDpostop, epi$Prov2extemMCF, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$DDpostop and epi$Prov2extemMCF
S = 3875.7, p-value = 0.2374
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.2186031

Warning message:
In cor.test.default(epi$DDpostop, epi$Prov2extemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$DDpostop, epi$Prov2extemMCF, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #DD vs EXTEM-CT
> cor.test(epi$DDpostop, epi$Prov2extemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$DDpostop and epi$Prov2extemCT
t = -2.5824, df = 29, p-value = 0.01513
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
```

```
 -0.6822053 -0.0921686
sample estimates:
       cor
-0.4323874

> cor.test(epi$DDpostop, epi$Prov2extemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$DDpostop and epi$Prov2extemCT
S = 6410.6, p-value = 0.1104
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.2924667

Warning message:
In cor.test.default(epi$DDpostop, epi$Prov2extemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$DDpostop, epi$Prov2extemCT, xlab="", ylab = "", cex.axis=3, cex=2.5,
pch=19, axes=F,abline(lm(epi$Prov2extemCT~ epi$DDpostop),lwd=3,lty=2))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(3.7,70,"r=-0.43*",cex=7)
> #Note: given the outler with a really high D-Dimer, and that the non-
parametric test does not give significance while the parametric one does, I
have counted this as a 'non-significant' result. /OT
>
> #DD vs INTEM-CT
> cor.test(epi$DDpostop, epi$Prov2intemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$DDpostop and epi$Prov2intemCT
t = -0.17456, df = 29, p-value = 0.8626
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3823491  0.3256805
sample estimates:
        cor
-0.03239841

> cor.test(epi$DDpostop, epi$Prov2intemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$DDpostop and epi$Prov2intemCT
S = 5913.5, p-value = 0.3002
alternative hypothesis: true rho is not equal to 0
sample estimates:
```

```
      rho 
-0.192234 

Warning message:
In cor.test.default(epi$DDpostop, epi$Prov2intemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$DDpostop, epi$Prov2intemCT, xlab="", ylab = "", cex.axis=3, cex=2.5, 
pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #DD vs FIBTEM-MCF
> cor.test(epi$DDpostop, epi$Prov2fibtemMCF, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$DDpostop and epi$Prov2fibtemMCF
t = 3.1564, df = 29, p-value = 0.003709
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1843580 0.7293265
sample estimates:
      cor 
0.5056653 

> cor.test(epi$DDpostop, epi$Prov2fibtemMCF, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$DDpostop and epi$Prov2fibtemMCF
S = 1948.5, p-value = 0.0002926
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.6071597 

Warning message:
In cor.test.default(epi$DDpostop, epi$Prov2fibtemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$DDpostop, epi$Prov2fibtemMCF, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2fibtemMCF~ epi$DDpostop),lwd=3))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(3.5, 22 , "r=0.51**", cex=7, pos=1)
> 
> #Fibrinogen vs EXTEM-MCF
> cor.test(epi$FIBpostop, epi$Prov2extemMCF, use="complete.obs", 
method="pearson")
```

```
    Pearson's product-moment correlation

data:  epi$FIBpostop and epi$Prov2extemMCF
t = 2.2847, df = 29, p-value = 0.02983
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.04203983 0.65434600
sample estimates:
     cor 
0.390562 

> cor.test(epi$FIBpostop, epi$Prov2extemMCF, use="complete.obs", 
method="spearman")

    Spearman's rank correlation rho

data:  epi$FIBpostop and epi$Prov2extemMCF
S = 3458.5, p-value = 0.09785
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.3027318 

Warning message:
In cor.test.default(epi$FIBpostop, epi$Prov2extemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$FIBpostop, epi$Prov2extemMCF, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2extemMCF~ epi
$FIBpostop),lwd=3,lty=2))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> epi$Prov2extemMCF
 [1] 71 76 74 75 77 73 73 73 75 68 77 74 66 70 NA 63 69 80 68 NA 71 64 72 65 63
[26] NA 60 54 NA NA 80 76 77 75 77 73 79 77
> text(6.4,58,"r=0.39*",cex=8)
> #NB given that the non-parametric test is non-significant, parametric sig.
> 
> #Fibrinogen vs EXTEM-CT
> cor.test(epi$FIBpostop, epi$Prov2extemCT, use="complete.obs", 
method="pearson")

    Pearson's product-moment correlation

data:  epi$FIBpostop and epi$Prov2extemCT
t = -1.6132, df = 29, p-value = 0.1175
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.58211669  0.07499732
sample estimates:
       cor 
-0.2869689 
```

```
> cor.test(epi$FIBpostop, epi$Prov2extemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$FIBpostop and epi$Prov2extemCT
S = 7078.1, p-value = 0.01658
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.4270374 

Warning message:
In cor.test.default(epi$FIBpostop, epi$Prov2extemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$FIBpostop, epi$Prov2extemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2extemCT~ epi
$FIBpostop),lwd=3,lty=2))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(5.5,30,"rho=-0.42*",cex=6)
> #NB given that the non-parametric but not the parametric test is significant,
I have not counted this as significant.
> 
> #Fibrinogen vs INTEM-CT
> cor.test(epi$FIBpostop, epi$Prov2intemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$FIBpostop and epi$Prov2intemCT
t = -0.13747, df = 29, p-value = 0.8916
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3764550  0.3318216
sample estimates:
        cor 
-0.02551897 

> cor.test(epi$FIBpostop, epi$Prov2intemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$FIBpostop and epi$Prov2intemCT
S = 4353.6, p-value = 0.5124
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.1222554 

Warning message:
In cor.test.default(epi$FIBpostop, epi$Prov2intemCT, use = "complete.obs",  :
```

```
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$FIBpostop, epi$Prov2intemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #Fibrinogen vs FIBTEM-MCF
> cor.test(epi$FIBpostop, epi$fibtemMCF, use="complete.obs", method="pearson")
Error in cor.test.default(epi$FIBpostop, epi$fibtemMCF, use =
"complete.obs",  :
  'x' and 'y' must have the same length
> cor.test(epi$FIBpostop, epi$fibtemMCF, use="complete.obs", method="spearman")
Error in cor.test.default(epi$FIBpostop, epi$fibtemMCF, use =
"complete.obs",  :
  'x' and 'y' must have the same length
> #RESULT:
> plot(epi$FIBpostop, epi$fibtemMCF, xlab="", ylab = "", cex.axis=3, cex=2.5,
pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #F2 vs EXTEM-MCF
> cor.test(epi$F2postop, epi$Prov2extemMCF, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F2postop and epi$Prov2extemMCF
t = 1.2043, df = 29, p-value = 0.2382
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1475097  0.5314781
sample estimates:
      cor
0.2182373

> cor.test(epi$F2postop, epi$Prov2extemMCF, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F2postop and epi$Prov2extemMCF
S = 4169.9, p-value = 0.392
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.1592969

Warning message:
In cor.test.default(epi$F2postop, epi$Prov2extemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
```

```
> #RESULT:
> plot(epi$F2postop, epi$Prov2extemMCF, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
> #F2 vs EXTEM-CT
> cor.test(epi$F2postop, epi$Prov2extemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F2postop and epi$Prov2extemCT
t = -1.5235, df = 29, p-value = 0.1385
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.57143614  0.09089247
sample estimates:
       cor
-0.2722148

> cor.test(epi$F2postop, epi$Prov2extemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F2postop and epi$Prov2extemCT
S = 6559.9, p-value = 0.07676
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.3225616

Warning message:
In cor.test.default(epi$F2postop, epi$Prov2extemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F2postop, epi$Prov2extemCT, xlab="", ylab = "", cex.axis=3, cex=2.5,
pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #F2 vs INTEM-CT
> cor.test(epi$F2postop, epi$Prov2intemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F2postop and epi$Prov2intemCT
t = -0.95783, df = 29, p-value = 0.3461
alternative hypothesis: true correlation is not equal to 0
```

```
95 percent confidence interval:
 -0.4985228  0.1910803
sample estimates:
       cor 
-0.1751165 

> cor.test(epi$F2postop, epi$Prov2intemCT, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F2postop and epi$Prov2intemCT
S = 5693.4, p-value = 0.4273
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.1478568 

Warning message:
In cor.test.default(epi$F2postop, epi$Prov2intemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F2postop, epi$Prov2intemCT, xlab="", ylab = "", cex.axis=3, cex=2.5, 
pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #F2 vs FIBTEM-MCF
> cor.test(epi$F2postop, epi$Prov2fibtemMCF, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F2postop and epi$Prov2fibtemMCF
t = 2.7334, df = 29, p-value = 0.01057
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1170382 0.6954189
sample estimates:
      cor 
0.4526081 

> cor.test(epi$F2postop, epi$Prov2fibtemMCF, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F2postop and epi$Prov2fibtemMCF
S = 3387.6, p-value = 0.08226
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.3170251 
```

```
Warning message:
In cor.test.default(epi$F2postop, epi$Prov2fibtemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F2postop, epi$Prov2fibtemMCF, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2fibtemMCF~ epi$F2postop),lwd=3,
lty=2))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.5,22,"r=0.45*",cex=7,pos=1)
>
>
>
> #F7 vs EXTEM-MCF
> cor.test(epi$F7postop, epi$Prov2extemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F7postop and epi$Prov2extemMCF
t = 0.97461, df = 29, p-value = 0.3378
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1881239  0.5008238
sample estimates:
      cor 
0.1780875 

> cor.test(epi$F7postop, epi$Prov2extemMCF, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F7postop and epi$Prov2extemMCF
S = 4588.5, p-value = 0.6889
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
0.07489179 

Warning message:
In cor.test.default(epi$F7postop, epi$Prov2extemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F7postop, epi$Prov2extemMCF, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
> #F7 vs EXTEM-CT
> cor.test(epi$F7postop, epi$Prov2extemCT, use="complete.obs",
```

```
method="pearson")

	Pearson's product-moment correlation

data:  epi$F7postop and epi$Prov2extemCT
t = -1.6856, df = 29, p-value = 0.1026
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.59055327  0.06220115
sample estimates:
       cor 
-0.2987229 

> cor.test(epi$F7postop, epi$Prov2extemCT, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F7postop and epi$Prov2extemCT
S = 7005.7, p-value = 0.02113
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.4124426 

Warning message:
In cor.test.default(epi$F7postop, epi$Prov2extemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F7postop, epi$Prov2extemCT, xlab="", ylab = "", cex.axis=3, cex=2.5, 
pch=19, axes=F,abline(lm(epi$Prov2extemCT~ epi$F7postop),lwd=3,lty=2))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.1,70,"rho=-0.41",cex=6)
> 
> #F7 vs intem-CT
> cor.test(epi$F7postop, epi$Prov2intemCT, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F7postop and epi$Prov2intemCT
t = -1.1018, df = 29, p-value = 0.2796
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.5179922  0.1656640
sample estimates:
       cor 
-0.2004424 

> cor.test(epi$F7postop, epi$Prov2intemCT, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho
```

```
data:  epi$F7postop and epi$Prov2intemCT
S = 5766.4, p-value = 0.3822
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
-0.162582 

Warning message:
In cor.test.default(epi$F7postop, epi$Prov2intemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F7postop, epi$Prov2intemCT, xlab="", ylab = "", cex.axis=3, cex=2.5, 
pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #F7 vs fibtem-MCF
> cor.test(epi$F7postop, epi$Prov2fibtemMCF, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F7postop and epi$Prov2fibtemMCF
t = 1.1696, df = 29, p-value = 0.2517
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.153646  0.526958
sample estimates:
      cor 
0.2122496 

> cor.test(epi$F7postop, epi$Prov2fibtemMCF, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F7postop and epi$Prov2fibtemMCF
S = 4154.7, p-value = 0.3829
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.1623541 

Warning message:
In cor.test.default(epi$F7postop, epi$Prov2fibtemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F7postop, epi$Prov2fibtemMCF, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
```

```
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
> #F9 vs EXTEM-MCF
> cor.test(epi$F9postop, epi$Prov2extemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F9postop and epi$Prov2extemMCF
t = 2.1374, df = 29, p-value = 0.04113
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.0167591 0.6396360
sample estimates:
      cor
0.3689085

> cor.test(epi$F9postop, epi$Prov2extemMCF, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F9postop and epi$Prov2extemMCF
S = 3572.5, p-value = 0.1275
alternative hypothesis: true rho is not equal to 0
sample estimates:
     rho
0.279731

Warning message:
In cor.test.default(epi$F9postop, epi$Prov2extemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F9postop, epi$Prov2extemMCF, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2extemMCF~ epi
$F9postop),lwd=3,lty=2))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(2,63,"r=0.37*",cex=7)
>
> #F9 vs EXTEM-CT
> cor.test(epi$F9postop, epi$Prov2extemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F9postop and epi$Prov2extemCT
t = -0.32209, df = 29, p-value = 0.7497
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4054660  0.3010043
sample estimates:
        cor
```

```
-0.05970371

> cor.test(epi$F9postop, epi$Prov2extemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F9postop and epi$Prov2extemCT
S = 5615.2, p-value = 0.4787
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.1320947

Warning message:
In cor.test.default(epi$F9postop, epi$Prov2extemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F9postop, epi$Prov2extemCT, xlab="", ylab = "", cex.axis=3, cex=2.5,
pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #F9 vs INTEM-CT
> cor.test(epi$F9postop, epi$Prov2intemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F9postop and epi$Prov2intemCT
t = -0.77183, df = 29, p-value = 0.4465
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4724640  0.2237109
sample estimates:
       cor
-0.1418756

> cor.test(epi$F9postop, epi$Prov2intemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F9postop and epi$Prov2intemCT
S = 4669.9, p-value = 0.7546
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
0.05849723

Warning message:
In cor.test.default(epi$F9postop, epi$Prov2intemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
```

```
> plot(epi$F9postop, epi$Prov2intemCT, xlab="", ylab = "", cex.axis=3, cex=2.5, 
pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #F9 vs FIBTEM-MCF
> cor.test(epi$F9postop, epi$Prov2intemMCF, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F9postop and epi$Prov2intemMCF
t = -0.79539, df = 29, p-value = 0.4328
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4758202  0.2195940
sample estimates:
       cor 
-0.1461155 

> cor.test(epi$F9postop, epi$Prov2intemMCF, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F9postop and epi$Prov2intemMCF
S = 4941.9, p-value = 0.9845
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho 
0.003645607 

Warning message:
In cor.test.default(epi$F9postop, epi$Prov2intemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F9postop, epi$Prov2intemMCF, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #F10 vs EXTEM-MCF
> cor.test(epi$F10postop, epi$Prov2extemMCF, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F10postop and epi$Prov2extemMCF
t = 2.4071, df = 29, p-value = 0.02267
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
```

```
 0.06282767 0.66610425
sample estimates:
      cor 
0.4080829 

> cor.test(epi$F10postop, epi$Prov2extemMCF, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F10postop and epi$Prov2extemMCF
S = 3348.5, p-value = 0.07453
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.3249012 

Warning message:
In cor.test.default(epi$F10postop, epi$Prov2extemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F10postop, epi$Prov2extemMCF, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2extemMCF~ epi
$F10postop),lwd=3,lty=2))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.2,58,"r=0.41*",cex=7)
> 
> #F10 vs EXTEM-CT
> cor.test(epi$F10postop, epi$Prov2extemCT, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F10postop and epi$Prov2extemCT
t = -0.74502, df = 29, p-value = 0.4623
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4686249  0.2283897
sample estimates:
       cor 
-0.1370408 

> cor.test(epi$F10postop, epi$Prov2extemCT, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F10postop and epi$Prov2extemCT
S = 6103.2, p-value = 0.2122
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.2304821 
```

```
Warning message:
In cor.test.default(epi$F10postop, epi$Prov2extemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F10postop, epi$Prov2extemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #F10 vs INTEM-CT
> cor.test(epi$F10postop, epi$Prov2intemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F10postop and epi$Prov2intemCT
t = -0.32822, df = 29, p-value = 0.7451
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4064152  0.2999704
sample estimates:
        cor
-0.06083604

> cor.test(epi$F10postop, epi$Prov2intemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F10postop and epi$Prov2intemCT
S = 4909, p-value = 0.9562
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
0.01028848

Warning message:
In cor.test.default(epi$F10postop, epi$Prov2intemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F10postop, epi$Prov2intemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #F10 vs FIBTEM-MCF
> cor.test(epi$F10postop, epi$Prov2intemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation
```

```
data:  epi$F10postop and epi$Prov2intemMCF
t = 0.59596, df = 29, p-value = 0.5558
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.2542543  0.4469167
sample estimates:
      cor 
0.1099956 

> cor.test(epi$F10postop, epi$Prov2intemMCF, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F10postop and epi$Prov2intemMCF
S = 4177.4, p-value = 0.3966
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.1577897 

Warning message:
In cor.test.default(epi$F10postop, epi$Prov2intemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F10postop, epi$Prov2intemMCF, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #F11 vs EXTEM-MCF
> cor.test(epi$F11postop, epi$Prov2extemMCF, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F11postop and epi$Prov2extemMCF
t = 1.7109, df = 29, p-value = 0.09778
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.05774782  0.59345628
sample estimates:
      cor 
0.3027881 

> cor.test(epi$F11postop, epi$Prov2extemMCF, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F11postop and epi$Prov2extemMCF
S = 4471, p-value = 0.5978
alternative hypothesis: true rho is not equal to 0
```

```
sample estimates:
       rho 
0.09858373 

Warning message:
In cor.test.default(epi$F11postop, epi$Prov2extemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F11postop, epi$Prov2extemMCF, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #F11 vs EXTEM-CT
> cor.test(epi$F11postop, epi$Prov2extemCT, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F11postop and epi$Prov2extemCT
t = -0.91083, df = 29, p-value = 0.3699
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4920325  0.1993526
sample estimates:
       cor 
-0.1667678 

> cor.test(epi$F11postop, epi$Prov2extemCT, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F11postop and epi$Prov2extemCT
S = 6159.3, p-value = 0.19
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.2417941 

Warning message:
In cor.test.default(epi$F11postop, epi$Prov2extemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F11postop, epi$Prov2extemCT, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #F11 vs INTEM-CT
> cor.test(epi$F11postop, epi$Prov2intemCT, use="complete.obs", 
```

```
method="pearson")

    Pearson's product-moment correlation

data:  epi$F11postop and epi$Prov2intemCT
t = -0.030361, df = 29, p-value = 0.976
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3592603  0.3494003
sample estimates:
         cor
-0.005637846

> cor.test(epi$F11postop, epi$Prov2intemCT, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F11postop and epi$Prov2intemCT
S = 4709.8, p-value = 0.7876
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
0.05043373

Warning message:
In cor.test.default(epi$F11postop, epi$Prov2intemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F11postop, epi$Prov2intemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #F11 vs FIBTEM-MCF
> cor.test(epi$F11postop, epi$Prov2fibtemMCF, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F11postop and epi$Prov2fibtemMCF
t = 2.5389, df = 29, p-value = 0.01674
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.08493867 0.67829026
sample estimates:
     cor
0.426444

> cor.test(epi$F11postop, epi$Prov2fibtemMCF, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho
```

```
data:  epi$F11postop and epi$Prov2fibtemMCF
S = 3423.5, p-value = 0.08991
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.3097777 

Warning message:
In cor.test.default(epi$F11postop, epi$Prov2fibtemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F11postop, epi$Prov2fibtemMCF, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2fibtemMCF~ epi
$F11postop),lwd=3,lty=2))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.5,19,"r=0.43*",cex=6)
> 
> #F12 vs EXTEM-MCF
> cor.test(epi$F12postop, epi$Prov2extemMCF, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F12postop and epi$Prov2extemMCF
t = 0.13599, df = 29, p-value = 0.8928
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3320659  0.3762193
sample estimates:
       cor 
0.02524455 

> cor.test(epi$F12postop, epi$Prov2extemMCF, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F12postop and epi$Prov2extemMCF
S = 5598.5, p-value = 0.4901
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.1287329 

Warning message:
In cor.test.default(epi$F12postop, epi$Prov2extemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F12postop, epi$Prov2extemMCF, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
```

```
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #F12 vs EXTEM-CT
> cor.test(epi$F12postop, epi$Prov2extemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F12postop and epi$Prov2extemCT
t = -1.6107, df = 29, p-value = 0.1181
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.58181687  0.07544813
sample estimates:
       cor
-0.2865528

> cor.test(epi$F12postop, epi$Prov2extemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F12postop and epi$Prov2extemCT
S = 6426.7, p-value = 0.1063
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.2956983

Warning message:
In cor.test.default(epi$F12postop, epi$Prov2extemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F12postop, epi$Prov2extemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #F12 vs INTEM-CT
> cor.test(epi$F12postop, epi$Prov2intemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F12postop and epi$Prov2intemCT
t = 0.94101, df = 29, p-value = 0.3545
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1940427  0.4962075
sample estimates:
      cor
0.1721328

> cor.test(epi$F12postop, epi$Prov2intemCT, use="complete.obs",
```

```
method="spearman")

	Spearman's rank correlation rho

data:  epi$F12postop and epi$Prov2intemCT
S = 4698.9, p-value = 0.7785
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
0.05264751 

Warning message:
In cor.test.default(epi$F12postop, epi$Prov2intemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F12postop, epi$Prov2intemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #F12 vs FIBTEM-MCF
> cor.test(epi$F12postop, epi$Prov2fibtemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F12postop and epi$Prov2fibtemMCF
t = 0.41489, df = 29, p-value = 0.6813
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.2852892  0.4197317
sample estimates:
       cor 
0.07681624 

> cor.test(epi$F12postop, epi$Prov2fibtemMCF, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F12postop and epi$Prov2fibtemMCF
S = 4808.6, p-value = 0.8705
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
0.03052984 

Warning message:
In cor.test.default(epi$F12postop, epi$Prov2fibtemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F12postop, epi$Prov2fibtemMCF, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
```

```
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
>
>
> #F13 vs EXTEM-MCF
> cor.test(epi$F13postop, epi$Prov2extemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F13postop and epi$Prov2extemMCF
t = 2.6074, df = 29, p-value = 0.01426
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.09631896 0.68443758
sample estimates:
      cor
0.4357859

> cor.test(epi$F13postop, epi$Prov2extemMCF, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F13postop and epi$Prov2extemMCF
S = 3359.7, p-value = 0.07668
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.3226419

Warning message:
In cor.test.default(epi$F13postop, epi$Prov2extemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F13postop, epi$Prov2extemMCF, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2extemMCF~ epi
$F13postop),lwd=3,lty=2))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1,60,"r=0.44*",cex=6)
>
>
> #F13 vs EXTEM-CT
> cor.test(epi$F13postop, epi$Prov2extemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F13postop and epi$Prov2extemCT
t = -0.96615, df = 29, p-value = 0.342
```

```
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4996641  0.1896156
sample estimates:
       cor 
-0.1765892 

> cor.test(epi$F13postop, epi$Prov2extemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F13postop and epi$Prov2extemCT
S = 5848.6, p-value = 0.3349
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
-0.179156 

Warning message:
In cor.test.default(epi$F13postop, epi$Prov2extemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F13postop, epi$Prov2extemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #F13 vs INTEM-CT
> cor.test(epi$F13postop, epi$Prov2intemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F13postop and epi$Prov2intemCT
t = 0.18351, df = 29, p-value = 0.8557
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3241954  0.3837659
sample estimates:
       cor 
0.03405699 

> cor.test(epi$F13postop, epi$Prov2intemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F13postop and epi$Prov2intemCT
S = 4576.8, p-value = 0.6795
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
0.07725669 
```

```
Warning message:
In cor.test.default(epi$F13postop, epi$Prov2intemCT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F13postop, epi$Prov2intemCT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #F13 vs FIBTEM-MCF
> cor.test(epi$F13postop, epi$Prov2fibtemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F13postop and epi$Prov2fibtemMCF
t = 2.8328, df = 29, p-value = 0.008309
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1331763 0.7037890
sample estimates:
      cor 
0.4655473 

> cor.test(epi$F13postop, epi$Prov2fibtemMCF, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F13postop and epi$Prov2fibtemMCF
S = 2650.5, p-value = 0.008296
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.4656307 

Warning message:
In cor.test.default(epi$F13postop, epi$Prov2fibtemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F13postop, epi$Prov2fibtemMCF, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2fibtemMCF~ epi
$F13postop)),lwd=3,lty=2)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(.85,20,"Rho=0.47**",cex=6)
>
>
>
>
>
```

```
> #EXTEM-MCF vs PT-INR
> cor.test(epi$Prov2extemMCF, epi$Prov2rutinPK, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2extemMCF and epi$Prov2rutinPK
t = -1.4426, df = 31, p-value = 0.1592
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.5470235  0.1012061
sample estimates:
       cor
-0.2508175

> cor.test(epi$Prov2extemMCF, epi$Prov2rutinPK, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2extemMCF and epi$Prov2rutinPK
S = 6546.7, p-value = 0.6027
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho
-0.09402775

Warning message:
In cor.test.default(epi$Prov2extemMCF, epi$Prov2rutinPK, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2extemMCF, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #EXTEM-MCF vs aPTT
> cor.test(epi$Prov2extemMCF, epi$Prov2rutinAPTT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2extemMCF and epi$Prov2rutinAPTT
t = -0.16956, df = 31, p-value = 0.8665
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3698837  0.3161730
sample estimates:
        cor
-0.03044012

> cor.test(epi$Prov2extemMCF, epi$Prov2rutinAPTT, use="complete.obs",
method="spearman")
```

```
	Spearman's rank correlation rho

data:  epi$Prov2extemMCF and epi$Prov2rutinAPTT
S = 5841.2, p-value = 0.8951
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
0.02386784 

Warning message:
In cor.test.default(epi$Prov2extemMCF, epi$Prov2rutinAPTT, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2extemMCF, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #EXTEM-MCF vs PIVKA
> cor.test(epi$Prov2extemMCF, epi$PIVKAMpostop, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2extemMCF and epi$PIVKAMpostop
t = -0.89872, df = 29, p-value = 0.3762
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4903501  0.2014808
sample estimates:
       cor 
-0.1646114 

> cor.test(epi$Prov2extemMCF, epi$PIVKAMpostop, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2extemMCF and epi$PIVKAMpostop
S = 6448.9, p-value = 0.1009
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.3001744 

Warning message:
In cor.test.default(epi$Prov2extemMCF, epi$PIVKAMpostop, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2extemMCF, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
```

```
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #EXTEM-MCF vs CRP
> cor.test(epi$Prov2extemMCF, epi$Prov2rutinCRP, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2extemMCF and epi$Prov2rutinCRP
t = -0.58792, df = 28, p-value = 0.5613
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4526865  0.2601939
sample estimates:
       cor
-0.1104267

> cor.test(epi$Prov2extemMCF, epi$Prov2rutinCRP, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2extemMCF and epi$Prov2rutinCRP
S = 4299.5, p-value = 0.8194
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
0.04350263

Warning message:
In cor.test.default(epi$Prov2extemMCF, epi$Prov2rutinCRP, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2extemMCF, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
>
> #EXTEM-CT vs PT-INR
> cor.test(epi$Prov2extemCT, epi$Prov2rutinPK, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2extemCT and epi$Prov2rutinPK
t = 1.1177, df = 31, p-value = 0.2723
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
```

```
 -0.1571117  0.5059370
sample estimates:
      cor
0.1968129

> cor.test(epi$Prov2extemCT, epi$Prov2rutinPK, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2extemCT and epi$Prov2rutinPK
S = 5462.4, p-value = 0.6296
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
0.08716727

Warning message:
In cor.test.default(epi$Prov2extemCT, epi$Prov2rutinPK, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2extemCT, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #EXTEM-CT vs aPTT
> cor.test(epi$Prov2extemCT, epi$Prov2rutinAPTT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2extemCT and epi$Prov2rutinAPTT
t = 0.96335, df = 31, p-value = 0.3428
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1835627  0.4853891
sample estimates:
      cor
0.1704904

> cor.test(epi$Prov2extemCT, epi$Prov2rutinAPTT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2extemCT and epi$Prov2rutinAPTT
S = 6474.8, p-value = 0.65
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho
-0.08202175
```

```
Warning message:
In cor.test.default(epi$Prov2extemCT, epi$Prov2rutinAPTT, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2extemCT, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #EXTEM-CT vs PIVKA
> cor.test(epi$Prov2extemCT, epi$PIVKAMpostop, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$Prov2extemCT and epi$PIVKAMpostop
t = -0.9842, df = 29, p-value = 0.3332
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.5021355  0.1864331
sample estimates:
       cor
-0.1797837

> cor.test(epi$Prov2extemCT, epi$PIVKAMpostop, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$Prov2extemCT and epi$PIVKAMpostop
S = 7649.9, p-value = 0.001624
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.5423156

Warning message:
In cor.test.default(epi$Prov2extemCT, epi$PIVKAMpostop, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2extemCT, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=2.7,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=2, labels=NA)
> axis(side=2,lwd=0,cex.axis=2.5, line=0)
>
> #EXTEM-CT vs CRP
> cor.test(epi$Prov2extemCT, epi$Prov2rutinCRP, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation
```

```
data:  epi$Prov2extemCT and epi$Prov2rutinCRP
t = 0.16566, df = 28, p-value = 0.8696
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3327281  0.3871963
sample estimates:
       cor
0.03129213

> cor.test(epi$Prov2extemCT, epi$Prov2rutinCRP, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2extemCT and epi$Prov2rutinCRP
S = 4190.2, p-value = 0.7218
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
0.06780432

Warning message:
In cor.test.default(epi$Prov2extemCT, epi$Prov2rutinCRP, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2extemCT, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
>
> #FIBTEM-MCF vs PT-INR
> cor.test(epi$Prov2fibtemMCF, epi$Prov2rutinPK, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2fibtemMCF and epi$Prov2rutinPK
t = -0.99309, df = 31, p-value = 0.3284
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4893990  0.1784758
sample estimates:
       cor
-0.1755922

> cor.test(epi$Prov2fibtemMCF, epi$Prov2rutinPK, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho
```

```
data:  epi$Prov2fibtemMCF and epi$Prov2rutinPK
S = 6137.7, p-value = 0.8872
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho 
-0.02568291 

Warning message:
In cor.test.default(epi$Prov2fibtemMCF, epi$Prov2rutinPK, use = 
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2fibtemMCF, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #fibtem-MCF vs aPTT
> cor.test(epi$Prov2fibtemMCF, epi$Prov2rutinAPTT, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2fibtemMCF and epi$Prov2rutinAPTT
t = -0.9046, df = 31, p-value = 0.3727
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4773939  0.1935995
sample estimates:
       cor 
-0.1603683 

> cor.test(epi$Prov2fibtemMCF, epi$Prov2rutinAPTT, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2fibtemMCF and epi$Prov2rutinAPTT
S = 6003.7, p-value = 0.9855
alternative hypothesis: true rho is not equal to 0
sample estimates:
         rho 
-0.003286168 

Warning message:
In cor.test.default(epi$Prov2fibtemMCF, epi$Prov2rutinAPTT, use = 
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2fibtemMCF, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
```

```
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #fibtem-MCF vs PIVKA
> cor.test(epi$Prov2fibtemMCF, epi$PIVKAMpostop, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2fibtemMCF and epi$PIVKAMpostop
t = -0.64842, df = 29, p-value = 0.5218
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4546267  0.2451816
sample estimates:
       cor
-0.1195442

> cor.test(epi$Prov2fibtemMCF, epi$PIVKAMpostop, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2fibtemMCF and epi$PIVKAMpostop
S = 5548.7, p-value = 0.5248
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.1186822

Warning message:
In cor.test.default(epi$Prov2fibtemMCF, epi$PIVKAMpostop, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2fibtemMCF, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #fibtem-MCF vs CRP
> cor.test(epi$Prov2fibtemMCF, epi$Prov2rutinCRP, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2fibtemMCF and epi$Prov2rutinCRP
t = -0.6738, df = 28, p-value = 0.506
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4654053  0.2451080
sample estimates:
       cor
-0.1263155
```

```
> cor.test(epi$Prov2fibtemMCF, epi$Prov2rutinCRP, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2fibtemMCF and epi$Prov2rutinCRP
S = 4530.6, p-value = 0.9669
alternative hypothesis: true rho is not equal to 0
sample estimates:
         rho
-0.007921481

Warning message:
In cor.test.default(epi$Prov2fibtemMCF, epi$Prov2rutinCRP, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2fibtemMCF, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
>
> #F2 vs PT-INR
> cor.test(epi$F2postop, epi$Prov2rutinPK, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F2postop and epi$Prov2rutinPK
t = -2.798, df = 29, p-value = 0.009041
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.7008942 -0.1275606
sample estimates:
       cor
-0.4610609

> cor.test(epi$F2postop, epi$Prov2rutinPK, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F2postop and epi$Prov2rutinPK
S = 7595.9, p-value = 0.002095
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.5314268

Warning message:
In cor.test.default(epi$F2postop, epi$Prov2rutinPK, use = "complete.obs",  :
  Cannot compute exact p-value with ties
```

```
> #RESULT:
> plot(epi$F2postop, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3, cex=2.5,
pch=19, axes=F,abline(lm(epi$Prov2rutinPK~ epi$F2postop),lwd=3))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.4,1.5,"r=-0.53**",cex=7)
>
> #F2 vs aPTT
> cor.test(epi$F2postop, epi$Prov2rutinAPTT, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F2postop and epi$Prov2rutinAPTT
t = -2.8248, df = 29, p-value = 0.008471
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.7031311 -0.1318968
sample estimates:
       cor
-0.4645266

> cor.test(epi$F2postop, epi$Prov2rutinAPTT, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F2postop and epi$Prov2rutinAPTT
S = 6623.8, p-value = 0.06508
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.3354347

Warning message:
In cor.test.default(epi$F2postop, epi$Prov2rutinAPTT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F2postop, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2rutinAPTT~ epi
$F2postop),lwd=3,lty=2))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.35,40,"r=-0.46*",cex=8)
>
> #F2 vs PIVKA
> cor.test(epi$F2postop, epi$PIVKAMpostop, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F2postop and epi$PIVKAMpostop
```

```
t = 0.62829, df = 29, p-value = 0.5347
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.2486658  0.4516782
sample estimates:
      cor 
0.1158852 

> cor.test(epi$F2postop, epi$PIVKAMpostop, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F2postop and epi$PIVKAMpostop
S = 3200, p-value = 0.05082
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.3548387 

> #RESULT:
> plot(epi$F2postop, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3, cex=2.5, 
pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #F2 vs CRP
> cor.test(epi$F2postop, epi$Prov2rutinCRP, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F2postop and epi$Prov2rutinCRP
t = -0.77348, df = 26, p-value = 0.4462
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4953380  0.2363232
sample estimates:
       cor 
-0.1499767 

> cor.test(epi$F2postop, epi$Prov2rutinCRP, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F2postop and epi$Prov2rutinCRP
S = 4133.1, p-value = 0.506
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.1311251 

Warning message:
```

```
In cor.test.default(epi$F2postop, epi$Prov2rutinCRP, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F2postop, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
>
> #F7 vs PT-INR
> cor.test(epi$F7postop, epi$Prov2rutinPK, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F7postop and epi$Prov2rutinPK
t = -3.7201, df = 29, p-value = 0.0008505
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.7680348 -0.2680127
sample estimates:
       cor
-0.5683756

> cor.test(epi$F7postop, epi$Prov2rutinPK, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F7postop and epi$Prov2rutinPK
S = 7645.4, p-value = 0.001659
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.5414184

Warning message:
In cor.test.default(epi$F7postop, epi$Prov2rutinPK, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F7postop, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3, cex=2.5,
pch=19, axes=F,abline(lm(epi$Prov2rutinPK~ epi$F7postop),lwd=3))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.2,1.5,"r=-0.57**",cex=6)
>
> #F7 vs aPTT
> cor.test(epi$F7postop, epi$Prov2rutinAPTT, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation
```

```
data:  epi$F7postop and epi$Prov2rutinAPTT
t = -1.8185, df = 29, p-value = 0.07934
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.60561656  0.03880751
sample estimates:
      cor
-0.319932

> cor.test(epi$F7postop, epi$Prov2rutinAPTT, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F7postop and epi$Prov2rutinAPTT
S = 5981, p-value = 0.2666
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.2058442

Warning message:
In cor.test.default(epi$F7postop, epi$Prov2rutinAPTT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F7postop, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
> #F7 vs PIVKA
> cor.test(epi$F7postop, epi$PIVKAMpostop, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F7postop and epi$PIVKAMpostop
t = 1.2953, df = 29, p-value = 0.2054
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1313587  0.5431934
sample estimates:
      cor
0.2338669

> cor.test(epi$F7postop, epi$PIVKAMpostop, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F7postop and epi$PIVKAMpostop
S = 3364, p-value = 0.07795
```

```
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.3217742 

> #RESULT:
> plot(epi$F7postop, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3, cex=2.5, 
pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #F7 vs CRP
> cor.test(epi$F7postop, epi$Prov2rutinCRP, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F7postop and epi$Prov2rutinCRP
t = -0.27418, df = 26, p-value = 0.7861
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4183889  0.3259125
sample estimates:
        cor 
-0.05369296 

> cor.test(epi$F7postop, epi$Prov2rutinCRP, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F7postop and epi$Prov2rutinCRP
S = 4240.2, p-value = 0.4148
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.1604161 

Warning message:
In cor.test.default(epi$F7postop, epi$Prov2rutinCRP, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F7postop, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> 
> #F9 vs PT-INR
> cor.test(epi$F9postop, epi$Prov2rutinPK, use="complete.obs", 
method="pearson")
```

```
    Pearson's product-moment correlation

data:  epi$F9postop and epi$Prov2rutinPK
t = -2.046, df = 29, p-value = 0.04992
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.6301952979 -0.0009432787
sample estimates:
       cor
-0.3551647

> cor.test(epi$F9postop, epi$Prov2rutinPK, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F9postop and epi$Prov2rutinPK
S = 6244.4, p-value = 0.1595
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.2589483

Warning message:
In cor.test.default(epi$F9postop, epi$Prov2rutinPK, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F9postop, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3, cex=2.5,
pch=19, axes=F,abline(lm(epi$Prov2rutinPK~ epi$F9postop),lwd=3,lty=2))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.95,1.55,"r=-0.36*",cex=7)
>
> #F9 vs aPTT
> cor.test(epi$F9postop, epi$Prov2rutinAPTT, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F9postop and epi$Prov2rutinAPTT
t = -1.2637, df = 29, p-value = 0.2164
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.5391469  0.1369781
sample estimates:
       cor
-0.2284503

> cor.test(epi$F9postop, epi$Prov2rutinAPTT, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho
```

```
data:  epi$F9postop and epi$Prov2rutinAPTT
S = 5896.5, p-value = 0.309
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.1888088 

Warning message:
In cor.test.default(epi$F9postop, epi$Prov2rutinAPTT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F9postop, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #F9 vs PIVKA
> cor.test(epi$F9postop, epi$PIVKAMpostop, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F9postop and epi$PIVKAMpostop
t = 0.23775, df = 29, p-value = 0.8137
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3151594  0.3923150
sample estimates:
       cor 
0.04410625 

> cor.test(epi$F9postop, epi$PIVKAMpostop, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F9postop and epi$PIVKAMpostop
S = 5260, p-value = 0.7459
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho 
-0.06048387 

> #RESULT:
> plot(epi$F9postop, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3, cex=2.5, 
pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #F9 vs CRP
> cor.test(epi$F9postop, epi$Prov2rutinCRP, use="complete.obs", 
```

```
method="pearson")

	Pearson's product-moment correlation

data:  epi$F9postop and epi$Prov2rutinCRP
t = 1.0772, df = 26, p-value = 0.2913
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1802788  0.5382686
sample estimates:
      cor 
0.2067003 

> cor.test(epi$F9postop, epi$Prov2rutinCRP, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F9postop and epi$Prov2rutinCRP
S = 2792.8, p-value = 0.2273
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.2356967 

Warning message:
In cor.test.default(epi$F9postop, epi$Prov2rutinCRP, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F9postop, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #F10 vs PT-INR
> cor.test(epi$F10postop, epi$Prov2rutinPK, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F10postop and epi$Prov2rutinPK
t = -2.4963, df = 29, p-value = 0.01848
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.67440010 -0.07781606
sample estimates:
       cor 
-0.4205599 

> cor.test(epi$F10postop, epi$Prov2rutinPK, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho
```

```
data:  epi$F10postop and epi$Prov2rutinPK
S = 6921.9, p-value = 0.02763
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.3955396

Warning message:
In cor.test.default(epi$F10postop, epi$Prov2rutinPK, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F10postop, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2rutinPK~ epi
$F10postop),lwd=3,lty=1))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.2,1.55,"r=-0.40*",cex=7)
>
> #F10 vs aPTT
> cor.test(epi$F10postop, epi$Prov2rutinAPTT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F10postop and epi$Prov2rutinAPTT
t = -2.9444, df = 29, p-value = 0.006314
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.7128916 -0.1510770
sample estimates:
       cor
-0.4797356

> cor.test(epi$F10postop, epi$Prov2rutinAPTT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F10postop and epi$Prov2rutinAPTT
S = 7046.9, p-value = 0.01842
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.4207554

Warning message:
In cor.test.default(epi$F10postop, epi$Prov2rutinAPTT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F10postop, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2rutinAPTT~ epi
$F10postop),lwd=3,lty=1))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
```

```
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.2,40,"r=-0.48*",cex=7)
>
> #F10 vs PIVKA
> cor.test(epi$F10postop, epi$PIVKAMpostop, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F10postop and epi$PIVKAMpostop
t = 0.72038, df = 29, p-value = 0.4771
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.2326811  0.4650804
sample estimates:
      cor
0.1325909

> cor.test(epi$F10postop, epi$PIVKAMpostop, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F10postop and epi$PIVKAMpostop
S = 4747, p-value = 0.8186
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
0.04294788

Warning message:
In cor.test.default(epi$F10postop, epi$PIVKAMpostop, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F10postop, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
> #F10 vs CRP
> cor.test(epi$F10postop, epi$Prov2rutinCRP, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F10postop and epi$Prov2rutinCRP
t = 0.39461, df = 26, p-value = 0.6963
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3046882  0.4376384
sample estimates:
       cor
```

```
0.07715958

> cor.test(epi$F10postop, epi$Prov2rutinCRP, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F10postop and epi$Prov2rutinCRP
S = 3224.9, p-value = 0.5517
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.1174377 

Warning message:
In cor.test.default(epi$F10postop, epi$Prov2rutinCRP, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F10postop, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #F11 vs PT-INR
> cor.test(epi$F11postop, epi$Prov2rutinPK, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F11postop and epi$Prov2rutinPK
t = -2.7558, df = 29, p-value = 0.01001
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.6973286 -0.1206935
sample estimates:
       cor 
-0.4555513 

> cor.test(epi$F11postop, epi$Prov2rutinPK, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F11postop and epi$Prov2rutinPK
S = 6819.1, p-value = 0.03775
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.3748259 

Warning message:
In cor.test.default(epi$F11postop, epi$Prov2rutinPK, use = "complete.obs",  :
  Cannot compute exact p-value with ties
```

```
> #RESULT:
> plot(epi$F11postop, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2rutinPK~ epi
$F11postop),lwd=3,lty=1))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.35,1.55,"r=-0.45*",cex=7)
>
> #F11 vs aPTT
> cor.test(epi$F11postop, epi$Prov2rutinAPTT, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F11postop and epi$Prov2rutinAPTT
t = -3.7572, df = 29, p-value = 0.0007701
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.7703469 -0.2732601
sample estimates:
       cor
-0.5721961

> cor.test(epi$F11postop, epi$Prov2rutinAPTT, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F11postop and epi$Prov2rutinAPTT
S = 7650.5, p-value = 0.001618
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
-0.542449

Warning message:
In cor.test.default(epi$F11postop, epi$Prov2rutinAPTT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F11postop, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2rutinAPTT~ epi
$F11postop),lwd=3,lty=1))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.2,40,"r=-0.48*",cex=7)
>
> #F11 vs PIVKA
> cor.test(epi$F11postop, epi$PIVKAMpostop, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation
```

```
data:  epi$F11postop and epi$PIVKAMpostop
t = 1.344, df = 29, p-value = 0.1894
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1227165  0.5493561
sample estimates:
      cor 
0.2421533 

> cor.test(epi$F11postop, epi$PIVKAMpostop, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F11postop and epi$PIVKAMpostop
S = 3231.8, p-value = 0.05475
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.3484222 

Warning message:
In cor.test.default(epi$F11postop, epi$PIVKAMpostop, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F11postop, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #F11 vs CRP
> cor.test(epi$F11postop, epi$Prov2rutinCRP, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F11postop and epi$Prov2rutinCRP
t = -1.3216, df = 26, p-value = 0.1978
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.5705603  0.1348068
sample estimates:
       cor 
-0.2508881 

> cor.test(epi$F11postop, epi$Prov2rutinCRP, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F11postop and epi$Prov2rutinCRP
S = 4382.3, p-value = 0.3092
alternative hypothesis: true rho is not equal to 0
sample estimates:
```

```
       rho 
-0.1993155 

Warning message:
In cor.test.default(epi$F11postop, epi$Prov2rutinCRP, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F11postop, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> 
> #F12 vs PT-INR
> cor.test(epi$F12postop, epi$Prov2rutinPK, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F12postop and epi$Prov2rutinPK
t = -1.9473, df = 29, p-value = 0.06124
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.61972276  0.01624047
sample estimates:
       cor 
-0.3400566 

> cor.test(epi$F12postop, epi$Prov2rutinPK, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F12postop and epi$Prov2rutinPK
S = 6396.2, p-value = 0.1141
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.2895475 

Warning message:
In cor.test.default(epi$F12postop, epi$Prov2rutinPK, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F12postop, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #F12 vs aPTT
```

```
> cor.test(epi$F12postop, epi$Prov2rutinAPTT, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F12postop and epi$Prov2rutinAPTT
t = -3.2114, df = 29, p-value = 0.003223
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.7334190 -0.1928443
sample estimates:
       cor
-0.5121855

> cor.test(epi$F12postop, epi$Prov2rutinAPTT, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$F12postop and epi$Prov2rutinAPTT
S = 7614.6, p-value = 0.00192
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.5351948

Warning message:
In cor.test.default(epi$F12postop, epi$Prov2rutinAPTT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F12postop, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2rutinAPTT~ epi
$F12postop),lwd=3,lty=1))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(1.1,40,"r=-0.51**",cex=7)
>
> #F12 vs PIVKA
> cor.test(epi$F12postop, epi$PIVKAMpostop, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$F12postop and epi$PIVKAMpostop
t = 2.0018, df = 29, p-value = 0.05474
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.006736402  0.625543087
sample estimates:
      cor
0.3484354

> cor.test(epi$F12postop, epi$PIVKAMpostop, use="complete.obs",
method="spearman")
```

```
	Spearman's rank correlation rho

data:  epi$F12postop and epi$PIVKAMpostop
S = 1978, p-value = 0.0004509
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.6012097 

> #RESULT:
> plot(epi$F12postop, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,ylim=c(0,110),abline(lm(epi$PIVKAMpostop~epi
$F12postop),lwd=3,lty=2))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(.95,90,"Rho=0.60**",cex=6)
> 
> #F12 vs CRP
> cor.test(epi$F12postop, epi$Prov2rutinCRP, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F12postop and epi$Prov2rutinCRP
t = -3.4561, df = 26, p-value = 0.001896
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.7724510 -0.2377528
sample estimates:
       cor 
-0.5610634 

> cor.test(epi$F12postop, epi$Prov2rutinCRP, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F12postop and epi$Prov2rutinCRP
S = 5854.6, p-value = 0.0006964
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.6022448 

Warning message:
In cor.test.default(epi$F12postop, epi$Prov2rutinCRP, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F12postop, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,abline(lm(epi$Prov2rutinCRP~ epi
$F12postop),lwd=3,lty=1))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
```

```
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> text(.95,250,"r=-0.56**",cex=6)
>
>
>
>
> #F13 vs PT-INR
> cor.test(epi$F13postop, epi$Prov2rutinPK, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F13postop and epi$Prov2rutinPK
t = -2.035, df = 29, p-value = 0.05109
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.6290361706  0.0009771294
sample estimates:
       cor
-0.3534854

> cor.test(epi$F13postop, epi$Prov2rutinPK, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F13postop and epi$Prov2rutinPK
S = 6076.1, p-value = 0.2236
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.2250186

Warning message:
In cor.test.default(epi$F13postop, epi$Prov2rutinPK, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F13postop, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
> #F13 vs aPTT
> cor.test(epi$F13postop, epi$Prov2rutinAPTT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F13postop and epi$Prov2rutinAPTT
t = -1.1949, df = 29, p-value = 0.2418
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
```

```
 -0.5302610  0.1491672
sample estimates:
       cor 
-0.2166227 

> cor.test(epi$F13postop, epi$Prov2rutinAPTT, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F13postop and epi$Prov2rutinAPTT
S = 5905.5, p-value = 0.3043
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
-0.190634 

Warning message:
In cor.test.default(epi$F13postop, epi$Prov2rutinAPTT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F13postop, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #F13 vs PIVKA
> cor.test(epi$F13postop, epi$PIVKAMpostop, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$F13postop and epi$PIVKAMpostop
t = -0.49414, df = 29, p-value = 0.6249
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4317363  0.2717645
sample estimates:
        cor 
-0.09137479 

> cor.test(epi$F13postop, epi$PIVKAMpostop, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$F13postop and epi$PIVKAMpostop
S = 3830, p-value = 0.2168
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.2278226 
```

```
> #RESULT:
> plot(epi$F13postop, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
> #F13 vs CRP
> cor.test(epi$F13postop, epi$Prov2rutinCRP, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F13postop and epi$Prov2rutinCRP
t = -0.27037, df = 26, p-value = 0.789
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4177741  0.3265782
sample estimates:
        cor
-0.05295006

> cor.test(epi$F13postop, epi$Prov2rutinCRP, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F13postop and epi$Prov2rutinCRP
S = 3859.1, p-value = 0.7767
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho
-0.05611826

Warning message:
In cor.test.default(epi$F13postop, epi$Prov2rutinCRP, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$F13postop, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
>
>
> #Fibrinogen vs PT-INR
> cor.test(epi$FIBpostop, epi$Prov2rutinPK, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation
```

```
data:  epi$FIBpostop and epi$Prov2rutinPK
t = -0.25778, df = 29, p-value = 0.7984
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3954537  0.3118094
sample estimates:
        cor 
-0.04781344 

> cor.test(epi$FIBpostop, epi$Prov2rutinPK, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$FIBpostop and epi$Prov2rutinPK
S = 4845, p-value = 0.9015
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
0.02318511 

Warning message:
In cor.test.default(epi$FIBpostop, epi$Prov2rutinPK, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$FIBpostop, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #FIB vs aPTT
> cor.test(epi$FIBpostop, epi$Prov2rutinAPTT, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$FIBpostop and epi$Prov2rutinAPTT
t = -0.033445, df = 29, p-value = 0.9735
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3597589  0.3488974
sample estimates:
         cor 
-0.006210473 

> cor.test(epi$FIBpostop, epi$Prov2rutinAPTT, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$FIBpostop and epi$Prov2rutinAPTT
S = 4704.6, p-value = 0.7833
alternative hypothesis: true rho is not equal to 0
```

```
sample estimates:
       rho 
0.05148571 

Warning message:
In cor.test.default(epi$FIBpostop, epi$Prov2rutinAPTT, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$FIBpostop, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #FIB vs PIVKA
> cor.test(epi$FIBpostop, epi$PIVKAMpostop, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$FIBpostop and epi$PIVKAMpostop
t = 0.92809, df = 29, p-value = 0.361
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1963158  0.4944241
sample estimates:
      cor 
0.1698387 

> cor.test(epi$FIBpostop, epi$PIVKAMpostop, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$FIBpostop and epi$PIVKAMpostop
S = 3822.1, p-value = 0.2144
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.2294167 

Warning message:
In cor.test.default(epi$FIBpostop, epi$PIVKAMpostop, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$FIBpostop, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #FIB vs CRP
```

```
> cor.test(epi$FIBpostop, epi$Prov2rutinCRP, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$FIBpostop and epi$Prov2rutinCRP
t = 1.5779, df = 26, p-value = 0.1267
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.08706656  0.60226770
sample estimates:
      cor 
0.2956126 

> cor.test(epi$FIBpostop, epi$Prov2rutinCRP, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$FIBpostop and epi$Prov2rutinCRP
S = 2812, p-value = 0.2381
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.2304426 

Warning message:
In cor.test.default(epi$FIBpostop, epi$Prov2rutinCRP, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$FIBpostop, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> 
> #PIVKA vs PT-INR
> cor.test(epi$PIVKAMpostop, epi$Prov2rutinPK, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$PIVKAMpostop and epi$Prov2rutinPK
t = -0.61612, df = 29, p-value = 0.5426
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4498893  0.2507709
sample estimates:
       cor 
-0.1136697 

> cor.test(epi$PIVKAMpostop, epi$Prov2rutinPK, use="complete.obs",
method="spearman")
```

```
    Spearman's rank correlation rho

data:  epi$PIVKAMpostop and epi$Prov2rutinPK
S = 5061.2, p-value = 0.9133
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho 
-0.02039946 

Warning message:
In cor.test.default(epi$PIVKAMpostop, epi$Prov2rutinPK, use = 
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$PIVKAMpostop, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F, xlim=c(0,140))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #PIVKAM vs aPTT
> cor.test(epi$PIVKAMpostop, epi$Prov2rutinAPTT, use="complete.obs", 
method="pearson")

    Pearson's product-moment correlation

data:  epi$PIVKAMpostop and epi$Prov2rutinAPTT
t = -1.239, df = 29, p-value = 0.2253
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.5359820  0.1413431
sample estimates:
       cor 
-0.2242271 

> cor.test(epi$PIVKAMpostop, epi$Prov2rutinAPTT, use="complete.obs", 
method="spearman")

    Spearman's rank correlation rho

data:  epi$PIVKAMpostop and epi$Prov2rutinAPTT
S = 5129, p-value = 0.8556
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho 
-0.03407076 

Warning message:
In cor.test.default(epi$PIVKAMpostop, epi$Prov2rutinAPTT, use = 
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$PIVKAMpostop, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3, 
```

```
cex=2.5, pch=19, axes=F, xlim=c(0,140))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
> #PIVKAM vs PIVKA
> cor.test(epi$PIVKAMpostop, epi$PIVKAMpostop, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$PIVKAMpostop and epi$PIVKAMpostop
t = Inf, df = 29, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 1 1
sample estimates:
cor
  1

> cor.test(epi$PIVKAMpostop, epi$PIVKAMpostop, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$PIVKAMpostop and epi$PIVKAMpostop
S = 0, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
rho
  1

> #RESULT:
> plot(epi$PIVKAMpostop, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
> #PIVKAM vs CRP
> cor.test(epi$PIVKAMpostop, epi$Prov2rutinCRP, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$PIVKAMpostop and epi$Prov2rutinCRP
t = -1.0739, df = 26, p-value = 0.2927
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.5378138  0.1808981
sample estimates:
       cor
```

```
-0.2060874 

> cor.test(epi$PIVKAMpostop, epi$Prov2rutinCRP, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$PIVKAMpostop and epi$Prov2rutinCRP
S = 4800.3, p-value = 0.104
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.3137148 

Warning message:
In cor.test.default(epi$PIVKAMpostop, epi$Prov2rutinCRP, use = 
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$PIVKAMpostop, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3, 
cex=2.5, pch=19, axes=F, xlim=c(0,140))
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #Plc vs PT-INR
> cor.test(epi$Prov2rutinTPK, epi$Prov2rutinPK, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinTPK and epi$Prov2rutinPK
t = -0.51222, df = 29, p-value = 0.6124
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4344523  0.2686654
sample estimates:
        cor 
-0.09468899 

> cor.test(epi$Prov2rutinTPK, epi$Prov2rutinPK, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinTPK and epi$Prov2rutinPK
S = 5501.5, p-value = 0.5588
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.1091649 

Warning message:
In cor.test.default(epi$Prov2rutinTPK, epi$Prov2rutinPK, use = 
```

```
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinTPK, epi$Prov2rutinPK, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
> #Prov2rutinTPK vs aPTT
> cor.test(epi$Prov2rutinTPK, epi$Prov2rutinAPTT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinTPK and epi$Prov2rutinAPTT
t = -0.6246, df = 29, p-value = 0.5371
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4511352  0.2493055
sample estimates:
       cor
-0.1152124

> cor.test(epi$Prov2rutinTPK, epi$Prov2rutinAPTT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinTPK and epi$Prov2rutinAPTT
S = 5473.7, p-value = 0.5793
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho
-0.1035621

Warning message:
In cor.test.default(epi$Prov2rutinTPK, epi$Prov2rutinAPTT, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinTPK, epi$Prov2rutinAPTT, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
>
>
> #Prov2rutinTPK vs PIVKA
> cor.test(epi$Prov2rutinTPK, epi$PIVKAMpostop, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation
```

```
data:  epi$Prov2rutinTPK and epi$PIVKAMpostop
t = -0.55884, df = 27, p-value = 0.5809
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4555833  0.2701612
sample estimates:
       cor
-0.1069325

> cor.test(epi$Prov2rutinTPK, epi$PIVKAMpostop, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$Prov2rutinTPK and epi$PIVKAMpostop
S = 4468.1, p-value = 0.6039
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
-0.100505

Warning message:
In cor.test.default(epi$Prov2rutinTPK, epi$PIVKAMpostop, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinTPK, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F,ylim=c(0,130))
>
>
>
> #Prov2rutinTPK vs CRP
> cor.test(epi$Prov2rutinTPK, epi$Prov2rutinCRP, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$Prov2rutinTPK and epi$Prov2rutinCRP
t = -1.4718, df = 28, p-value = 0.1522
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.5729300  0.1021591
sample estimates:
       cor
-0.2679728

> cor.test(epi$Prov2rutinTPK, epi$Prov2rutinCRP, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$Prov2rutinTPK and epi$Prov2rutinCRP
S = 4873.1, p-value = 0.6585
alternative hypothesis: true rho is not equal to 0
sample estimates:
```

```
        rho 
-0.08412151 

Warning message:
In cor.test.default(epi$Prov2rutinTPK, epi$Prov2rutinCRP, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2rutinTPK, epi$Prov2rutinCRP, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> 
> #Prov2extemMCF vs PIVKA
> cor.test(epi$Prov2extemMCF, epi$PIVKAMpostop, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$Prov2extemMCF and epi$PIVKAMpostop
t = -0.89872, df = 29, p-value = 0.3762
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4903501  0.2014808
sample estimates:
       cor 
-0.1646114 

> cor.test(epi$Prov2extemMCF, epi$PIVKAMpostop, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$Prov2extemMCF and epi$PIVKAMpostop
S = 6448.9, p-value = 0.1009
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
-0.3001744 

Warning message:
In cor.test.default(epi$Prov2extemMCF, epi$PIVKAMpostop, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> #RESULT:
> plot(epi$Prov2extemMCF, epi$PIVKAMpostop, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3, labels=NA)
> axis(side=2,lwd=0,cex.axis=3, line=0)
> 
> #Correlation between fibrinogen and Fibtem
```

```
> dev.new(width=5)
> # plot(epi$FIBpreop, epi$Prov2fibtemMCF, xlab="P-fibrinogen (g/L)", ylab =
"ROTEM FIBTEM MCF (mm)", abline(lm(epi$Prov2fibtemMCF~ epi
$FIBpreop)),cex.main=1.3, ylim=c(10,52),cex.lab=1.4, main="FIBTEM-MCF vs
Fibrinogen")
> plot(epi$FIBpreop, epi$Prov2fibtemMCF, xlab="P-fibrinogen (g/L)", ylab =
"ROTEM FIBTEM MCF (mm)",cex.main=1.3, ylim=c(10,52),cex.lab=1.4, main="FIBTEM-
MCF vs Fibrinogen")
> cor.test(epi$FIBpreop, epi$Prov2fibtemMCF, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$FIBpreop and epi$Prov2fibtemMCF
t = 1.3124, df = 30, p-value = 0.1993
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1259042  0.5379999
sample estimates:
      cor 
0.2330198 

> cor.test(epi$FIBpreop, epi$Prov2fibtemMCF, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$FIBpreop and epi$Prov2fibtemMCF
S = 4097, p-value = 0.1692
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.2490805 

Warning message:
In cor.test.default(epi$FIBpreop, epi$Prov2fibtemMCF, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> #result: NS
> # text(x=6, y=41, "N/S", pos=3, cex=2)
> arrows(1.85,9,,25,code=0,lwd=2,lty=3)
> arrows(2,9,4,,code=0,lwd=2,lty=3)
> 
> 
> plot(epi$FIBpostop, epi$Prov2fibtemMCF, xlab="", ylab = "", cex.axis=3,
cex=2.5, pch=19, axes=F)
> axis(side=1,lwd=4,cex.axis=3, labels=NA)
> axis(side=1,lwd=0,cex.axis=3, line=1)
> axis(side=2,lwd=4,cex.axis=3)
> #axis(side=2,lwd=4,cex.axis=3)
> 
> 
> #Correlation between fibrinogen and withdrawal time
> 
> plot(epi$withdrawaltime, epi$FIBpreop, xlab="Day of epidural withdrawal",
ylab = "P-fibrinogen (g/L)",abline(lm(epi$FIBpreop~epi
$withdrawaltime)),cex.main=1.3, cex.lab=1.4)
```

```
> cor.test(epi$withdrawaltime, epi$FIBpreop, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$withdrawaltime and epi$FIBpreop
t = 0.50375, df = 30, p-value = 0.6181
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.2655909  0.4266535
sample estimates:
       cor
0.09158469

> cor.test(epi$withdrawaltime, epi$FIBpreop, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho

data:  epi$withdrawaltime and epi$FIBpreop
S = 4996.4, p-value = 0.6467
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.0842434

Warning message:
In cor.test.default(epi$withdrawaltime, epi$FIBpreop, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=14, y=4.5, "N/S", pos=3, cex=2)
> #text(x=13, y=640, "r=0.56", pos=3, cex=2)
>
> #Correlation between aPTT and INTEM-MCF
>
> plot(epi$Prov2rutinAPTT, epi$Prov2intemMCF, xlab="aPTT (s)", ylab = "ROTEM
INTEM MCF (mm)", abline(lm(epi$Prov2intemMCF~epi$Prov2rutinAPTT)),cex.main=1.3,
cex.lab=1.4)
> cor.test(epi$Prov2rutinAPTT, epi$Prov2intemMCF, use="complete.obs",
method="pearson")

    Pearson's product-moment correlation

data:  epi$Prov2rutinAPTT and epi$Prov2intemMCF
t = -0.34078, df = 31, p-value = 0.7356
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.3960925  0.2882640
sample estimates:
        cor
-0.06109077

> cor.test(epi$Prov2rutinAPTT, epi$Prov2intemMCF, use="complete.obs",
method="spearman")

    Spearman's rank correlation rho
```

```
data:  epi$Prov2rutinAPTT and epi$Prov2intemMCF
S = 5773.4, p-value = 0.8459
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
0.03518698 

Warning message:
In cor.test.default(epi$Prov2rutinAPTT, epi$Prov2intemMCF, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=40, y=62, "N/S", pos=3, cex=2)
> #text(x=13, y=640, "r=0.56", pos=3, cex=2)
> 
> #Correlation between aPTT and INTEM-CT
> 
> plot(epi$Prov2rutinAPTT, epi$Prov2intemCT, xlab="aPTT (s)", ylab = "ROTEM
INTEM CT (s)", abline(lm(epi$Prov2intemCT~epi$Prov2rutinAPTT)),cex.main=1.3,
cex.lab=1.4)
> cor.test(epi$Prov2rutinAPTT, epi$Prov2intemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinAPTT and epi$Prov2intemCT
t = -0.89483, df = 31, p-value = 0.3778
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.4760559  0.1952656
sample estimates:
       cor 
-0.1586808 

> cor.test(epi$Prov2rutinAPTT, epi$Prov2intemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinAPTT and epi$Prov2intemCT
S = 6583.8, p-value = 0.5789
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
-0.100237 

Warning message:
In cor.test.default(epi$Prov2rutinAPTT, epi$Prov2intemCT, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=39, y=170, "N/S", pos=3, cex=2)
> #text(x=13, y=640, "r=0.56", pos=3, cex=2)
> 
> #Correlation between PT-INR and EXTEM-CT
> plot(epi$Prov2rutinPK, epi$Prov2extemCT, xlab="PT-INR", ylab = "ROTEM EXTEM
CT (s)", abline(lm(epi$Prov2extemCT~epi$Prov2rutinPK)),cex.main=1.3,
cex.lab=1.4)
```

```
> cor.test(epi$Prov2rutinPK, epi$Prov2extemCT, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinPK and epi$Prov2extemCT
t = 1.1177, df = 31, p-value = 0.2723
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1571117  0.5059370
sample estimates:
      cor 
0.1968129 

> cor.test(epi$Prov2rutinPK, epi$Prov2extemCT, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2rutinPK and epi$Prov2extemCT
S = 5462.4, p-value = 0.6296
alternative hypothesis: true rho is not equal to 0
sample estimates:
       rho 
0.08716727 

Warning message:
In cor.test.default(epi$Prov2rutinPK, epi$Prov2extemCT, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=1.5, y=45, "N/S", pos=3, cex=2)
> #text(x=13, y=640, "r=0.56", pos=3, cex=2)
> 
> 
> 
> #Correlation between PT-INR and EXTEM-MCF
> plot(epi$Prov2rutinPK, epi$Prov2extemMCF, xlab="PT-INR", ylab = "ROTEM EXTEM
MCF (mm)", abline(lm(epi$Prov2extemMCF~epi$Prov2rutinPK)),cex.main=1.3,
cex.lab=1.4)
> cor.test(epi$Prov2rutinPK, epi$Prov2extemMCF, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2rutinPK and epi$Prov2extemMCF
t = -1.4426, df = 31, p-value = 0.1592
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.5470235  0.1012061
sample estimates:
       cor 
-0.2508175 

> cor.test(epi$Prov2rutinPK, epi$Prov2extemMCF, use="complete.obs",
method="spearman")
```

```
	Spearman's rank correlation rho

data:  epi$Prov2rutinPK and epi$Prov2extemMCF
S = 6546.7, p-value = 0.6027
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho 
-0.09402775 

Warning message:
In cor.test.default(epi$Prov2rutinPK, epi$Prov2extemMCF, use =
"complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=1.5, y=65, "N/S", pos=3, cex=2)
> #text(x=13, y=640, "r=0.56", pos=3, cex=2)
> 
> 
> 
> 
> #Correlation between FII and PIVKA
> #Preop
> plot(epi$F2preop, epi$PIVKAMpreop, xlab="Preoperative FII (kIE/L)", ylab =
"Preoperative mean PIVKA (µg/L)", abline(lm(epi$PIVKAMpreop~epi
$F2preop)),cex.main=1.3, cex.lab=1.4)
> cor.test(epi$F2preop, epi$PIVKAMpreop, use="complete.obs", method="pearson")

	Pearson's product-moment correlation

data:  epi$F2preop and epi$PIVKAMpreop
t = 0.81739, df = 36, p-value = 0.4191
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.1930289  0.4358591
sample estimates:
     cor 
0.134984 

> cor.test(epi$F2preop, epi$PIVKAMpreop, use="complete.obs", method="spearman")

	Spearman's rank correlation rho

data:  epi$F2preop and epi$PIVKAMpreop
S = 7512.8, p-value = 0.2852
alternative hypothesis: true rho is not equal to 0
sample estimates:
     rho 
0.177936 

Warning message:
In cor.test.default(epi$F2preop, epi$PIVKAMpreop, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> text(x=1, y=10, "Spearman: Rho=0.17//P=0.029", pos=3, cex=2)
> text(x=1, y=20, "Pearson: t=0.81//P=0.042", pos=3, cex=2)
> 
> #Postop
> plot(epi$postop, epi$PIVKAMpostop, xlab="Postoperative FII (kIE/L)", ylab =
```

```
"Postoperative mean PIVKA (µg/L)", abline(lm(epi$PIVKAMpostop~epi
$F2postop)),cex.main=1.3, cex.lab=1.4)
Error in xy.coords(x, y, xlabel, ylabel, log) :
  'x' and 'y' lengths differ
> cor.test(epi$F2postop, epi$PIVKAMpostop, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$F2postop and epi$PIVKAMpostop
t = 0.62829, df = 29, p-value = 0.5347
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.2486658  0.4516782
sample estimates:
      cor
0.1158852

> cor.test(epi$F2postop, epi$PIVKAMpostop, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho

data:  epi$F2postop and epi$PIVKAMpostop
S = 3200, p-value = 0.05082
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.3548387

> text(x=1.2, y=300, "Spearman: Rho=0.35//P=0.051", pos=3, cex=2)
> text(x=1, y=200, "Pearson: t=0.62//P=0.53", pos=3, cex=2)
>
> #####
> #Correlation between postop extem MCF och F13.
> plot(epi$Prov2extemMCF, epi$F13postop, xlab="postop extem MCF", ylab =
"postop F13", abline(lm(epi$F13postop~epi$Prov2extemMCF)),cex.main=1.3,
cex.lab=1.4)
> cor.test(epi$Prov2extemMCF, epi$F13postop, use="complete.obs",
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2extemMCF and epi$F13postop
t = 2.6074, df = 29, p-value = 0.01426
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.09631896 0.68443758
sample estimates:
      cor
0.4357859

> cor.test(epi$Prov2extemMCF, epi$F13postop, use="complete.obs",
method="spearman")

	Spearman's rank correlation rho
```

```
data:  epi$Prov2extemMCF and epi$F13postop
S = 3359.7, p-value = 0.07668
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.3226419 

Warning message:
In cor.test.default(epi$Prov2extemMCF, epi$F13postop, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> 
> #Correlation between postop intem MCF och F13.
> plot(epi$Prov2intemMCF, epi$F13postop, xlab="postop intem MCF", ylab = 
"postop F13", abline(lm(epi$F13postop~epi$Prov2intemMCF)),cex.main=1.3, 
cex.lab=1.4)
> cor.test(epi$Prov2intemMCF, epi$F13postop, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2intemMCF and epi$F13postop
t = 1.7327, df = 29, p-value = 0.09377
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.05389246  0.59595588
sample estimates:
      cor 
0.3062968 

> cor.test(epi$Prov2intemMCF, epi$F13postop, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2intemMCF and epi$F13postop
S = 3332.6, p-value = 0.07155
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.3281047 

Warning message:
In cor.test.default(epi$Prov2intemMCF, epi$F13postop, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> 
> #Correlation between postop fibtem MCF och F13.
> plot(epi$Prov2fibtemMCF, epi$F13postop, xlab="postop fibtem MCF", ylab = 
"postop F13", abline(lm(epi$F13postop~epi$Prov2fibtemMCF)),cex.main=1.3, 
cex.lab=1.4)
> cor.test(epi$Prov2fibtemMCF, epi$F13postop, use="complete.obs", 
method="pearson")

	Pearson's product-moment correlation

data:  epi$Prov2fibtemMCF and epi$F13postop
```

```
t = 2.8328, df = 29, p-value = 0.008309
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1331763 0.7037890
sample estimates:
      cor 
0.4655473 

> cor.test(epi$Prov2fibtemMCF, epi$F13postop, use="complete.obs", 
method="spearman")

	Spearman's rank correlation rho

data:  epi$Prov2fibtemMCF and epi$F13postop
S = 2650.5, p-value = 0.008296
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho 
0.4656307 

Warning message:
In cor.test.default(epi$Prov2fibtemMCF, epi$F13postop, use = "complete.obs",  :
  Cannot compute exact p-value with ties
> 
```