Article title: Validation of distal radius failure load predictions by homogenized- and micro- Finite Element analyses based on second generation high resolution peripheral quantitative CT images.

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Electronic Supplementary Material 4: Scripts and tasks to perform the homogenized- and micro- FE analyses

mFE analysis

```
$!
$!       _/_/_/  _/_/_/    _/
$!        _/    _/    _/  _/         Image Processing Language
$!       _/    _/_/_/    _/
$!      _/    _/       _/           (c) Eindhoven Univ. of Technology
$!    _/_/_/  _/      _/_/_/_/          Bert v. Rietbergen
$!
$!
$! Script for XtremeCT2 micro-FE analysis.
$! Requires SCANCO IPLFE v1.16 or higher to run
$!
$! Call as: @mFE.com disk2:[microct.data.00001234.00005678]c0001234.aim
$!
$! with the numbers 00001234 and 00005678 replaced by the correct sample number and
$! measurement number respectively, and the filename c0001234 replaced by the correct file
$! name. In case the data is stored at another disk also the disk specification should be replaced.
$!
$! This script uses the E5E6 cortical/cancellous compartment definitions
$! Required input files: _SEG.AIM and .GOBJ
$!
$! ------------------------------------------------------------------------------
$! Definition of base filename and jobname:
$  FILENAME    = F$PARSE("'P1'",,,"NAME") - "_SEG"
$  DEV         = F$PARSE("'P1'",,,"DEVICE")
$  DIR         = F$PARSE("'P1'",,,"DIRECTORY")
$  FILEBASE    = DEV + DIR + FILENAME
$  JOB_NAME    = FILEBASE + "_MFE"
$! ------------------------------------------------------------------------------
$! Definition of symbols used in the script:
$  IPL_SEGAIM   = FILEBASE + "_SEG.AIM"        ! input: segmented aim file
$  IPL_FNAME0   = JOB_NAME + ".AIM"            ! output: FE aim file
$  IPL_FNAME1   = JOB_NAME + "_RESULT.AIM"     ! output: FE result aim file
$  IPL_GOBJ0    = FILEBASE + ".GOBJ"           ! input: periosteal contour
$  IPL_PROBLEM  = 33                           ! problem_nr
$  IPL_FEPAR_NO = 43                           ! variable_nr for post-proc.
$  IPL_FEA0     = 10000                        ! Young's modulus trab. tissue
$  IPL_FEA1     = 10000                        ! Young's modulus cort. tissue
$  IPL_FEA2     = "-0.05"                      ! Critical_volume for strength
$  IPL_FEA3     = "0.01"                       ! Critical_value   ,,     ,,
$!
$! ---- Check if the required input files exist
$!
```

```
$  IF (F$SEARCH(IPL_SEGAIM) .EQS. "")
$  THEN
$    WRITE SYS$OUTPUT " ------------------------------------------------------------------------"
$    WRITE SYS$OUTPUT " ERROR: cannot find file: ",IPL_SEGAIM
$    WRITE SYS$OUTPUT " This task can only run after the standard patient evaluation is
completed
$    WRITE SYS$OUTPUT " ------------------------------------------------------------------------"
$    STOP
$  ENDIF
$  IF (F$SEARCH(IPL_GOBJ0) .EQS. "")
$  THEN
$    WRITE SYS$OUTPUT " ------------------------------------------------------------------------"
$    WRITE SYS$OUTPUT " ERROR: cannot find file: ",IPL_GOBJ0
$    WRITE SYS$OUTPUT " This task can only run after the standard patient evaluation is
completed
$    WRITE SYS$OUTPUT " ------------------------------------------------------------------------"
$    STOP
$  ENDIF
$  ON ERROR THEN EXIT
$! ---------------------------------------------------------------------------
$! First part of the IPL script: pre-processing
$! ---------------------------------------------------------------------------
$  IPLFE_BATCH

! ---- Read segmented aim generated by the default image processing. For XT2
!      this file already has different values for the cort/trab compartments

/read
  -name                 comb
  -filename              "IPL_SEGAIM

! ---- only include the regions indicated by the gobj

/gobj_maskaimpeel_ow
  -input_output           comb
  -gobj_filename          "IPL_GOBJ0
  -peel_iter              0

! ---- Delete unconnected parts

/cl_rank_extract
  -input                comb
  -output               cl
  -first_rank           1
  -last_rank            1
  -connect_boundary       false
  -value_in_range         1
```

```
/multiply_volumes
 -input1                comb
 -input2                cl
 -output                out
 -common_region_only       false
 -multiply_zero_pixels     true

/del comb
/del cl

! ---- Remove empty space around the bone, if any

/bounding_box_cut
 -input                 out
 -output                fem
 -z_only                false
 -border                0 0 0

/del out

/write
 -name                  fem
 -filename               "IPL_FNAME0        ! (_MFE.AIM)
 -compress_type            bin
..
$! ----------------------------------------------------------------------------
$! Second part of the IPL script: the actual FE-analysis
$! ----------------------------------------------------------------------------
$  IPLFE_BATCH

/read
 -name                  fem
 -filename               "IPL_FNAME0        ! (_MFE.AIM)

/fe_solve3
 -in                  fem
 -fea_file_name           "JOB_NAME         ! (_MFE)
 -problem_nr             "IPL_PROBLEM
 -scale_factor           -0.01
 -list_option            1
 -tolerance_force         1.000000E-03
 -tolerance_displ         1.000000E+00
 -max_nr_iter            50000
 -restart_option          0
 -comp_val_mat_001        126
 -Ymodulus_mat_001        "IPL_FEA0
 -Poissonr_mat_001        3.000000E-01
 -comp_val_mat_002        127
```

```
  -Ymodulus_mat_002         "IPL_FEA1
  -Poissonr_mat_002         3.000000E-01
  -comp_val_mat_003         0
  -Ymodulus_mat_003         1.000000E+04
  -Poissonr_mat_003         3.000000E-01
..
$! ---------------------------------------------------------------------------
$! Third part of the IPL script: post-processing
$! ---------------------------------------------------------------------------
$  IPLFE_BATCH

/db_scanco_activate
  -write                    true

! ---- use the voxgobj to get the correct threshold in the database

/read
  -name                     fem
  -filename                 "IPL_FNAME0        ! (_MFE.AIM)

/voxgobj_scanco_param
  -input                    fem
  -gobj_filename            "IPL_GOBJ0
  -peel_iter                -1
  -region_number            0

/del fem

! ---- do the postprocessing and store results in the database

/fe_post
  -post_file_name           "JOB_NAME          ! (_MFE)
  -output                   res
  -variable_nr              "IPL_FEPAR_NO
  -loadcase_nr              1
  -list_option              1
  -interpol_option          1
  -averaging_option         0
  -test_dir                 0
  -critical_variable_nr     "IPL_FEPAR_NO      ! Not available in FE v01.*
  -critical_volume          "IPL_FEA2
  -critical_value           "IPL_FEA3

/write
  -name                     res
  -filename                 "IPL_FNAME1        ! (_MFE_RESULT.AIM)
..
$!
```

hFE analysis

```
$!
$!       _/_/_/  _/_/_/   _/
$!        _/   _/   _/  _/         Image Processing Language
$!       _/   _/_/_/   _/
$!      _/   _/       _/          (c) Eindhoven Univ. of Technology
$!    _/_/_/  _/      _/_/_/_/          Bert v. Rietbergen
$!
$!
$! Script for XtremeCT2 homogenized-FE analysis
$! Requires SCANCO IPLFE v2.01 or higher to run
$!
$! Call as: @hFE.com disk2:[microct.data.00001234.00005678]c0001234.aim
$!
$! with the numbers 00001234 and 00005678 replaced by the correct sample number
$! and measurement number respectively, and the filename c0001234 replaced by
$! the correct file name. In case the data is stored at another disk also the
$! disk specification should be replaced.
$!
$! This script uses the E5E6 cortical/cancellous compartment definitions
$! Required input files: .AIM, _SEG.AIM, .GOBJ and _TRAB_MASK.GOBJ
$!
$! ------------------------------------------------------------------------------
$! Definition of base filename and jobname:
$  FILENAME    = F$PARSE("'P1'",,,"NAME") - "_SEG"
$  DEV         = F$PARSE("'P1'",,,"DEVICE")
$  DIR         = F$PARSE("'P1'",,,"DIRECTORY")
$  FILEBASE    = DEV + DIR + FILENAME
$  JOB_NAME    = FILEBASE + "_HFE"
$!
$! Definition of symbols used in the script:
$  IPL_AIM     = FILEBASE + ".AIM"             ! input: aim file
$  IPL_SEGAIM  = FILEBASE + "_SEG.AIM"         ! input: segmented aim
$  IPL_FNAME0  = JOB_NAME + ".INP"             ! output: FE input inp
$  IPL_FNAME1  = JOB_NAME + "_FST_INC_RESULT.AIM"! output: first inc res.
$  IPL_FNAME2  = JOB_NAME + "_LST_INC_RESULT.AIM"! output: last inc res.
$  IPL_FNAME3  = JOB_NAME + "_BASE.INP"        ! temp: model input
$  IPL_FNAME4  = JOB_NAME + "_TRAB.INP"        ! temp: model input
$  IPL_GOBJ0   = FILEBASE + ".GOBJ"            ! input: perios. contour
$  IPL_GOBJ1   = FILEBASE + "_TRAB_MASK.GOBJ"  ! input: endost. contour
$  IPL_MISC1_0 = 28                            ! downscale factor
$  IPL_MISC1_1 = 1                             ! meshing_option
$  IPL_MISC1_2 = 1                             ! fabric_option
$  IPL_PROBLEM = 33                            ! problem_nr
$  IPL_FEPAR_NO = 42                           ! var. for first inc.
$  IPL_FEA0    = 120                           ! var. for last inc.
```

```
$!
$! ---- Check if the required input files exist
$!
$  IF (F$SEARCH(IPL_AIM) .EQS. "")
$  THEN
$    WRITE SYS$OUTPUT " ------------------------------------------------------------------------------"
$    WRITE SYS$OUTPUT " ERROR: cannot find file: ",IPL_AIM
$    WRITE SYS$OUTPUT " This task can only run after the standard patient evaluation is
completed
$    WRITE SYS$OUTPUT " ------------------------------------------------------------------------------"
$    STOP
$  ENDIF
$  IF (F$SEARCH(IPL_SEGAIM) .EQS. "")
$  THEN
$    WRITE SYS$OUTPUT " ------------------------------------------------------------------------------"
$    WRITE SYS$OUTPUT " ERROR: cannot find file: ",IPL_SEGAIM
$    WRITE SYS$OUTPUT " This task can only run after the standard patient evaluation is
completed
$    WRITE SYS$OUTPUT " ------------------------------------------------------------------------------"
$    STOP
$  ENDIF
$  IF (F$SEARCH(IPL_GOBJ0) .EQS. "")
$  THEN
$    WRITE SYS$OUTPUT " ------------------------------------------------------------------------------"
$    WRITE SYS$OUTPUT " ERROR: cannot find file: ",IPL_GOBJ0
$    WRITE SYS$OUTPUT " This task can only run after the standard patient evaluation is
completed
$    WRITE SYS$OUTPUT " ------------------------------------------------------------------------------"
$    STOP
$  ENDIF
$  IF (F$SEARCH(IPL_GOBJ1) .EQS. "")
$  THEN
$    WRITE SYS$OUTPUT " ------------------------------------------------------------------------------"
$    WRITE SYS$OUTPUT " ERROR: cannot find file: ",IPL_GOBJ1
$    WRITE SYS$OUTPUT " This task can only run after the standard patient evaluation is
completed
$    WRITE SYS$OUTPUT " ------------------------------------------------------------------------------"
$    STOP
$  ENDIF
$!
$! ---- When using hex elements, use a low mask threshold such that any element
$!      touching the mask is included. When using tet elements, threshold at 50%
$!      to get the proper contours
$!
$  IF (IPL_MISC1_1 .EQ. 1)
$  THEN
$    SCALE_THRESHOLD == 10
$  ELSE
```

```
$    IF (IPL_MISC1_1 .EQ. 2)
$    THEN
$      SCALE_THRESHOLD == 500
$    ELSE
$      WRITE SYS$OUTPUT " ------------------------------------------------------"
$      WRITE SYS$OUTPUT " Invalid meshing option: ", IPL_MISC1_1
$      WRITE SYS$OUTPUT " Valid options are 1 and 2 only
$      WRITE SYS$OUTPUT " ------------------------------------------------------"
$      EXIT 2
$    ENDIF
$  ENDIF
$  ON ERROR THEN EXIT
$! ----------------------------------------------------------------------------
$! First part of the IPL script: pre-processing and homogenization
$! ----------------------------------------------------------------------------
$  IPLFE_BATCH

! ---- Read the original input files

/read
  -name                org_in
  -filename             "IPL_AIM

/read
  -name                seg_in
  -filename             "IPL_SEGAIM

/gobj_to_aim
  -gobj_filename          "IPL_GOBJ0
  -output              full_mask_in
  -peel_iter            0

/gobj_to_aim
  -gobj_filename          "IPL_GOBJ1
  -output              trab_mask_in
  -peel_iter            0

! ---- Make a common 'canvas' to which all images will be pasted to ensure
!      they are positioned in the proper way relative to each other when
!      removing the pos later

/threshold
  -input                org_in
  -output                tmp
  -lower_in_perm_aut_al     999999
  -upper_in_perm_aut_al     0
  -value_in_range          0
  -unit                 0
```

```
! ---- Set a border of downscale_factor voxels around the canvas in x/y-dir
!      This is needed later for better density interpolation when using tet elements

/border_change
  -input                tmp
  -output               canvas
  -border               "IPL_MISC1_0 "IPL_MISC1_0 0

/del tmp

! ---- Now place all images in the canvas

/concat
  -input1               canvas
  -input2               org_in
  -output               org_canv
  -common_region_only       false
  -add_not_overlay          false

/del org_in

/concat
  -input1               canvas
  -input2               seg_in
  -output               seg_canv
  -common_region_only       false
  -add_not_overlay          false

/del seg_in

/concat
  -input1               canvas
  -input2               full_mask_in
  -output               full_mask_canv
  -common_region_only       false
  -add_not_overlay          false

/del full_mask_in

/concat
  -input1               canvas
  -input2               trab_mask_in
  -output               trab_mask_canv
  -common_region_only       false
  -add_not_overlay          false

/del trab_mask_in
```

```
! ---- Now all images are pasted in the same canvas, crop all images to the volume of
!      interest (voi) which is defined as the volume of seg with a border in x/y-dir
!      of downscale_factor voxels.
!      This will remove any slices potentially lost due to slice matching from all images.

! ---- first get the voi

/gobj_maskaimpeel_ow
  -input_output            seg_canv
  -gobj_filename           "IPL_GOBJ0
  -peel_iter               0

/bounding_box_cut
  -input                   seg_canv
  -output                  voi
  -z_only                  false
  -border                  "IPL_MISC1_0 "IPL_MISC1_0 0              ! Create the voi border in x/y-dir only

/set_value
  -input                   voi
  -value_object            0
  -value_background        0

! ---- then crop all images to the voi dim and pos

/concat
  -input1                  voi
  -input2                  org_canv
  -output                  org
  -common_region_only      true
  -add_not_overlay         false

/del org_canv

/concat
  -input1                  voi
  -input2                  seg_canv
  -output                  seg
  -common_region_only      true
  -add_not_overlay         false

/del seg_canv

/concat
  -input1                  voi
  -input2                  full_mask_canv
  -output                  full_mask
```

```
 -common_region_only       true
 -add_not_overlay         false

/del full_mask_canv

/concat
 -input1               voi
 -input2               trab_mask_canv
 -output               trab_mask
 -common_region_only       true
 -add_not_overlay         false

/del trab_mask_canv
/del voi

/exa org geo
/exa seg geo
/exa trab_mask geo
/exa full_mask geo

! ---- Set the pos of all files to zero such that alignment of downscaled and
!     high-resolution images is exact for any down_scale_factor.
!     For example, if this is not done and the pos was 49 and the downscale
!     factor 10, the downscaled image would have a pos of 4. The error in the
!     pos thus would be 9 voxels in size. This would affect the calculation of
!     the element density/fabric later. By setting the pos to zero, no such
!     errors occur

/header_geo_set
 -input               org
 -off_new              -1  -1  -1
 -pos_new               0   0   0
 -el_size_mm_new         -1.0 -1.0 -1.0

/header_geo_set
 -input               seg
 -off_new              -1  -1  -1
 -pos_new               0   0   0
 -el_size_mm_new         -1.0 -1.0 -1.0

/header_geo_set
 -input               full_mask
 -off_new              -1  -1  -1
 -pos_new               0   0   0
 -el_size_mm_new         -1.0 -1.0 -1.0

/header_geo_set
 -input               trab_mask
```

```
  -off_new                -1   -1   -1
  -pos_new                 0    0    0
  -el_size_mm_new          -1.0 -1.0 -1.0

/exa trab_mask geo

! ------ create the cortical and trabecular compartment masks

/subtract_aims
  -input1                 full_mask
  -input2                 trab_mask
  -output                 cort_mask

/set_value
  -input                  trab_mask
  -value_object           1
  -value_background       0

/set_value
  -input                  cort_mask
  -value_object           2
  -value_background       0

! ---- Generate the mesh

/fe_mesh
  -in                   full_mask
  -out_filename         "IPL_FNAME3       ! (_HFE_BASE.INP)
  -output_format         abaqus
  -down_scale_factor      "IPL_MISC1_0
  -threshold_value       "SCALE_THRESHOLD
  -threshold_unit        6
  -max_nr_groups          0
  -meshing_option         "IPL_MISC1_1
  -element_order          1
  -use_hex_as_tet         false
  -oddcase_start          true
  -optimize_bw            fasle
  -max_aspect_ratio       1.000000
  -min_side_length        0.100000
  -global_pos_flag        true
  -problem_nr             0
  -max_nr_mat             0
  -density_option         0
  -ref_density            1.000000
  -Emod_const_a           10000.000000
  -Emod_const_b           0.000000
  -Emod_const_p           1.000000
```

```
 -Poissons_ratio          0.300000

/del full_mask

! ---- calculate element density and fabric for the trabecular elements

/hfe_homogenize
 -org                 org
 -seg                 seg
 -mask                  trab_mask
 -mesh_infile_name        "IPL_FNAME3        ! (_HFE_BASE.INP)
 -mesh_outfile_name       "IPL_FNAME4        ! (_HFE_TRAB.INP)
 -VOI_radius            2.000000
 -volfrac_option          2
 -volfrac_ref_density     1200.000000
 -volfrac_min           0.001
 -fabric_option          "IPL_MISC1_2
 -fabric_min_volume       8.000000
 -fabric_min_volfrac      0.050000
 -fabric_power_transform   1.0
 -MIL_peel_iter          0
 -MIL_ip_sigma           0.000000
 -MIL_ip_support         0
 -MIL_ip_threshold        50
 -MIL_nr_ave_iter         2
 -MIL_t_dir_radius        2
 -MIL_epsilon           1.200000
 -list_option           2

/del trab_mask

! ---- calculate element density but no fabric for the cortical elements
!     Set a very small radius: will be set to element size by /hfe_homogenize

/hfe_homogenize
 -org                 org
 -seg                 seg
 -mask                  cort_mask
 -mesh_infile_name        "IPL_FNAME4        ! (_HFE_TRAB.INP)
 -mesh_outfile_name       "IPL_FNAME0        ! (_HFE.INP)
 -VOI_radius            0.010000
 -volfrac_option          2
 -volfrac_ref_density     1200.000000
 -volfrac_min           0.001
 -fabric_option          0
 -fabric_min_volume       8.000000
 -fabric_min_volfrac      0.050000
 -fabric_power_transform   1.0
```

```
  -MIL_peel_iter           0
  -MIL_ip_sigma            0.000000
  -MIL_ip_support          0
  -MIL_ip_threshold        50
  -MIL_nr_ave_iter         2
  -MIL_t_dir_radius        2
  -MIL_epsilon             1.200000
  -list_option             2

/del org
/del seg
/del cort_mask
..
$  DEL 'IPL_FNAME3';*
$  DEL 'IPL_FNAME4';*
$!
$! ----------------------------------------------------------------------------
$! Second part of the IPL script: the actual FE-analysis
$! ----------------------------------------------------------------------------
$!
$  IPLFE_BATCH

/hfe_solve
  -in_file_name            "IPL_FNAME0        ! (_HFE.INP)
  -job_file_name           "JOB_NAME          ! (_HFE_XT2_STD)
  -Eparams                 19010. 7851 0.223
  -Epowers                 2.00 0.96 1.00
  -Sparams                 131. 166. 67.3
  -Spowers                 1.82 0.79 1.00
  -CHI                   0.23 0.26
  -Dparams                 0.750 7.000
  -Hparams                 100.000 0.020
  -problem_nr              "IPL_PROBLEM
  -scale_factor            -0.05000000
  -nod_select_tol          0.010
  -nr_steps                100
  -tolerance               0.001
  -max_nr_iter             20
  -assembly_every_iters     3
  -max_force_drop          0.020000
  -list_option             1
..
$!
$! ----------------------------------------------------------------------------
$! Third part of the IPL script: additional post-processing
$! ----------------------------------------------------------------------------
$!
$  POST1:
```

```
$  IF (IPL_FEPAR_NO.EQ.0) THEN GOTO POST2
$  IPLFE_BATCH

/db_scanco_activate
  -write                true

! ---- use the voxgobj to get the correct threshold in the database

/read
  -name                 in
  -filename              "IPL_SEGAIM

/voxgobj_scanco_param
  -input                in
  -gobj_filename          "IPL_GOBJ0
  -peel_iter             -1
  -region_number          0

! ---- create first plot

/hfe_post
  -job_file_name          "JOB_NAME         ! (_HFE_XT2_STD)
  -out                  res
  -dim_out               -1 -1 -1
  -pos_out               -1 -1 -1
  -el_size_mm_out         -1 -1 -1
  -variable_nr            "IPL_FEPAR_NO
  -loadstep_nr            1
  -interpol_option        2
  -defplot_scaling        0.000000
  -list_option            1

/write
  -name                 res
  -filename              "IPL_FNAME1       ! (_HFE_FST_INC_RESULTS.AIM)
  -compress_type          bin
..
$!
$  POST2:
$  IF (IPL_FEA0.EQ.0) THEN EXIT
$  IPLFE_BATCH

/db_scanco_activate
  -write                true

! ---- create 2nd plot

/hfe_post
```

```
 -job_file_name          "JOB_NAME         ! (_HFE_XT2_STD)
 -out                 res
 -dim_out              -1 -1 -1
 -pos_out              -1 -1 -1
 -el_size_mm_out         -1 -1 -1
 -variable_nr           "IPL_FEA0
 -loadstep_nr           99999
 -interpol_option        2
 -defplot_scaling       0.000000
 -list_option           1

/write
 -name                res
 -filename             "IPL_FNAME2       ! (_HFE_LST_INC_RESULTS.AIM)
 -compress_type          bin
..
$!
```