HOW TO DEFINE AN ANALYSIS WITH THE GP-TOOL

General

The name of the analysis will be combined from the settings of the analysis. This allows to identify analysis easily by name.

It is defined by the loading name, the material name, the values a, b and biological growth, the loading factor, the number of iterations and the growth method separated by "_".

Example: "generic_mat1_a_0.02_b_0.01_bio_double_f_1_iter_1_FNDD"

Loading Conditions

1. Define a name that you can identify the loading conditions easily later (e.g.: "generic" for generic MSK model, "personalized" for model with AVA and NSA of participant. …)
2. Create a loading file (.mat) prior to creating an analysis with the previous TAB ("Loading"). Then, **select the created loading file** when creating the analysis.
3. Specify, if you want to apply the hip joint contact force only in one desired direction. **Typically, do not check anything. This applies the total hip joint contact force.**
4. Specify whether you want to **reduce/increase** the hip joint contact force by a **factor**.

Material Properties

Define a name that you can identify the material properties easily later (e.g.: mat1, mat2, mat3, …)

The femur is split into 5 different parts depending on the segmentation you provided (see programs README for an example, section "Femur Segmentation"):

- Trabecular proximal: this is the part on top (above and below the growth plate
- Growth plate
- Cortical bone: this is the outer part of the femoral shaft
- Bone marrow: this is the inner part of the femoral shaft
- Trabecular distal: this is the part below the femoral shaft

Each parts' material properties (Youngs' modulus (stiffness) and Poisson-ratio) can be defined. A transition zone between trabecular proximal and growth plate will be added where material properties will be interpolated.

Keep in mind, that too low values lead to very high deformation and maybe, the analysis will not converge. **If the analysis is not converging, try to use higher Youngs' moduli.**

Growth Parameters

Currently, growth is prediction is under construction. It possible to either model growth by FEBio with nodal forces (default) or with Abaqus and "Thermal expansion".
Each element / node will have applied a growth direction and a growth amount depending on the selected properties.

Select the desired growth method. There are different methods to predict femoral bone growth:

- Femoral Neck Deflection Direction (FNDD) (Yadav et al., 2016)
- Principal Stress Direction (PSD) (Yadav et al., 2016)
- Normal to growth plate orientation (NORM)

"Avoid negative growth" replaces negative growth values by zero.

"biological growth = 2 * mechanical growth" adds twice the maximum occurring mechanical growth value (osteogenic index) to all elements

"growth factor" is just a factor to scale the applied growth

"nr of growth iterations" defines in how many iterations the growth should be simulated. For each iteration the "grown" geometry of the last iteration will be used to calculate stresses etc.
This is also described by (Carriero et al., 2011)

Read this paper for more information:

Carriero, A., Jonkers, I., and Shefelbine, S. J. (2011). Mechanobiological prediction of proximal femoral deformities in children with cerebral palsy. *Computer Methods in Biomechanics and Biomedical Engineering* 14, 253–262. doi: 10.1080/10255841003682505.

Yadav, P., Shefelbine, S. J., and Gutierrez-Farewik, E. M. (2016). Effect of growth plate geometry and growth direction on prediction of proximal femoral morphology. *Journal of Biomechanics* 49, 1613–1619. doi: 10.1016/j.jbiomech.2016.03.039.