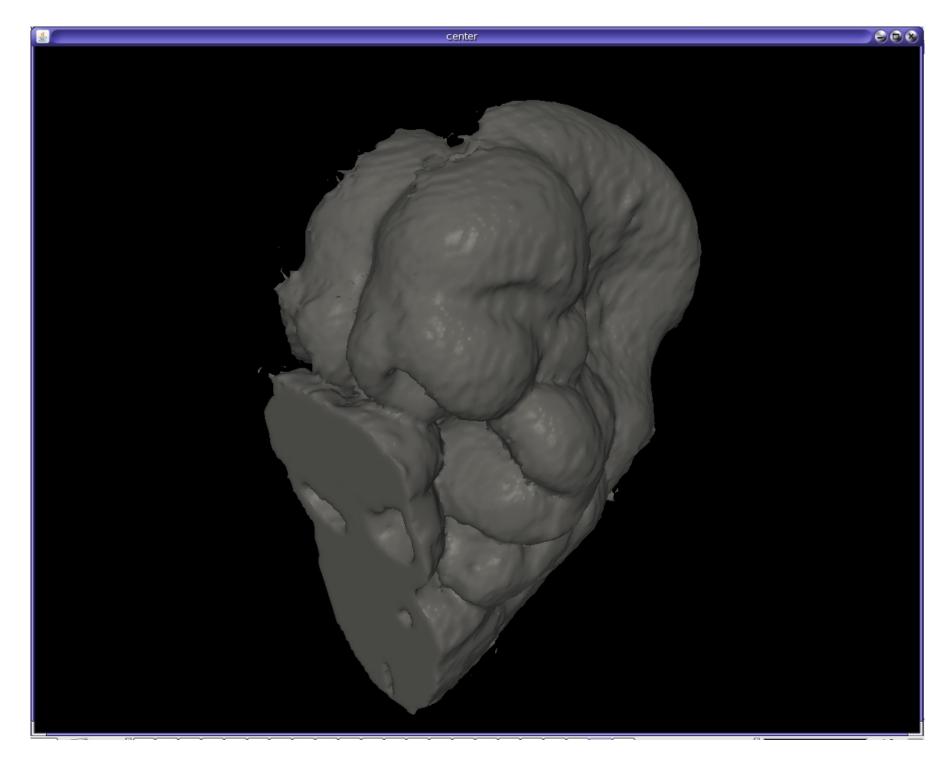
## Integrating Cell Proliferation and Morphometrical Data for Development Analysis of Mice

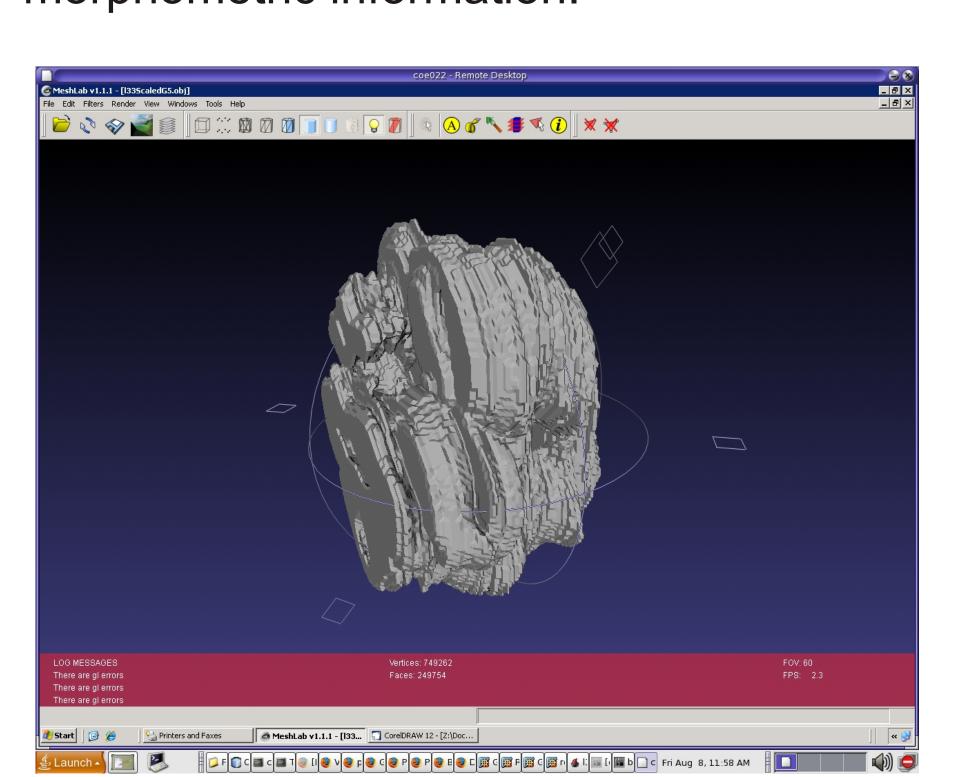
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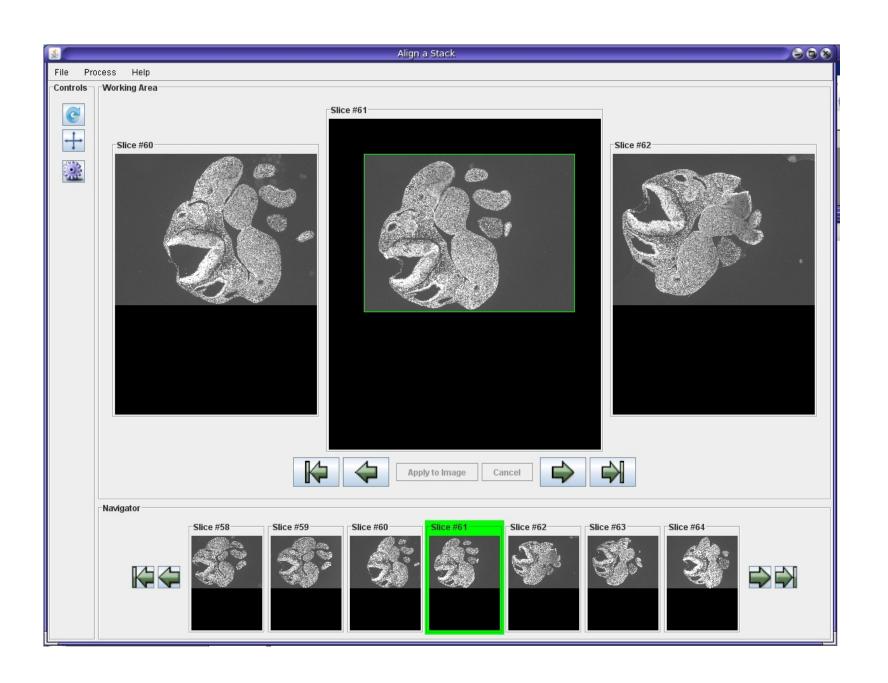
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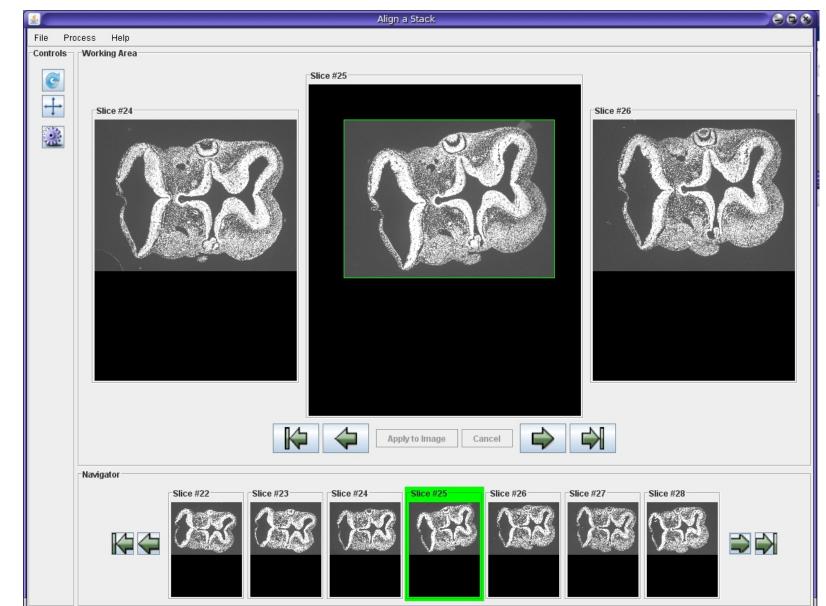
Identifying cell proliferation changes within and across subjects at different stages of growth is important in morphometrics research. We want to model the relationship between cell proliferation patterns and external facial morphology and its relation with cleft lip malformation in mice. To investigate this relationship, we compared 3D representations obtained by processing MRI, CT or micro-CT scans with histological data.



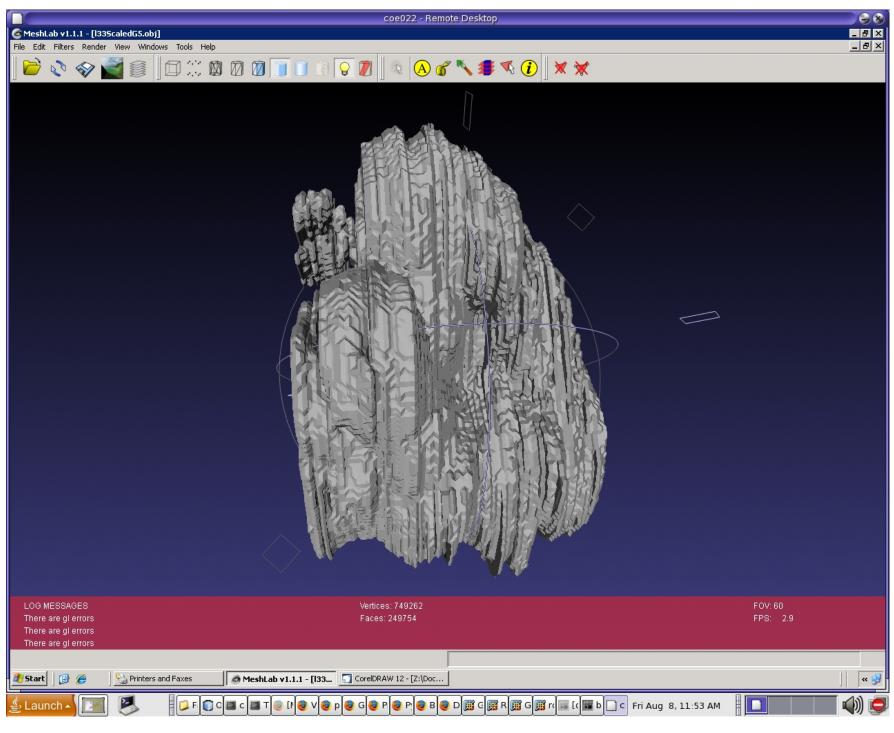
Our subjects are mouse embryos. Here we show the 3D surface model obtained from a micro-CT scan that was taken before a subject was sectioned in thin slices. The surface model is used to obtain morphometric information.

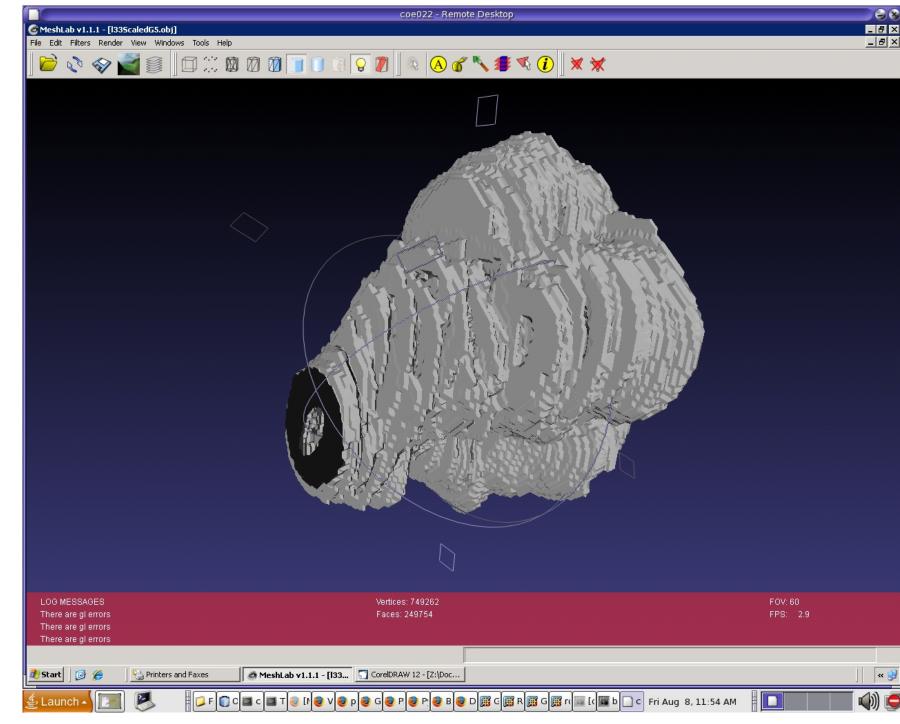




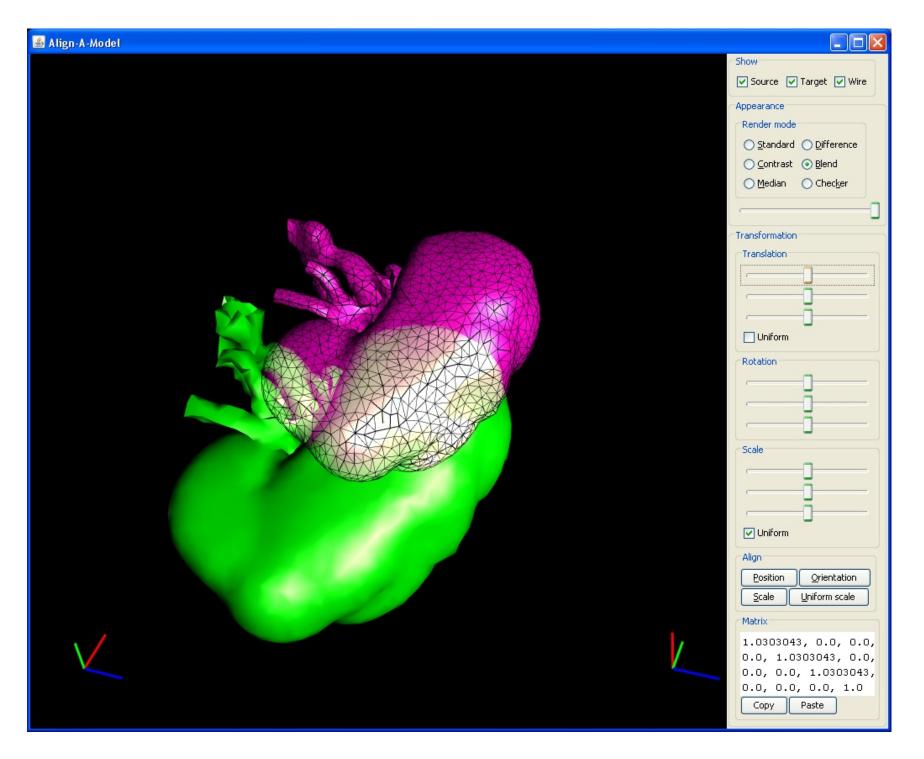


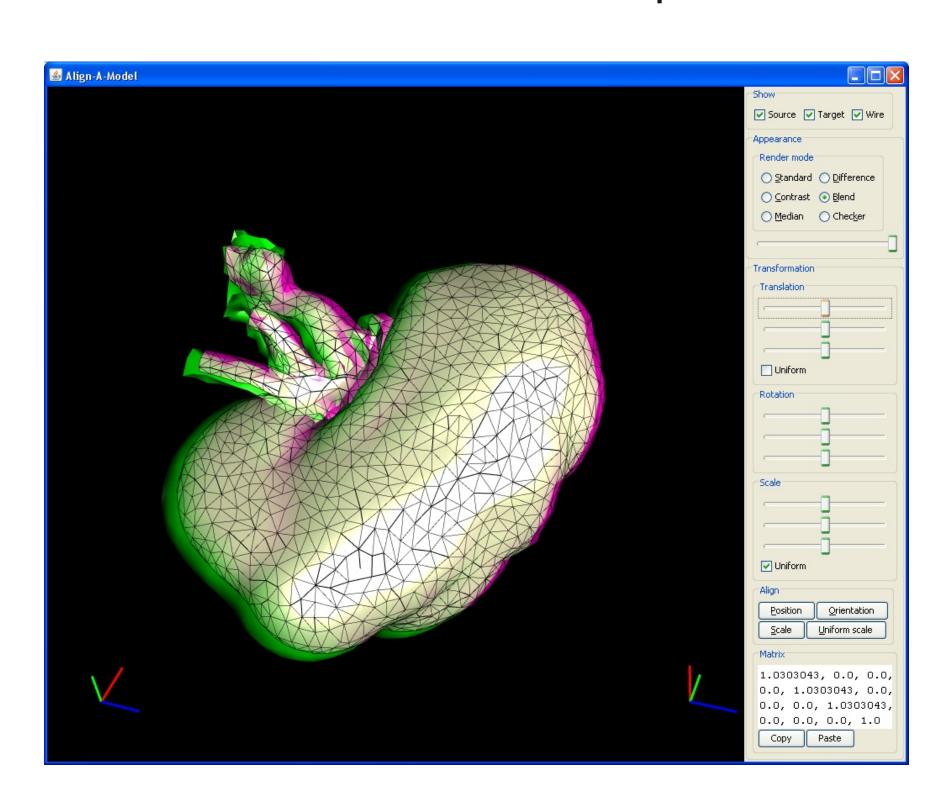
The model is sliced and photographed to obtain cell proliferation data. During this process the images produced are misaligned with respect to each other, so we need to align the whole stack to reconstruct the original positioning of the slices. We use interactive and automatic alignment tools for this purpose. Here we show snapshots of 'AlignAStack' the interactive tool. Automatic alignment is performed using ITK.

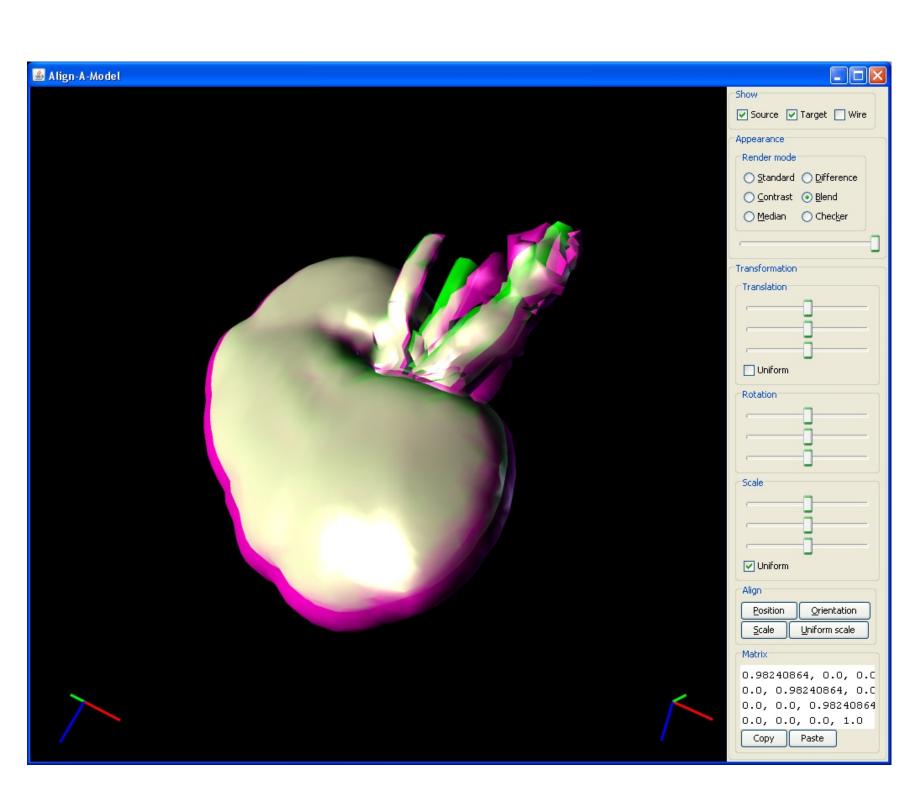




Once the stack of images has been aligned, we use a surface reconstruction algorithm (marching cubes) to recreate the surface model that comes from the tissue slices taken from the subject. This model will be aligned with the one obtained from CT scans to analyze and compare histological data contained in the slices with morphometric data obtained from the scanned 3D model.







To compare both datastes in 3D space, we need to find the correspondence between the data contained in the slices and the morphometric data. To find this correspondence, we use AlignAModel, an interactive and semi-automatic alignment tool that helps us find an affine transformation that associates both datasets.

Data from several subjects will be collected and combined to test hypothesis that describe the relationship between cell proliferation patterns and morphology of the mouse embryo during development. This data can be used to guide further efforts in the simulation of cell proliferation and development of facial features, as well as malformations such as cleft palate.