Diploma thesis review

Thesis autor: **Bc. Jan Hereš**

Thesis title: **Reconstruction of a patient-specific surface model of the humerus bone**

The presented diploma thesis deals with completing a 3D model of the humerus bone from a partial model that only captures the proximal part, reconstructed from a CT scan via means of isosurface reconstruction. The topic is important and practical, and the need for a practical solution is documented by the breath of the literature on the topic.

Having studied the presented document, the proposed method and its implementation in the 3D Slicer software, I see several issues with the presented work, which lead me to hesitation whether or not the thesis should be recommended for defense.

First of all, the proposed method of addressing the problem is in my opinion inappropriate. The procedure starts with building a mean 3D model of a humerus, one for males and one for females. This model is then rigidly and non-rigidly aligned with the available partial model, declaring the resulting complete model a "reconstruction". Even though the author uses the term Statistical Shape Model (SSM) for the mean model, it is not what literature understands as SSM. In SSM, a shape **variability**, learned/extracted from a large sample of known data, is captured via a mean model **and** usually a PCA space of model variations. Such a model could capture the possible correlation of the shape of the proximal and distal part of the humerus, truly reconstructing one form the other. Using a universal (albeit sex-specific) mean model, however, has no such property. The distal part is **essentially replaced** by the mean model, effectively ignoring most of the patient-specific shape information that could be extracted from the known proximal part. The fact that the mean model is not truly a mean model, but a specific model biased by the manual choice of the specific base model on which others are registered (as admitted by the author, which I appreciate) is only a minor flaw, since finding a mean shape in a set of shapes is a difficult problem addressed by a wide literature (some of which could have been referenced).

The second major issue is the lack of any verification, apart from very few qualitative personal assessments. Any sort of quantitative analysis is missing, although the scenario naturally lends itself to many possible evaluations. For example, full humerus scans could be truncated, reconstructed and then compared with the original data, using various metrics, such as Hausdorff distance, intersection over union difference or any other out of a plethora of shape (dis)similarity metrics. The choice may be difficult, but choosing not to perform such evaluation at all is in my opinion not justified. At the same time, a quantitative evaluation could have provided means of determining optimal parameters of the several steps of the algorithm, which is currently another major issue with the implementation: the parameters must be manually fine-tuned in order to even achieve qualitatively correct results. This problem certainly hinders practical applicability of the presented solution.

From the computer science point of view, the presented work is not particularly impressive either. The core of the solution is a Pyhton script that links several libraries, and another script that defines a module GUI in the 3D Slicer environment. None of the actual processing is done by the delivered script, essentially it merely takes the parameters from the user and calls the routines of imported libraries. The core logic of the implementation is a script on 458 lines, including 127 lines of self-documenting commentary.

Also, the final model denoted "merged" is in fact not merged at all, but simply consists of the triangles of both the known proximal part and the fitted mean model, i.e. it has two surfaces in the proximal part. The purpose of such output is unclear to me.

As for the presented document, it is written in English of quite good quality, in fact the Czech version of the abstract is the weakest part of the document from stylistic point of view (repeated words, mixed up proximal/distal adjectives, …). There are occasional awkward formulations ("…precision of the landmarks can be non-negligible."), and on several occasions, sentences are unfinished. However, overall, the document is easy to follow and easy to understand, which I appreciate, and represents in my opinion one of the strengths of the thesis. On the other hand, the author presents full listings of complex algorithms (figs 2.3 and 2.4), which are incomprehensible without more details on how they work. Also, from the description, I am not sure that the author knows how the Radon / inverse Radon transformation works.

Overall, I feel that the thesis is borderline acceptable at best. It provides a GUI to known tools, which, when manually correctly configured, provides a qualitatively acceptable model of a humerus that in a certain sense matches the input proximal part. The used model is in my opinion inferior to the state of the art and does not deserve the description SSM. Testing is lacking.

On the other hand, the author has managed to devise a working solution for a complex problem that lies outside of his main field of expertise, and was able to describe it in a concise and clear manner, even identifying some of the weak spots of the solution (bias in selecting the base model for establishing the mean shape). For these reasons, I believe that he deserves a chance to defend his work, **I recommend it for defense** and suggest the grade "**good**".

I suggest the following topics for defense discussion:

1) Why did you not choose a true SSM, where the shape variability is captured by a PCA model, as suggested in the literature?
2) Why did you not perform a proper quantitative analysis of the achieved results?
3) Is there a way to automatically determine the appropriate configuration parameters of the procedure?

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