Abstract Title: Computer-assisted Allograft selection for transepiphyseal tumor resection at the knee

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Introduction: Preservation of the epiphysis in high-grade metaphyseal osteosarcoma at the knee is a surgical alternative for carefully selected patients. Crucial factors needed to obtain local tumor control and achieve an acceptable functional result include, but are not limited to, a positive response to chemotherapy, accurate preoperative assessment of tumor extension to the epiphysis, and appropriate choice of fixation techniques for intercalary allografts. Manual surgical planning of allograft interventions for tumor-induced deformations of the femur is a non-trivial and time consuming task and efforts to enhance the currently available methods are required.

In order to select the best matching donor bone, we propose, apply, and validate an automatic computerized method to localize within a bone databank, the most appropriate donor bone as well as the best region matching the part to be resected and replaced, based on size and shape information of the metaphyseal area extracted from a mirrored version of the healthy contralateral femur.

Methods: Two preoperative computed tomography (CT) scans of diseased femurs were segmented and used to apply the presented technique. The femurs presented large distal tumors that required surgical removal and allograft replacement.

Symmetry between the left and right femurs [1] of the same patient is used as a tool to guide the search for the best donor bone from a 3D virtual bone databank consisting of ten cadaver femurs, scanned, manually segmented, and stored digitally. After applying the adequate affine transformations on the healthy femur in order to align it with its diseased counterpart, the part that corresponds to the region containing the tumor is isolated and used as a template.

The template is then aligned and compared to a set of cadaver femurs stored in the bone databank. For each cadaver model, the template is repeatedly moved cranially and caudally across the main axis of the femur. Iterative closest point (ICP) is used to establish the correspondence between the different shapes at every iteration. The Mean surface error is computed at every step and the location that produces the least mean surface error is stored. This is repeated for each cadaver femur. Finally, the lowest global mean surface error, together with the proper positioning of the cut part, indicates the best fit of the allograft, and delineates the location of the cutting planes to be applied on the chosen cadaver femur. Figure 1 shows the progress of the search algorithm as it searches along the vertical direction and finds the best fitting of the template for one of the two studied cases. Manual adjustment by an experienced personnel can be later carried out in order to make the fit optimal and adequate for clinical applications.

Validation of the method was carried out by resecting a part of the mirrored contralateral femur of each one of the cadaver bones and considering it the search template. Results are shown in Table 1, where the mean and standard deviation of the mean surface error resulting from the search along the vertical axis are presented.

Results: Qualitatively, visual comparison of the healthy contralateral limb in mirror lapping and the future allograft allows for the inspection of the scene in a virtual scenario, thus giving the surgeon the possibility to investigate potential underlying differences as well as to obtain more pre-operative information predicting the behavior of the allograft during the surgery.

Quantitatively, the validation tests showed that the algorithm was able to find the correct match in 60% of the tested instances. However, in the rest of the cases, the final outcome was very close to being a correct match.

Conclusion: The proposed method allows for automatic allograft selection from a bone databank, enabling fast and accurate localization of the donor bone and region in the databank that best matches the patient's required allograft. The method further enables optimization of the databank usage. Furthermore, Inspection of the outcome of the proposed method by an experienced surgeon confirmed the validity of the results, as minimal steps were observed while maintaining a high contact surface between the graft and the remaining parts of the diseased femur.

	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10
MF1	**6.95 ± 0.76**	7.76 ± 0.95	7.24 ± 0.9	7.21 ± 0.65	7.55 ± 0.51	8.09 ± 1.33	6.94 ± 0.82	8.07 ± 0.49	7.99 ± 0.68	8.16 ± 0.98
MF2	8.32 ± 0.84	**6.25 ± 0.92**	9.21 ± 0.49	8.38 ± 0.9	8.87 ± 0.67	9.51 ± 1.4	8.22 ± 0.77	9.77 ± 0.5	8.94 ± 0.67	9.5 ± 0.85
MF3	7.69 ± 0.77	9.54 ± 1.36	**6.5 ± 0.77**	7.78 ± 1.31	6.82 ± 0.58	8.22 ± 1.78	6.98 ± 1.11	8.39 ± 0.4	8.07 ± 0.74	8.2 ± 1.22
MF4	7.03 ± 0.68	7.39 ± 0.78	7.33 ± 0.37	**6.39 ± 1.01**	7.05 ± 0.45	7.53 ± 1.6	6.54 ± 0.85	8.47 ± 0.29	7.26 ± 0.56	7.98 ± 1
MF5	7.34 ± 1.36	8.69 ± 1.06	7.25 ± 0.86	7.58 ± 1.3	**6.51 ± 0.89**	8.18 ± 1.8	6.82 ± 1.05	7.75 ± 0.67	7.59 ± 1.23	8.31 ± 1.48
MF6	7.1 ± 0.28	8.04 ± 0.46	6.97 ± 0.59	6.76 ± 0.41	7.31 ± 0.36	**6.24 ± 0.83**	6.11 ± 0.35	8.18 ± 0.42	7.85 ± 0.55	7.16 ± 0.51
MF7	7.15 ± 0.96	8.15 ± 0.75	6.87 ± 0.34	6.83 ± 1.23	6.46 ± 0.55	7.11 ± 1.43	**5.83 ± 0.83**	7.34 ± 0.28	7.11 ± 0.59	7.19 ± 1.15
MF8	8.41 ± 1.29	9.69 ± 1.61	6.99 ± 1.13	7.95 ± 1.37	6.82 ± 0.8	9.07 ± 1.91	7.27 ± 1.2	**7.37 ± 0.83**	8.35 ± 1.17	8.84 ± 1.31
MF9	7.82 ± 0.33	8.58 ± 0.85	6.79 ± 0.46	7.42 ± 0.8	7.12 ± 0.5	8.14 ± 1.14	6.84 ± 0.65	8.22 ± 0.77	**7.16 ± 0.62**	8.16 ± 0.62
MF10	7.02 ± 0.28	8.29 ± 0.64	6.47 ± 0.51	7.21 ± 0.4	6.74 ± 0.34	6.89 ± 1.07	6.05 ± 0.76	7.71 ± 0.31	7.85 ± 0.36	**7.28 ± 0.6**

Table 1: Mean and standard deviation of the mean surface error (in millimeter) of the validation tests. MF indicates the mirrored template. F indicates the cadaver femur from the databank.

References:

[1] Seiler C, Weber S, Schmidt W, Fischer F, Reimers N, and Reyes M, "Automatic landmark propagation for left and right symmetry assessment of tibia and femur: a computational anatomy based approach," in *Proceedings of the 9th Annual Meeting of CAOS-International*, pp. 195-198, 2009.

Figure 1: Localization of the best allograft by searching in the databank of donor bones and finding the best fit of the template.