

## Motivation

Our work is motivated by the need to measure bone mineral density (BMD) from CT images. The BMD values are useful in a number of applications. For example, the loss of BMD is an important bio-marker for foot bone deformities in Diabetes patients with Charcot Neuroarthropathy (Figure 1). In an on-going project, the primary goal is to determine the BMD in each of the 26 bones in the foot.

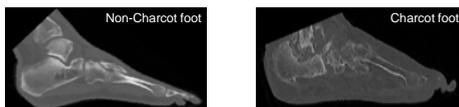
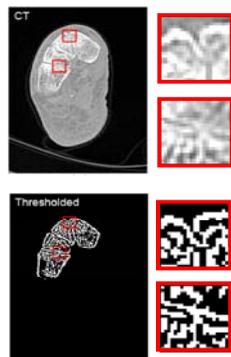


Figure 1: A Charcot foot exhibits much less bone density than a normal foot.

## Problem



To quantify the BMD in a bone, a prerequisite is to identify **individual** bones from the CT volume. This task can be broken into two sub-tasks:

**1. Bone segmentation:** Segment bone tissue from the rest of the CT volume.

- A relatively easy task due to higher tissue density of the bones.
- Typically done by thresholding or edge-detection (Figure 2).

**2. Bone separation:** Different bones are often connected in the segmented volume (Figure 2), which need to be separated.

- This poster presents a solution to the **bone separation problem**.

Figure 2: Segmenting bones by thresholding. The thumbnails show places where bones are connected after segmentation.

## Challenges and Current Solutions

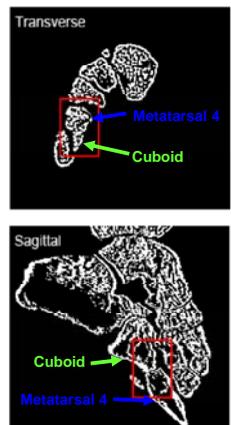


Figure 3: Bone interfaces can be difficult to identify on a single 2D view (e.g., transverse).

### Challenges in bone separation:

- Quantity.** Bone connections are often of a large number.
- Ambiguity.** Bone connections can be difficult to identify (Figure 3).

### Current solutions:

- Computational:** filter the CT volume [Westin *et al.* 98] or use special mask [Kang *et al.* 03].
  - Can not eliminate connections, or only applicable to specific bones (e.g., femur head).
- Manual:** go through each 2D slice and label each bone, checking all 3 directions
  - Laborious: **2.4 hours** for 12 foot bones in a CT volume.

## Interactive Tool

We introduce a new interactive tool for semi-automatic bone separation. The user only needs to mark a small number of voxels (called *seeds*) by bone labels on a few slices (Figure 4), and the tool automatically labels the rest of the voxels (Figure 5). If the separation is unsatisfactory, the user can provide more seeds and iterate the process.

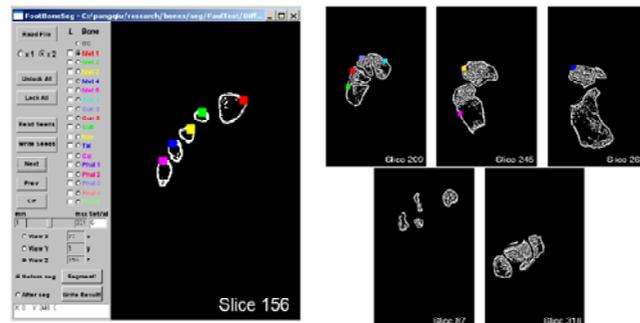


Figure 4: User interface for bone separation (left), and slices on which the user places the seeds (colored boxes, left and right) colored by the corresponding bone. For example, 1<sup>st</sup> metatarsal is red, 2<sup>nd</sup> metatarsal is green, etc.

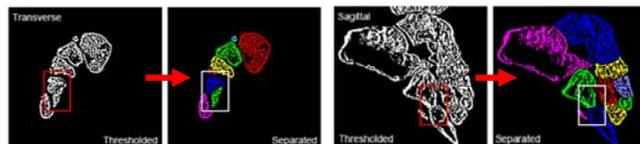


Figure 5: Given the seeds in Figure 4, the tool automatically labels all other voxels, achieving bone separation.

## Algorithm

We formulate the bone separation task as a graph-cut problem. Voxels in the segmented CT volume are represented as a connected graph with auxiliary terminal nodes, where seeds are connected to terminals of corresponding labels (Figure 6 top). To separate the bones, we find the minimal-size cut in the graph so that terminals of different labels become disconnected (Figure 6 bottom). The cut breaks the graph into disconnected components, each to be labeled by the terminal it is connected to.

**1. Graph construction:** The graph is designed to help place the min-cut at bone interfaces:

- Each seed is grown into a collection of seeds
  - Preventing min-cuts around the seeds
- Edges weighted by the density of 6-connected voxels in the edge's neighborhood
  - Preventing min-cuts in the middle of the bone (Figure 7), where the voxels are denser.

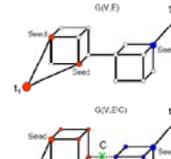


Figure 6: A graph (top) and a cut that disconnects the terminals (bottom).

**2. Graph cut:** K-way multi-cut [Dahlhaus *et al.* 94]

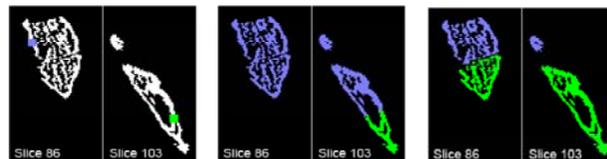


Figure 7: Comparing graph-cut result in the un-weighted (middle) and weighted (right) graph, given two seeds (left) in the 2<sup>nd</sup> cuneiform (blue) and 2<sup>nd</sup> metatarsal (green).

## Refining the Results

When starting with a noisy binary segmentation, graph cut may not give the desired result. We provide convenient controls to refine separation along bone interfaces, in the same graph-cut framework.

- Locking tool:** restricting graph-cut to only bones of concern.
  - Increased efficiency
- Fine seeding:** placing seeds without seed-growth
  - For fine-tuning along border
  - Useful for processing noisy data (Figure 8)

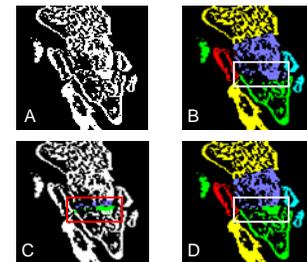


Figure 8: Initial separation (B) errs on the interface between 2<sup>nd</sup> metatarsal (green) and 2<sup>nd</sup> cuneiform (blue). After placing fine seeds (C), a correct separation is obtained (D).

## Performance and Validation

**Setup:** The tool is tested on 10 CT volumes for separating 12 foot bones on a 2GHz PC with 2GB RAM. Two people used the tool in three independent sessions to separate the same data.

**Performance:** Less than 50 seeds were used for each volume, with an average interaction time of **18 minutes** per volume (comparing to 2.4 hours of manual effort).

**Validation:** Interactive separation resulted in less than 1.5% difference from manual separation without using the tool, and less than 0.25% variation among the three sessions.

## Conclusion and Future Work

We present an interactive method for separating connected bone components from segmented (binary) CT volumes.

**Technical contribution:** Novel means for graph construction from binary volumes to locate bone interfaces as graph min-cuts.

**Practical usage:** Dramatically reduces manual effort without losing accuracy. Currently deployed at Washington University Medical School for bone density analysis in Charcot patients.

**Work in progress:** An interactive tool for filling the interior of a separated bone (Figure 9), to obtain a solid bone mask.

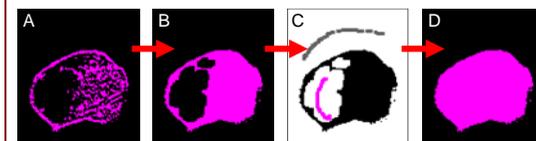


Figure 9: To fill the interior of a bone (A), we first apply morphological closing and 2D flood filling (B), then use a similar graph-cut method that takes user-drawn seeds (C, purple for inside and gray for outside) and obtain the fill (D).

## Acknowledgement

This work is supported by NIH grant R21DK79457 and NSF grant CCF-0702662.