# CropDicom

User Guide: CropDicomTool

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- The idea of the CropDicomTool is to prepare the images for the harris lines tool (HL tool)
- Each input image for the HL tool has to be in the dicom format and contain one single bone, which is vertically oriented

- the buttons on the right hand side are used from top to down

(1) open dicom or tiff image

- black background needed, otherwise 'invert' the image
- currently only tiff and dicom images can be loaded (other formats upon request [Contact](#))
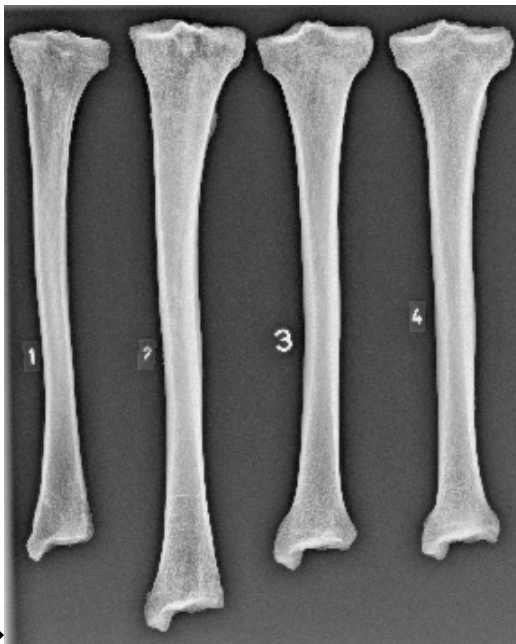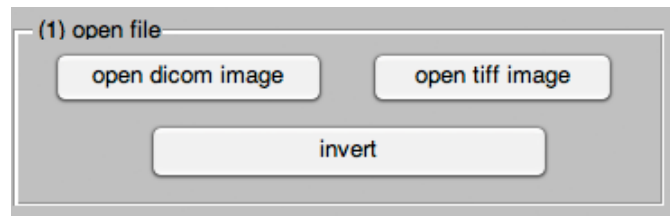
(1) open file   opening panel

(2) extract bones

- threshold the input image such that you see your bones in white on the right image
- calculate the automatic threshold (with button)
- tune / adjust the calculated threshold with the offset (play with negative or positive small offsets)
- every bone should be clearly separated from other things, i.e., no connecting white line should be visible between the bones
- small numbers or box artefacts should also be separated, they can be removed later
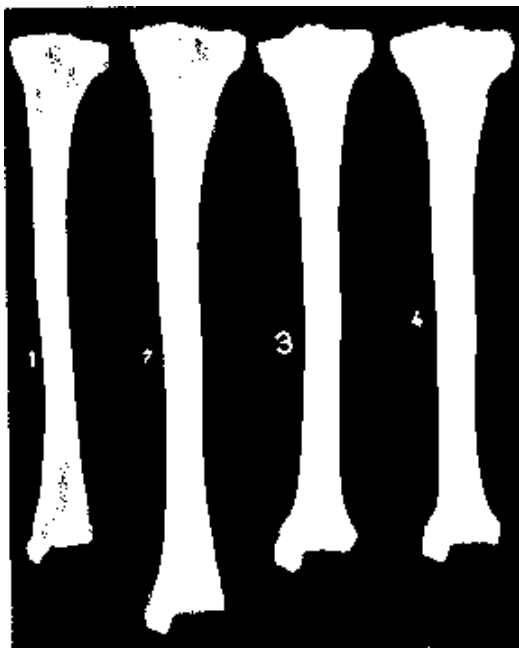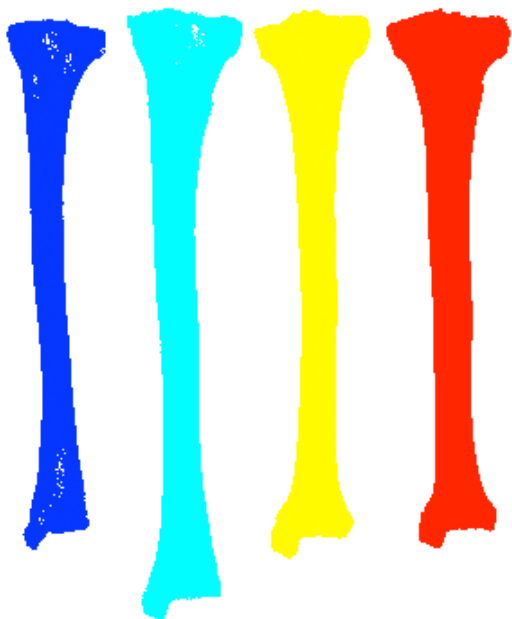
(2) thresholded bones   threshold panel

(3) separate bones

- one color per bone
- mark each single bone with a separate color (play with the input field to increase or decrease the number)
- e.g, by increasing the value (min area size), small numbers or similar things can be removed

(3) labeled bones (one color per bone)   labeling panel

(4) save single bones

- one dcm-file per bone
- each colored bone is extracted and saved
- you have to provide a file name for every bone
- before saving, each image is displayed such that you can give the correct name to it
- artifacts are also saved, but they can be manually deleted after the saving procedure
- the bone should be oriented vertically (if this is not the case, it needs to be rotated in another tool, rotation is currently not provided in the CropDicomTool)

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