# After-class exercise: genome liftover

**You are provide with a genomic file in .tsv format. Your task is to convert the coordinates to hg38 for all the data entires using local programs.**

1. Convert other files to the BED format (programmatically).

2. Use the liftOver program locally:
   a) Copy the liftOver program to you local folder
   b) Try it out: ./liftOver
   c) Read the help of liftOver and understand the basic parameters
   d) convert the segments file, which you should have converted to the BED format, to hg38 using liftOver locally.

3. Use segment_liftover:
   a) Read the paper or github of segment_liftover and understand what does it do
   b) Setup Python virtual environment:
      python3 -m venv myenv
      source myenv/bin/activate
      pip install --upgrade pip
   c) Install segment_liftover: pip install segment_liftover
   d) Read the instructions of segment_liftover
   e) Use segment_liftover to convert the segment file again.
   f) Compare the results with liftOver and make a simple analysis.
   g) When you finish: deactivate