

Pile|Line

Example #5.
Browsing Genomic Position files.



Step 1.

Download and uncompress the Genomic Position example files :

PileLineGUI Guided Example #1

1. Download and uncompress GP files (pileup format) and Annotation files to your working directory:

REFERENCE GENOME

- Human Genome 18 in FASTA (.fa) and indexed FASTA (.fai). The sequence names are without the 'chr' prefix.
[hg18.zip](#) (929MB)

EXPERIMENT FILES

- GP files-Experiment 1. Each .zip file contains 2 files: a complete and a variants-only pileup.
[Control1Files.zip](#) (36MB)
[Case1Files.zip](#) (36MB)

Note: there is only data for the chromosome 10

- GP files-Experiment 2. Each .zip file contains 2 files: a complete and a variants-only pileup.
[Control2Files.zip](#) (38MB)
[Case2Files.zip](#) (38MB)

Note: there is only data for the chromosome 10

ANNOTATION FILES

- Gene Annotation .BED file.Ensembl Genes for the Human Genome 18.
[Hg18_hgnc_ensembl_genes.bed.zip](#) (365KB)
- SNPs from dbSNP version 36.3 for the Human Genome 18.
[DbSNP_36.3.bed.bgz.zip](#) (150MB)

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Step 2.

Load uncompressed Genomic Position files:

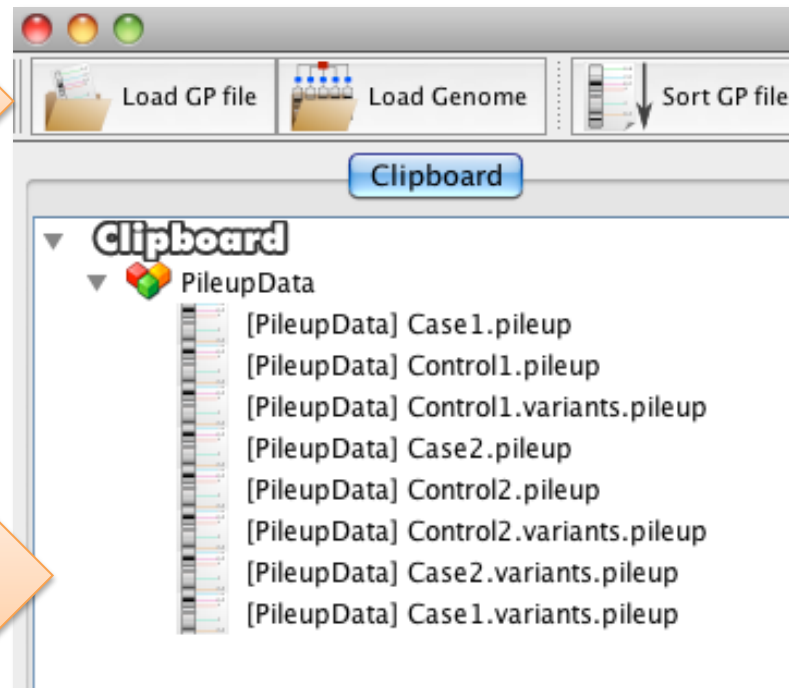
Case1.pileup

Case1.variants.pileup

Control1.pileup

Control1.variants.pileup

*Click on
'Load GP'
button*



*Find the
loaded
files in the
clipboard*

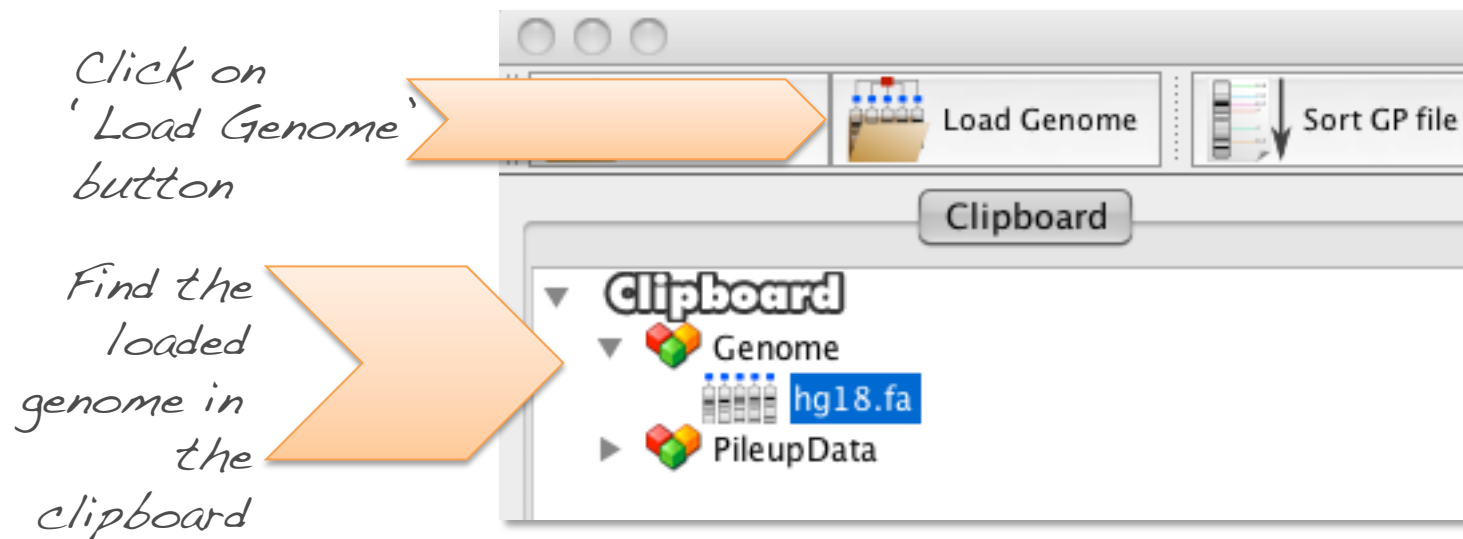


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Step 3.

Load uncompressed Reference Genome FASTA file.

Note: Require .fai index



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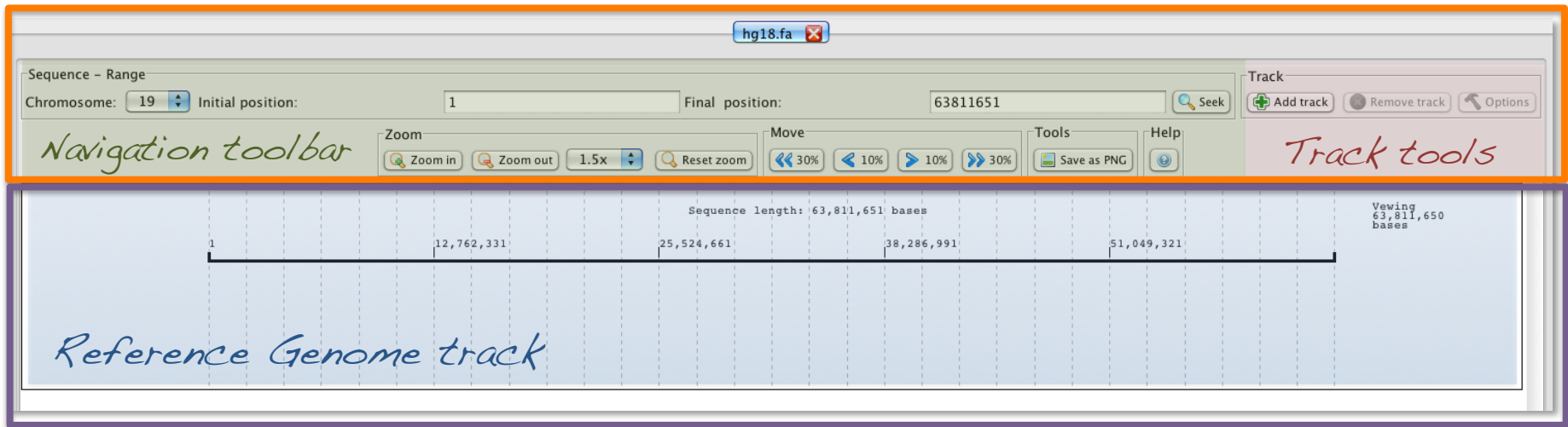
Step 4.

Summary of the the Browser interface .

Help



Tools area



The screenshot displays the Pile|Line browser interface. At the top, a tab labeled 'hg18.fa' is visible. Below it, the 'Sequence - Range' section shows 'Chromosome: 19', 'Initial position: 1', and 'Final position: 63811651'. A 'Seek' button is located to the right. The 'Navigation toolbar' includes 'Zoom in', 'Zoom out', '1.5x', and 'Reset zoom' buttons. The 'Move' section contains navigation buttons for 30%, 10%, and 30% increments. The 'Tools' section has a 'Save as PNG' button. The 'Track' section on the right includes 'Add track', 'Remove track', and 'Options' buttons. The 'Reference Genome track' is shown below the toolbar, displaying a sequence length of 63,811,651 bases. The track shows a horizontal line with vertical markers at positions 1, 12,762,331, 25,524,661, 38,286,991, and 51,049,321. The text 'Vewing 63,811,650 bases' is visible on the right side of the track.

Browsing area

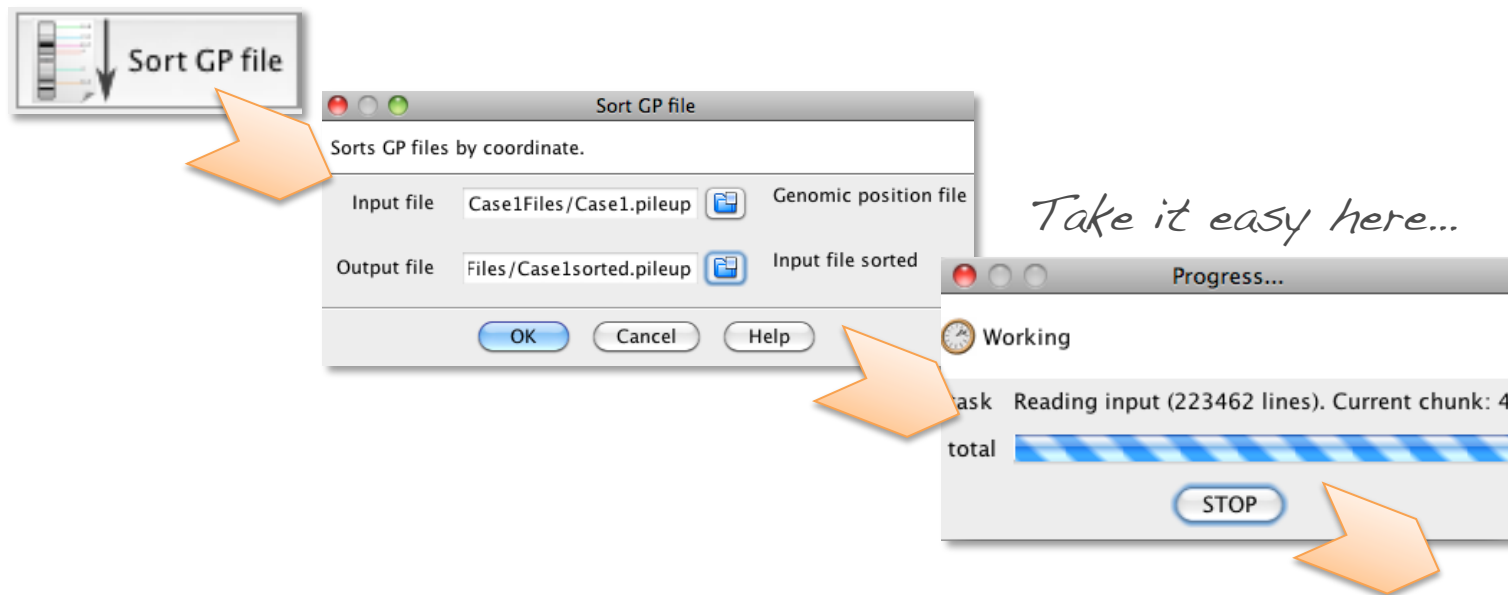
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Step 5.

Adding new tracks I

IMPORTANT:

GP files MUST be sorted. Use 'Sort GP file' button to sort your Case1.pileup file.

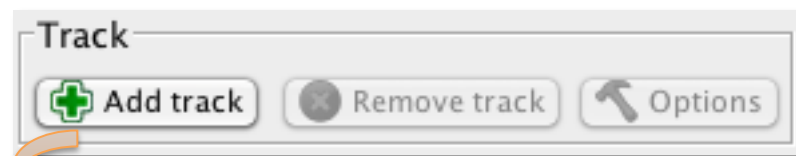


Case1sorted.pileup file.

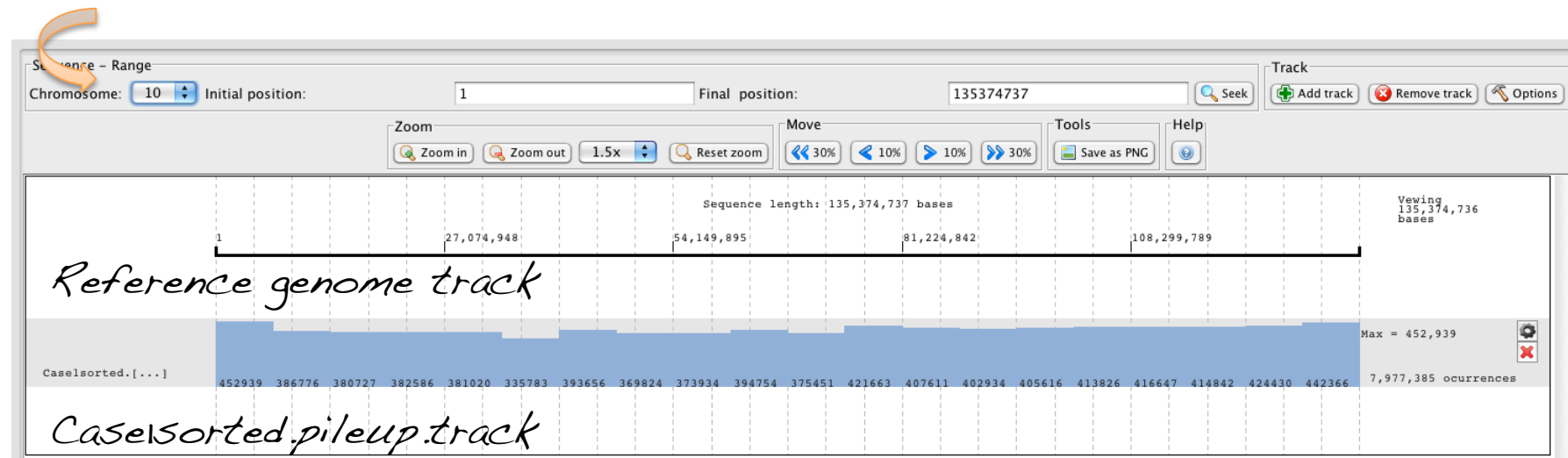
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Step 6.

Adding new tracks II



Case1sorted.pileup file.



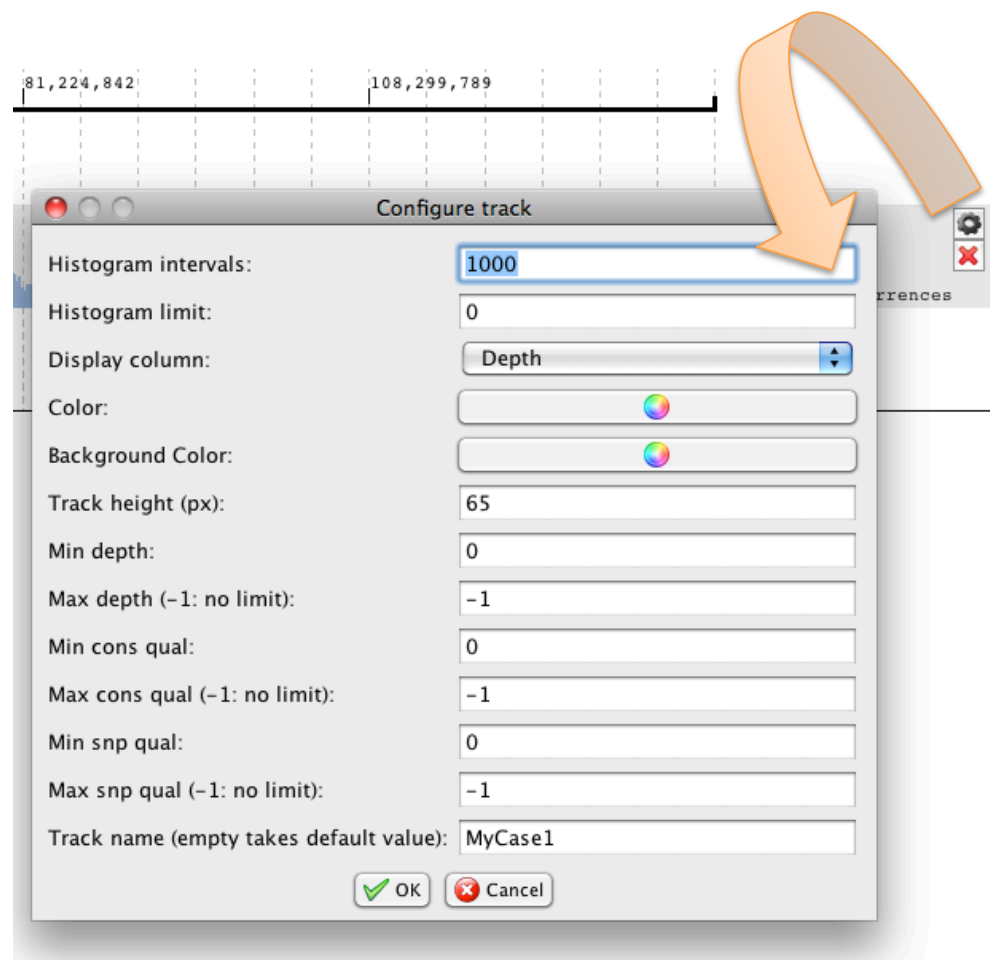
Reminder:

Example files only includes values for chromosome 10.

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Step 7.

Configuring tracks



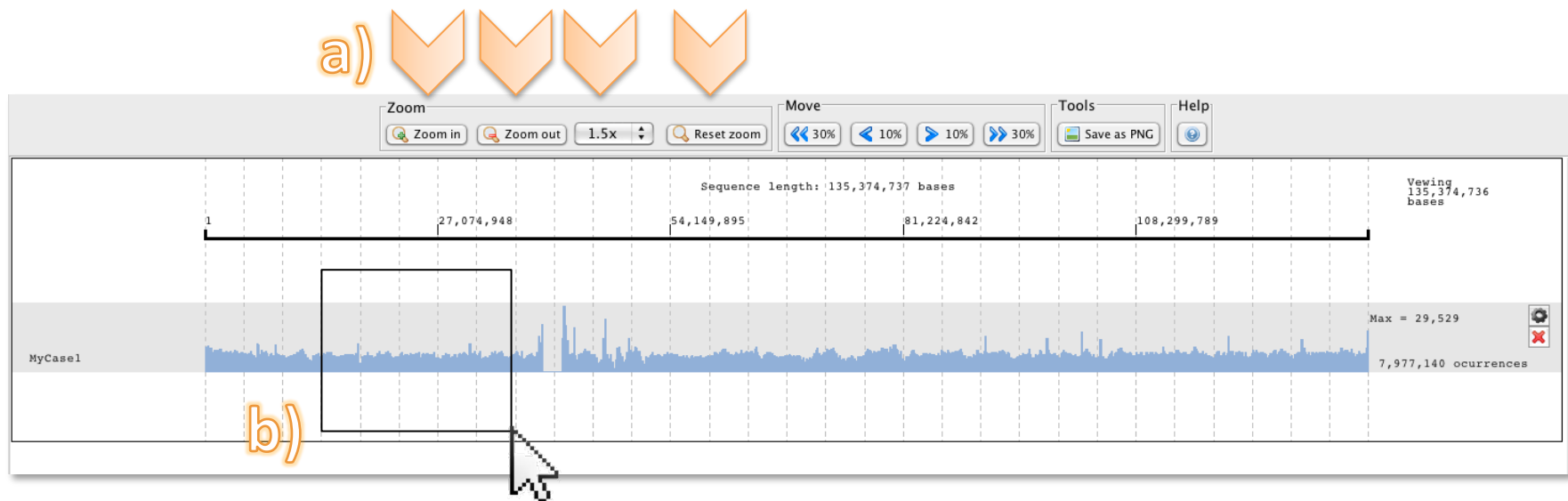
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Step 8.

Zoom

Two ways to make zoom:

a) Use zoom buttons or b) roll over desired genomic region directly.





For further info see PileLineGUI Documentation at:

<http://sing.ei.uvigo.es/pileline/pilelineguihelp/>