

# Analysis of Geuvadis Dataset using Flux-Capacitor.

Hi all,

Hopefully this is the correct place to ask this question.

I'm looking to use flux-capacitor to reference the Geuvadis dataset against gencodeV18.gtf. I want to keep the methodology **exactly the same** as was done in the original mapping, changing only the size of the .bam files (sliced BAM).

So far, I have:

- Downloaded all .bam files for CEU population from ArrayExpress
- Sliced bam files for particular genomic locations using samtools.
- Sorted and indexed bam files.
- Downloaded gencodev18.gtf
- Created parameter file:

```
ANNOTATION_FILE gencode.v12.annotation.gtf
READ_DESCRIPTOR {ID}/{MATE}[1,2]
```

```
ANNOTATION_MAPPING PAIRED
```

Please could someone let me know the next steps?

Do I need to convert to BED format as stated in [Geuvadis Quantifications](#) ?

And what are the exact command line arguments for the annotation using flux-capacitor (**identical** to the original methodology)?

Thank you in advance,

Chris O