Geuvadis Quantifications

Flux Version

Flux Capacitor 1.0.1

Read Mappings

Unfiltered GEM read mappings were employed, after converting them to BED format.

Annotation File

The quantifications are based on the Gencode (v12) reference annotation:

gencode.v12.annotation.gtf.gz

Parameter File

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

Command Line

```
flux-capacitor -p <parameter_file> -i <sample.bam> -o <output.gtf>
```

Pipeline

To speed up computation of the big dataset, the JIP pipeline system has been employed. All datasets were quantified in parallel, splitting each dataset on a per-chromosome base.