# RNA-degradation bias normalization



Dice whole-experiment coverage into per-gene coverage matrices ($L_i$ x $p$)

RNA-Seq .bam, .bai files ($p$ experiments)

Experiment 1 .bam, .bai file
Experiment 2 .bam, .bai file
⋮
Experiment $p$ .bam, .bai file

Gene annotation (.gtf)

5'                    3'

Start

DegNorm NMF-based normalization

DegNorm output directory

DI score summary

Adjusted read counts

| Sample 1 | ... | Sample $p$ |
|----------|-----|-----------|
| 195 | ... | 320 |
| 1191 | ... | 1459 |
| ... | ... | ... |

DI score correlation map

End