

5'-peak in read coverage

Hello

I got a strong 5' bias. First positions in a transcript have a high(very high coverage) . The window that follows has almost no reads.

I believe the figure should speak for itself. I join also the parameters file used.

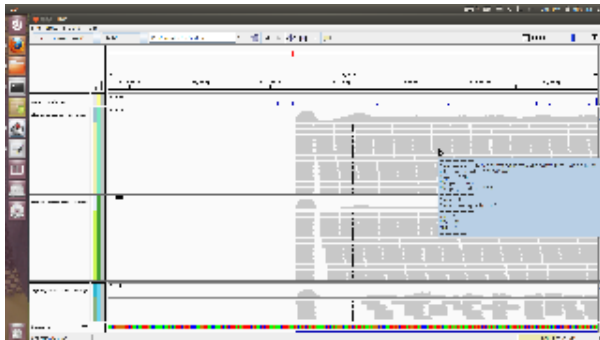
I noticed that accepting variability in TSS position reduces this bias but I want to simulate data with a fixed TSS.

Any suggestions on how to reduce this bias?

Thank you,

Bogdan

[5bias.png](#)



Parameters

```
NB_MOLECULES      50000
TSS_MEAN          NaN
POLYA_SCALE       50
POLYA_SHAPE       2
```

```
## Fragmentation
FRAG_SUBSTRATE     RNA
FRAG_METHOD        UR
FRAG_NB_LAMBDA    50
```

```
## RT parameters
RTRANSCRIPTION YES
RT_PRIMER          RH
RT_LOSSLESS        YES
RT_MIN             2000
RT_MAX             6000
```

```
## PCR / Filtering
## no [GC] bias to not observe sequence based biases
```

```
PCR_DISTRIBUTION  default
PCR_PROBABILITY  0.5
GC_MEAN          NaN
FILTERING         YES
SIZE_SAMPLING     MH
```

```
# Sequencing
FASTA             true
READ_NUMBER       1000000
READ_LENGTH       50
PAIRED_END        NO
```