

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.

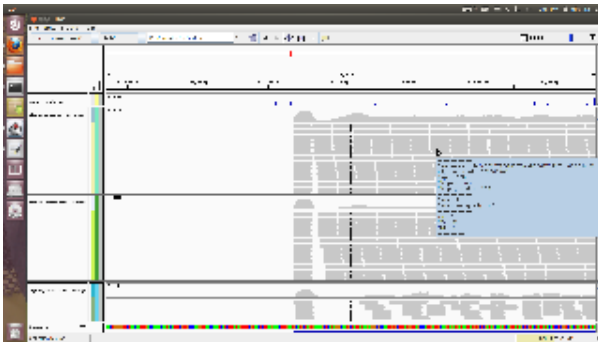
I noticed that accepting variability in TSS position reduces this bias but I want to simulate data with a fixed TSS.

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