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- .ERR Error Model
 - DEPRECATED: pre-2009 .ERR format
 - DEPRECATED: pre-2011 .ERR format
- .FASTA/FASTQ Read Sequences
- .GTF Gene Annotations
- .LIB Library Fragments
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 - Biological replicates
 - Control error model for longer reads and polyA-tails in bed alignments.
 - Does the reads generated contain adaptor sequences as in real read data ?

- FPKM from PRO
- Generating a library with reads which are specific to one locus
- How do I post a new question in the forum?
- How do I reproduce a simulation?
- How many files do I need to run the Flux Simulator?
- How to cite the Flux Simulator
- how to generate paired-end read strand specific
- How to output results in a user specified directory?
- How to simulate a bad experiment?
- how to simulate the 3 primer's bias?
- I followed the paramater file and useage ,the error that java
nullpointerexception occurred.
- Is it possible to force the simulation to produce reads with the exact same
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- Is there any way to find out which exon is sequenced?
- Stil an error while preparing sequences
- Why so many reads are truncated?
- D.2 - Gene / Transcript Expression
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 - Correct gene expression profile formula
 - Differential expression and alternative splicing
 - Empirical expression vector as input
 - Exact number of individual AS events
 - flux simulator .pro file
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 - How to simulate alternative splicing?
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 - How to simulate SNP?
 - NB_MOLECULES and READ_NUMBER
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 - Anchored primers for RT
 - Error at library preparation step
 - How do I modify the PCR amplification protocol?
 - New error at library preparation step
 - Noise while preparing library
 - Source of strong bias towards 5' ends
 - Understanding behaviour of the RT_MOTIF simulation parameter
 - What paramters should I change if I would like to observe strong GC bias?
 - What paramters should I use to create a strong positional (3') bias?
 - Why do I obtain reads that are shorter than my specified READ_LENGTH
in the .PAR file?
 - Why no fragmentation by sonication?
 - Why simulating fragment lengths obtained by hydrolysis by Weibull
distributions?
- D.4 - Sequencing and Errors
 - Compatibility of Mapping Files between Simulator and Capacitor
 - Covered fraction of a simulated transcript
 - Error simulating large number of reads
 - Exact position where reads come from
 - field missing, sequence preparation errors
 - fix read length / indel errors
 - How to creat a custom error model
 - how to fix the insert size and deviation for paired-end reads?
 - Missing Data in the Genome
 - Oversequencing the final library
 - Running time
 - Strand Specific Library?
 - Which bases are mutated?

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May 29, 2018 • commented by [Micha Sammeth](#)

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May 25, 2018 • commented by [Yuande Tan](#)

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Aug 07, 2017 • created by [Deepak Grover](#)

[Still an error while preparing sequences](#)

Jun 22, 2017 • commented by [Vitor Lima Coelho](#)

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