

# Home

## 1 - Introduction

## 2 - Download

- 1.0.1 Release notes
- 1.0.2 Release notes
- 1.0.3 Release Notes
- 1.1 Release Notes
- 1.2 Release Notes
- 1.2.1 Release Notes

## 3 - Getting Started

- 3.1 - System Requirements
- 3.2 - Starting the Flux Simulator
- 3.3 - Setting Up Simulations
  - follow the parameter file and usage ,the error that java nullpointerexception occurred

## 4 - The Simulation Pipeline

- 4.1 - Gene Expression
  - 4.1.1 - Gene Expression Profile
  - 4.1.2 - Transcript Modifications
- 4.2 - Reverse Transcription
- 4.3 - Fragmentation
  - 4.3.1 - RNA Hydrolysis
  - 4.3.2 - DNA Nebulization
  - 4.3.3 - DNA Digestion
- 4.4 - Final Library Preparation
  - 4.4.1 - Size Selection
  - 4.4.2 - PCR Amplification
- 4.5 - Sequencing
  - 4.5.1 - The Sequencing Process
  - 4.5.2 - Read Identifiers
  - 4.5.3 - Output Read Sequences
  - 4.5.4 - Error Models
  - 4.5.5 - Uniformity Measurements

## 5 - Example Simulations

- 5.1 RNA Hydrolysis Protocol (M.musculus)
- 5.2 Directional RNA-Seq Protocol (H.sapiens)
- 5.3 Poly-dT Priming and DNase Digestion (S.cerevisiae)
- 5.4 Poly-dT Priming and Nebulization (A.thaliana)
- Demo - Create Fastq file

## Appendix A - File Format Specifications

- .BED Mapping Locations
- .ERR Error Model
  - DEPRECATED: pre-2009 .ERR format
  - DEPRECATED: pre-2011 .ERR format
- .FASTA/FASTQ Read Sequences
- .GTF Gene Annotations
- .LIB Library Fragments
- .PAR Simulation Parameters
- .PRO Transcriptome Profile

## Appendix B - Frequently Asked Questions (FAQ)

## Appendix C - JIRA Issue Tracker

## Appendix D - Forum

- D.1 - General Questions
  - 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 length?
- 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
  - An error at library preparation step
  - 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
  - Generating paired-end reads longer than 100nt
  - How to simulate alternative splicing?
  - How to simulate reads not containing introns
  - How to simulate SNP?
  - NB\_MOLECULES and READ\_NUMBER
  - Noise Within Introns
  - Simulate Differential Expression (DE)
  - Simulate Exon Skipping Frequencies
  - Simulating RNA-Seq in different Individuals
  - Using .gtf files from iGenomes: "not sorted!"
- D.3 - Library Preparation
  - 5'-peak in read coverage
  - 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?

## Community Forum

### Recently Updated

[2 - Download](#)

Dec 13, 2018 • updated by Micha Sammeth

• [view change](#)

[5.3 Poly-dT Priming and DNase Digestion \(S. cerevisiae\)](#)

Nov 28, 2018 • updated by Micha Sammeth

• [view change](#)

[1.0.1 Release notes](#)

Aug 27, 2018 • updated by Micha Sammeth

• [view change](#)

### [1.0.2 Release notes](#)

Aug 27, 2018 • updated by Micha Sammeth  
• view change

### [1.0.3 Release Notes](#)

Aug 27, 2018 • updated by Micha Sammeth  
• view change

### [1.1 Release Notes](#)

Aug 27, 2018 • updated by Micha Sammeth  
• view change

### [1.2 Release Notes](#)

Aug 27, 2018 • updated by Micha Sammeth  
• view change

### [1.2.1 Release Notes](#)

Aug 27, 2018 • updated by Micha Sammeth  
• view change

### [D.1 - General Questions](#)

May 29, 2018 • commented by Micha  
Sammeth

### [D.1 - General Questions](#)

May 25, 2018 • commented by Yuande Tan

### [3.2 - Starting the Flux Simulator](#)

May 25, 2018 • commented by Yuande Tan

### [FPKM from PRO](#)

Aug 07, 2017 • created by Deepak Grover

### [Stil an error while preparing sequences](#)

Jun 22, 2017 • commented by Vitor Lima  
Coelho

I followed the paramater file and useage ,the error  
that java nullpointerexception occurred.

Jun 22, 2017 • commented by Vitor Lima  
Coelho

I followed the paramater file and useage ,the error  
that java nullpointerexception occurred.

Jun 22, 2017 • created by longyuqi