

3.1 - System Requirements

Java Virtual Machine

The Flux Simulator is written in 100% pure Java, therefore no platform-specific compiling of the bytecode is required. A Java Virtual Machine (JVM) with level 1.6 or higher has to be installed on the system, however, it is recommended to update to the newest Java binaries provided by Oracle for the corresponding platform (i.e., Linux, Solaris, or Windows); Mac OSX users are encouraged to use the automatic software update functionality to obtain the newest virtual machine from Apple. The following command confirms the correct installation of a valid JVM:

shell (Linux /Unix)	<pre>\$ java -version java version "1.6.0" OpenJDK Runtime Environment (build 1.6.0-b09) OpenJDK 64-Bit Server VM (build 1.6.0-b09, mixed mode)</pre>	cmd (Windows)	<pre>C:\>java -version java version "1.6.0_20" Java (TM) SE Runtime Environment (build 1.6.0_20-b02) Java HotSpot(TM) Client VM (build 16.3-b01, mixed mode)</pre>
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RAM

Random Access Memory (RAM) consumption of the Flux Simulator increases drastically with the simulation of sequence-dependent biases; an RNA-Seq experiment involving a typical mammalian transcriptome, for instance, can be simulated in substantially less than 1Gb of RAM when disregarding sequence specific biases. When sequence motifs are provided, however, the memory requirements increase to >3Gb of memory. Note that RAM requirements scale with the number of different transcripts that are simulated, regardless of how many expressed RNA molecules, fragments or reads are obtained from these in the end.

A custom amount of memory can be reserved for simulations by setting the environment variable FLUX_MEM before starting the Flux Simulator:

shell (Linux/Unix)	<pre>\$ export FLUX_MEM="4G"</pre>	cmd (Windows)	<pre>C:\>set FLUX_MEM="4G"</pre>
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Disk Space

In contrast to RAM, the disk space required by a simulation scales linearly with an increasing number of molecules, respectively fragments and reads obtained from them: during *in silico* expression and library preparation, on average about 50 bytes of disk space are required to store an RNA molecule or fragment, i.e., about 1Gb per 20 million reads; simulated reads stored in the bed format require about twice the space, here 10 million reads occupy ~1Gb. In order to estimate additional disk capacity in bytes required for storing simulated read sequences and qualities in a FastQ file (

Unknown macro: 'latex-inline'), the following function on the number of reads (

Unknown macro: 'latex-inline') may be employed:

Unknown macro: 'latex-block'

Before each simulation it is to be assured that the disk space is available in the temporary directory as well as in the output folder exceeds *twice* the amount required to store intermediary files that describe RNA molecules, respectively the amount required for the sequenced reads.