

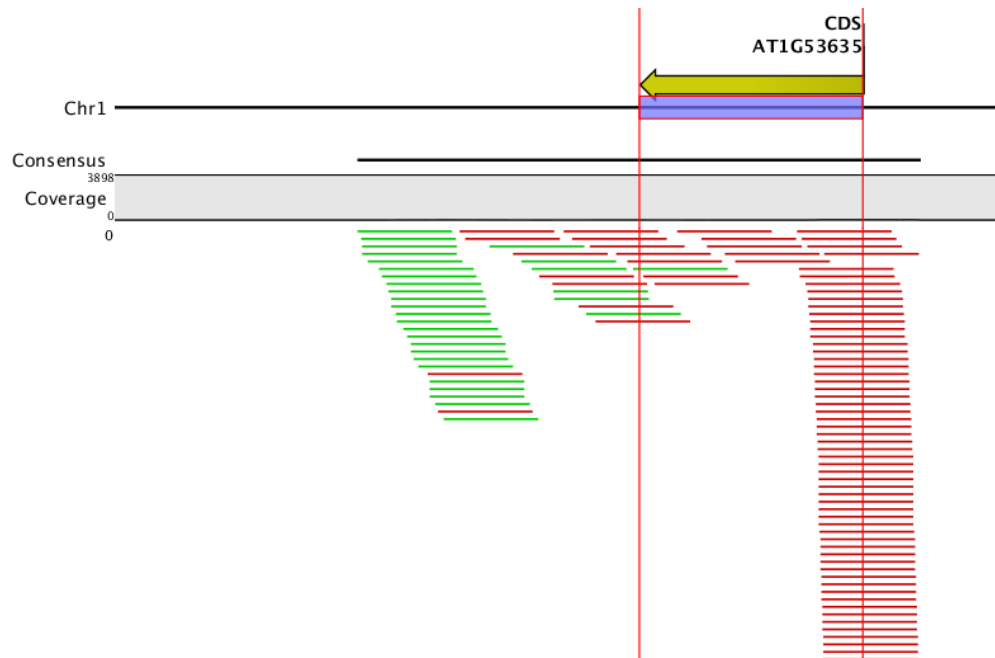
How to simulate reads not containing introns

Hi,

having using Flux simulator for a couple of weeks, I have two questions:

1. Not sure if I ran Flux correctly or not, is it possible to simulate reads only containing exons? Both the simulated reads: the example Poly-dT Priming and Nebulization (A.thaliana) and my custom case contains reads having sequence from introns or UTRs, but I only want reads containing sequence from exons. The parameters I used to simulate are in the attachments.
2. Is it possible to calculate sequencing coverage for the simulation? For example: $\text{Sum of (read number} \times \text{read length)} / \text{Sum of (expressed number} \times \text{transcript length)}$

Any response is appreciated!



Attachments:
[t9_nebulization.par](#)
[A11_A21.par](#)