Reviewer Report

Title: Trans-NanoSim characterizes and simulates nanopore RNA-seq data

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Reviewer name: Andrey D. Prjibelski, M.Sc.

Reviewer Comments to Author:

General comments
The paper entitled "Trans-NanoSim characterizes and simulates nanopore RNA-seq data" describes a new tool for simulating long ONT RNA reads. The authors extend their previous tool NanoSim by adding several modifications, such as transcript abundance and intron retention events. Considering rapid growth of interest to long RNA reads, Trans-NanoSim is a valuable instrument for the scientific community.
The tool itself is available on GitHub, well-documented, easy to install and launch, which, indeed, is a positive aspect of this work. I was able to run quantification and simulation pipelines on my data without any problem, and I'm looking forward to using this tool in my work. Overall, the paper is well-structured and easy to follow. Below I summarize a few non-crucial issues, which, in my opinion, may improve the quality of the manuscript and the tool itself.
Major comments
- My main suggestion is to add a comparison against IsoSeqSim (https://github.com/yunhaowang/IsoSeqSim). Although it was released quite some time ago and may not have such functionality as introducing intron retention, it still has main simulation features such as truncating transcripts and introducing errors according to given profiles.
Minor comments
- Would be useful to provide some trained models for 1-2 typical ONT experiments in the package to allow a user to make a quick start.
- For the same reason, it could be helpful to add the possibility to simulate reads without transcript abundance file. Instead of real abundances, one can use some approximation (e.g. negative binomial distribution).
- Quality of plots used in the manuscript can be improved, preferably to vector quality.

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