

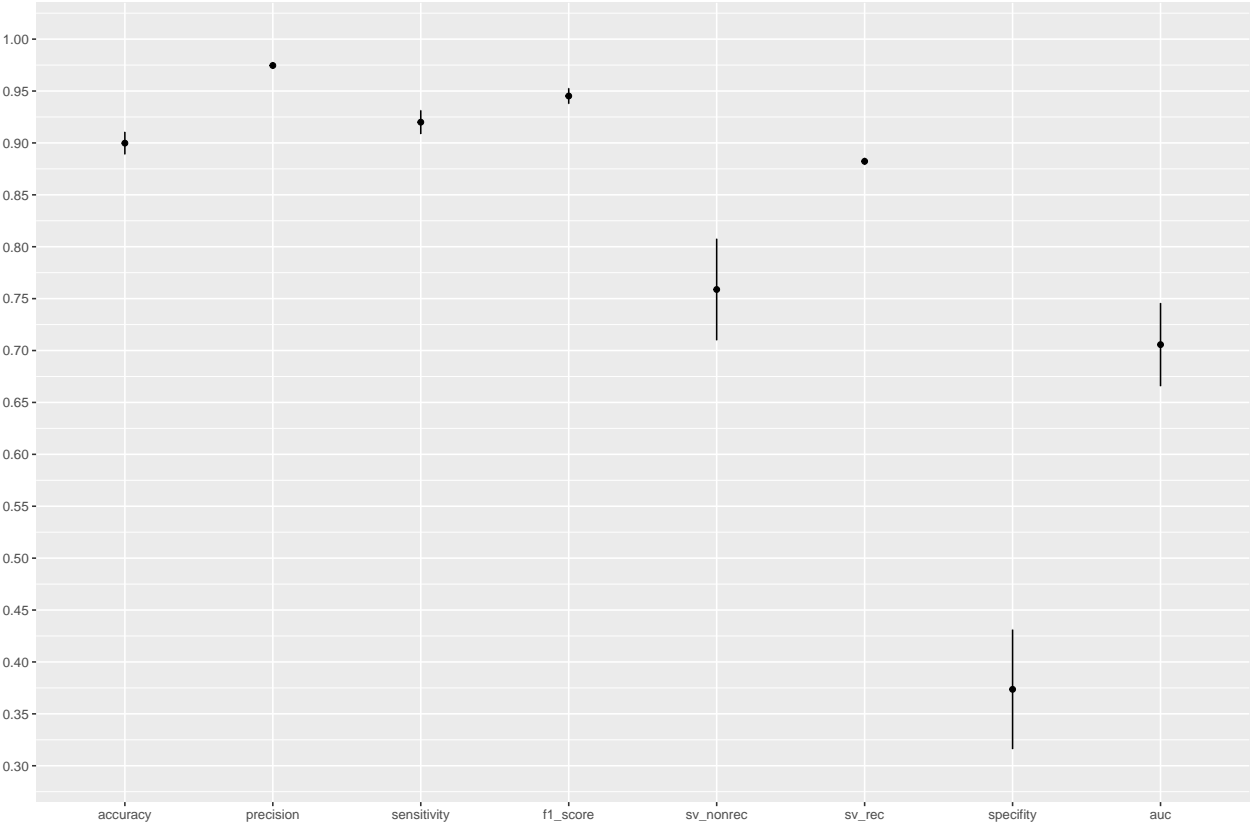
simulation results analysis for mix recombinants

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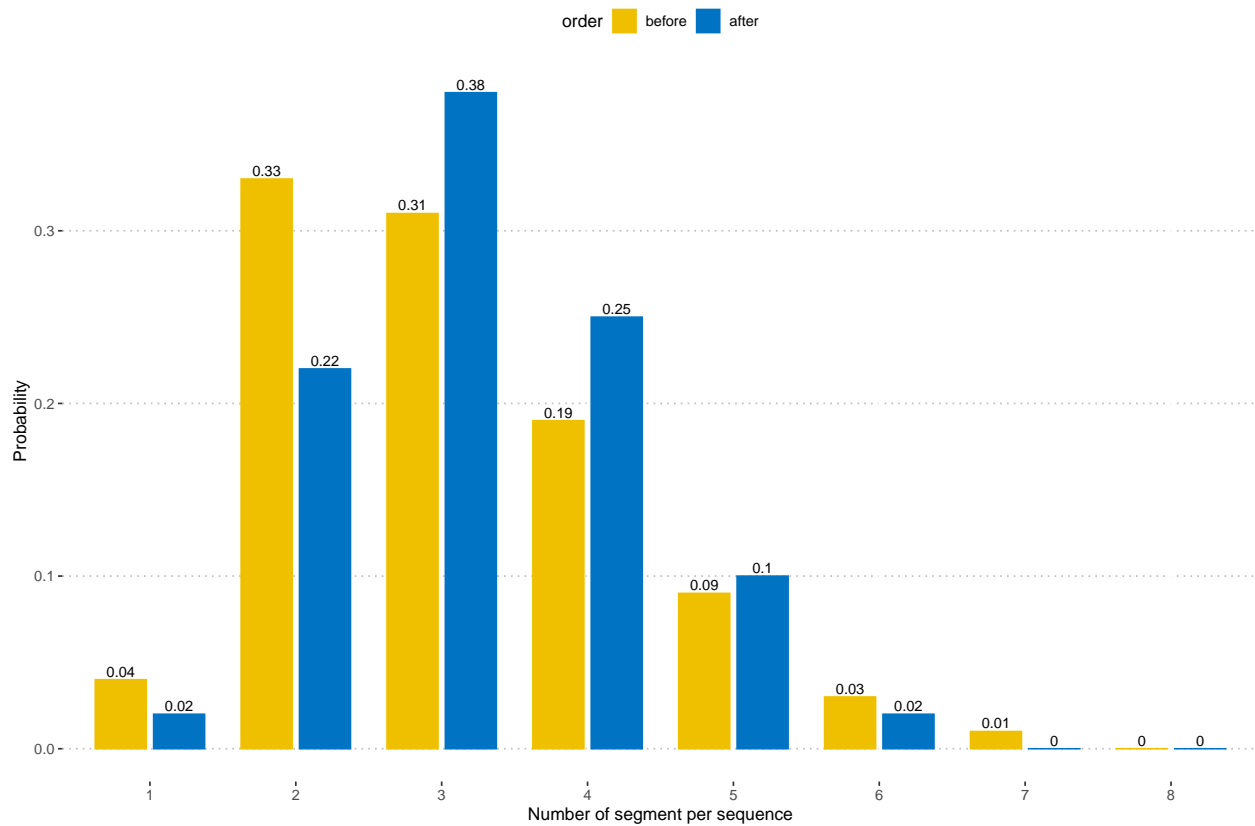
This file is for analyzing the simulation results for mix recombinants. The combination of recombinants per replicate was sampled from Ghana real data.

Classification measures: accuracy, precision, sensitivity, specifity, f1_score, sv_nonrec, sv_rec, auc



Mosaic three pars

##	mosaic_pars	value	CI.L	CI.R
##	delta	1 0.0021	0.001904004	0.002295996
##	epsilon	2 0.9677	0.961898507	0.973501493
##	rho	3 0.0129	0.012723603	0.013076397



Above original distribution before mosaic step seems to move towards to right. Conclusion is when I generate recombinants from real data mosaic output, the simulated dataset tend to generate more segments per target sequence after mosaic implementation.

I think we are trying to solve the low specificity issue. How to control the number of recombinants in multiple_source partial alignment case?

