This supplement accompanies

Statistically-Consistent k-mer Methods for Phylogenetic Tree Reconstruction

by E.S. Allman, J.A. Rhodes, and S. Sullivant.

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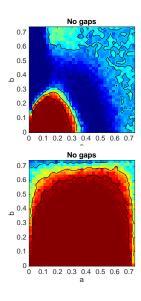
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1 Simulation results using d_{JC} + Neighbor Joining, 1000 bp

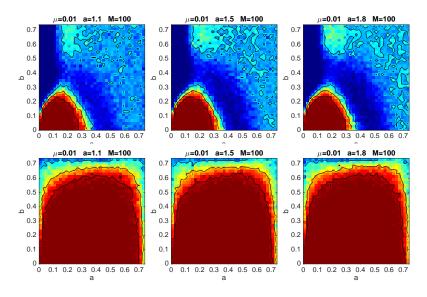
Each pair of rows corresponds to 100 datasets simulated with a fixed rate of insertions/deletions. Columns correspond to varying Lavalette parameters. In each pair of rows, the top row shows alignment+NJ, and the bottom row shows true alignment+NJ. Sequences have length 1000 bp.

1.1 JC with no indel process.

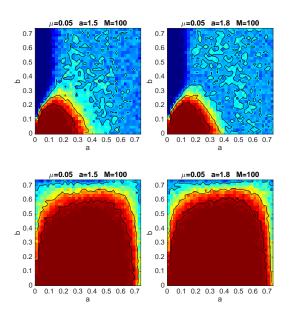


100 80 60 40 20

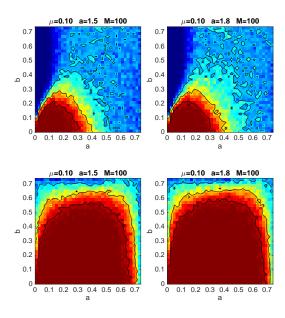
1.2 JC with mutation rate $\mu = 0.01$ for the indel process.



1.3 JC with mutation rate $\mu = 0.05$ for the indel process.



1.4 JC with mutation rate $\mu = 0.10$ for the indel process.

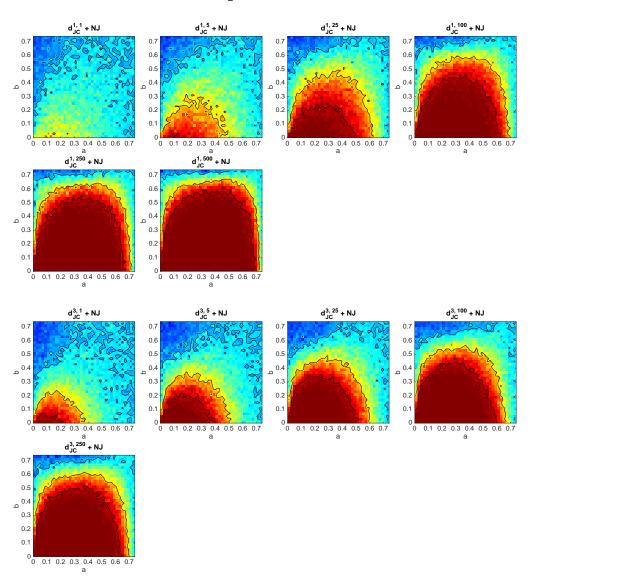


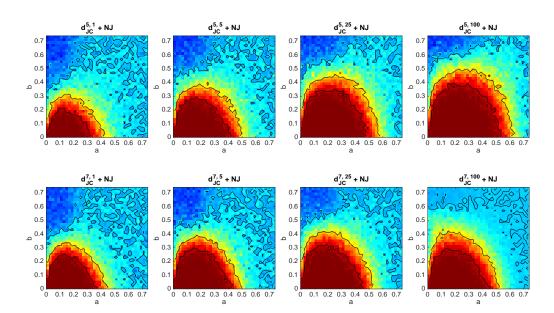
2 Simulation results using $d_{JC}^{k,B}$ + Neighbor Joining, 1000 bp

Each subgroup of figures corresponds to a fixed setting for the model parameters used to generate sequences. Titles indicate the value of k and the number of blocks used for computing $d_{JC}^{k,B}$. Sequences have length 1000 bp.

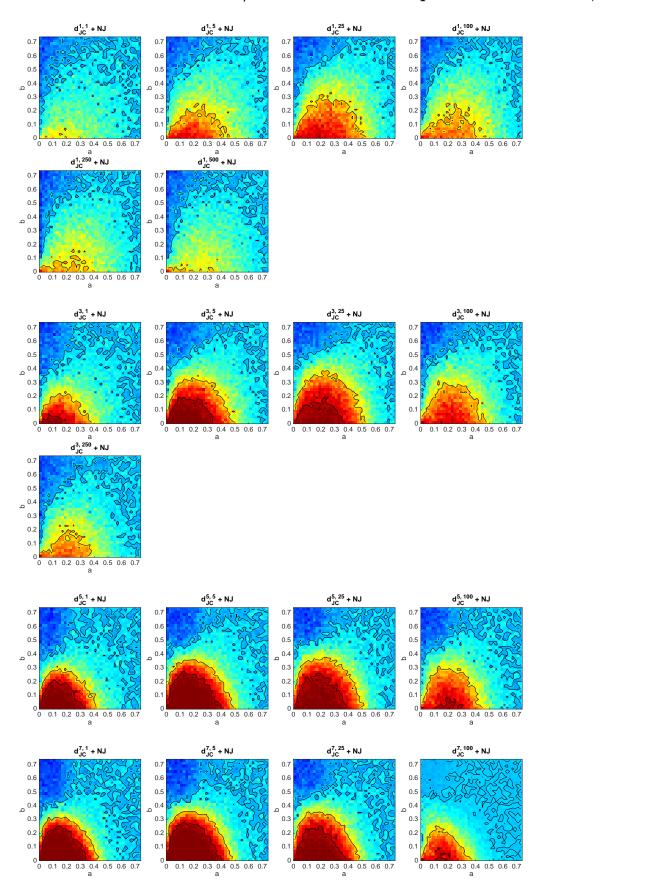
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2.1 JC with no indel process.

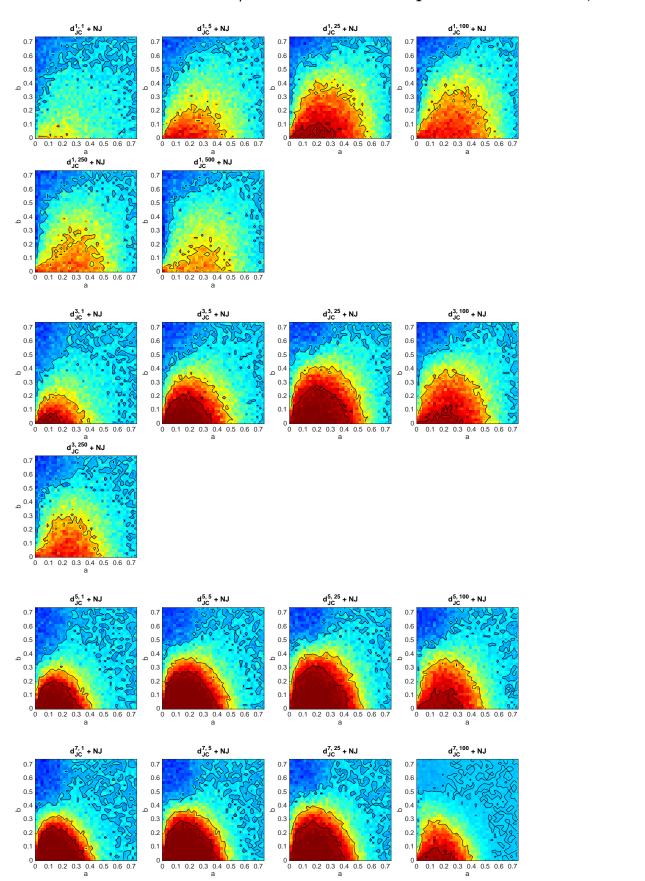




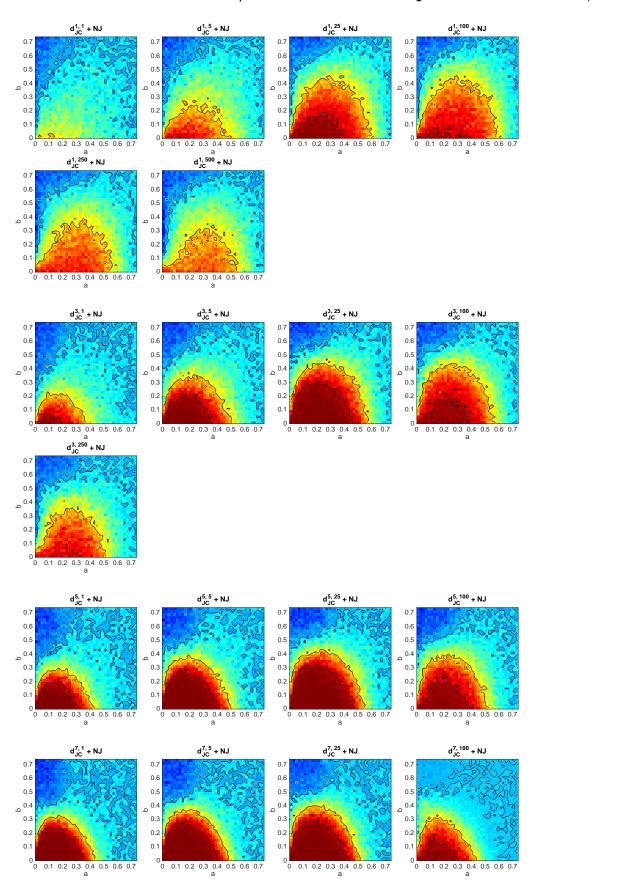
2.2 JC with indel rate $\mu=0.01$. Lavalette parameters $a=1.1,\,M=100$.



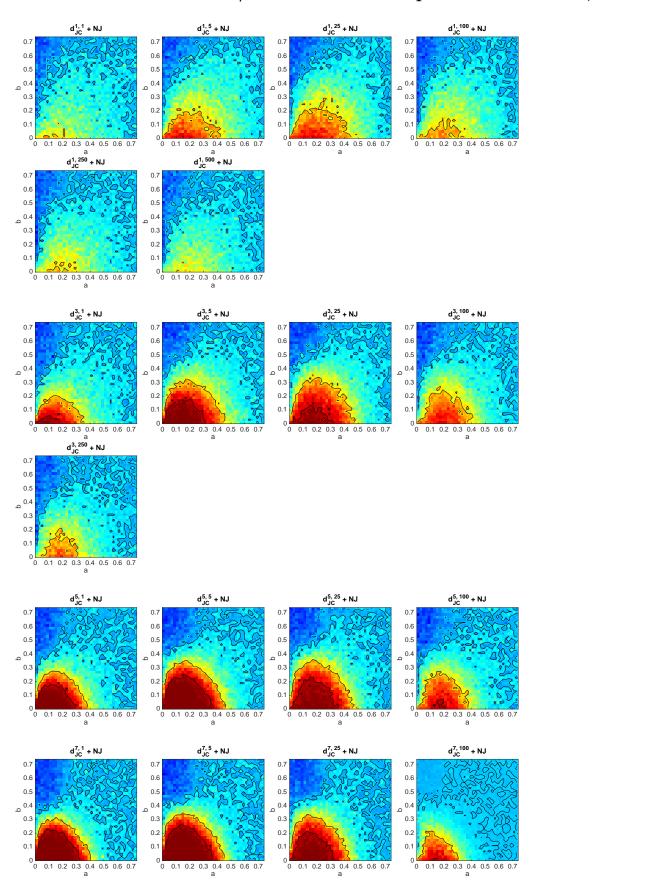
2.3 JC with indel rate $\mu=0.01$. Lavalette parameters $a=1.5,\,M=100$.



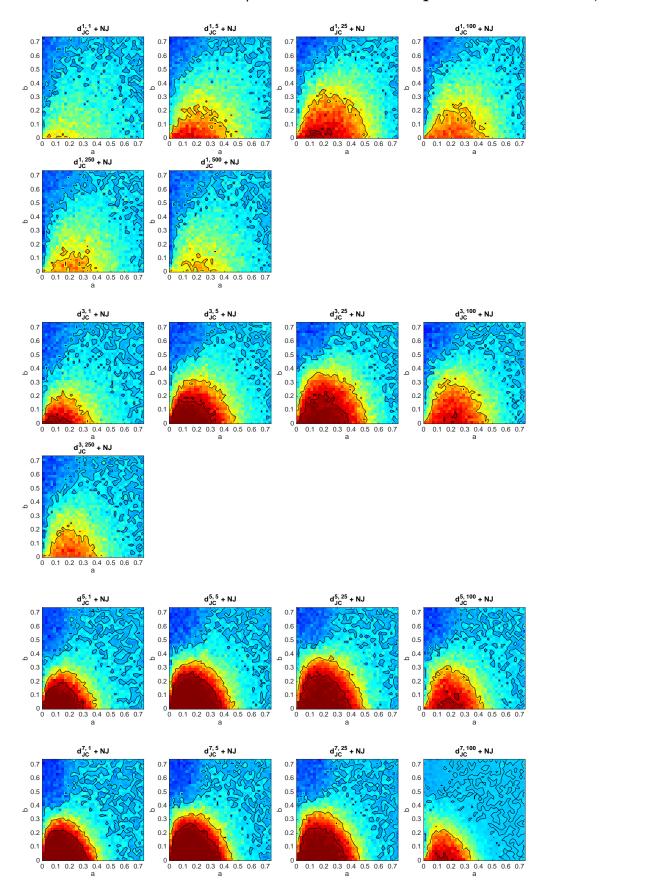
2.4 JC with indel rate $\mu=0.01$. Lavalette parameters $a=1.8,\,M=100$.



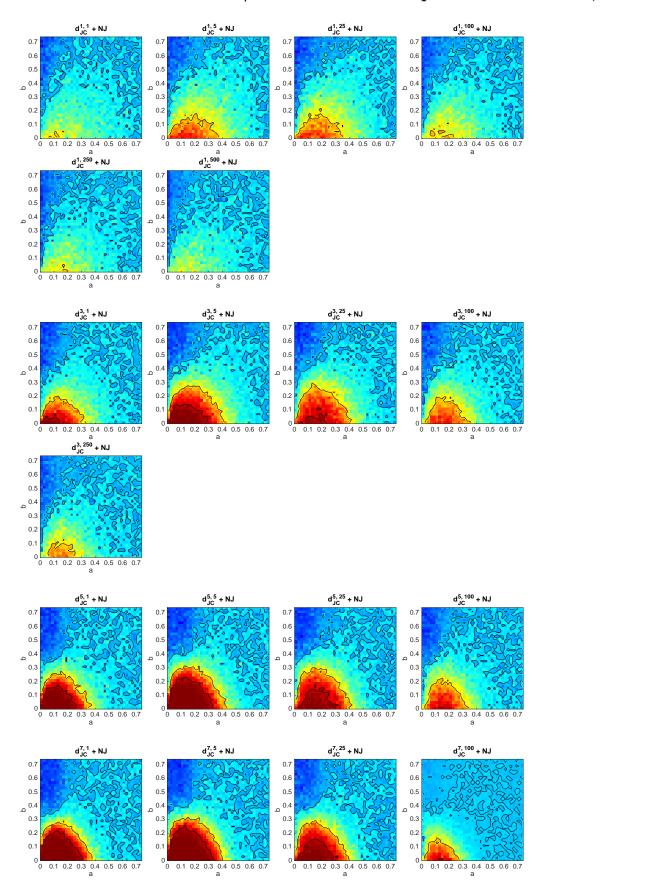
2.5 JC with indel rate $\mu=0.05$. Lavalette parameters $a=1.5,\,M=100$.



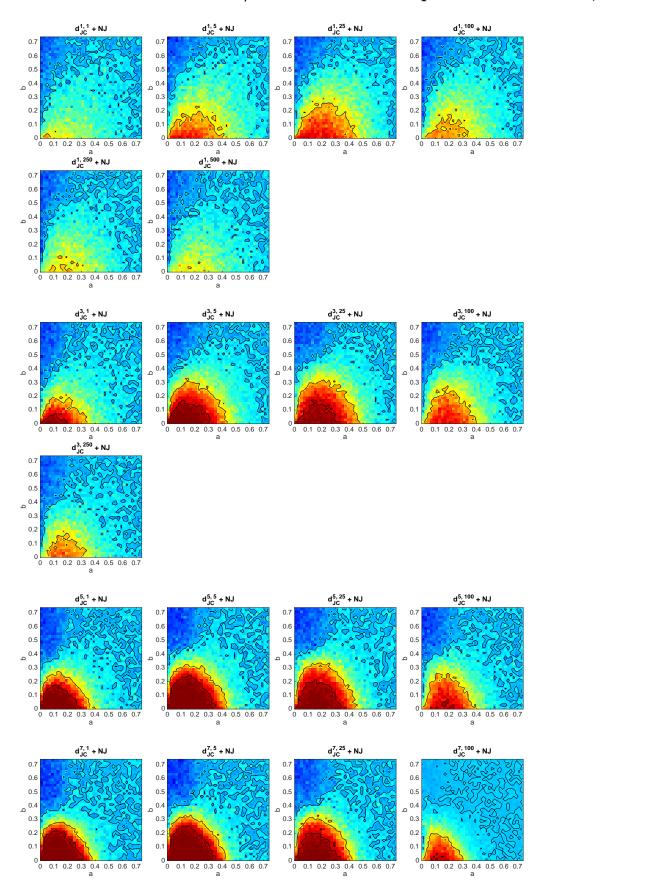
2.6 JC with indel rate $\mu=0.05$. Lavalette parameters $a=1.8,\,M=100$.



2.7 JC with indel rate $\mu=0.10$. Lavalette parameters $a=1.5,\,M=100$.



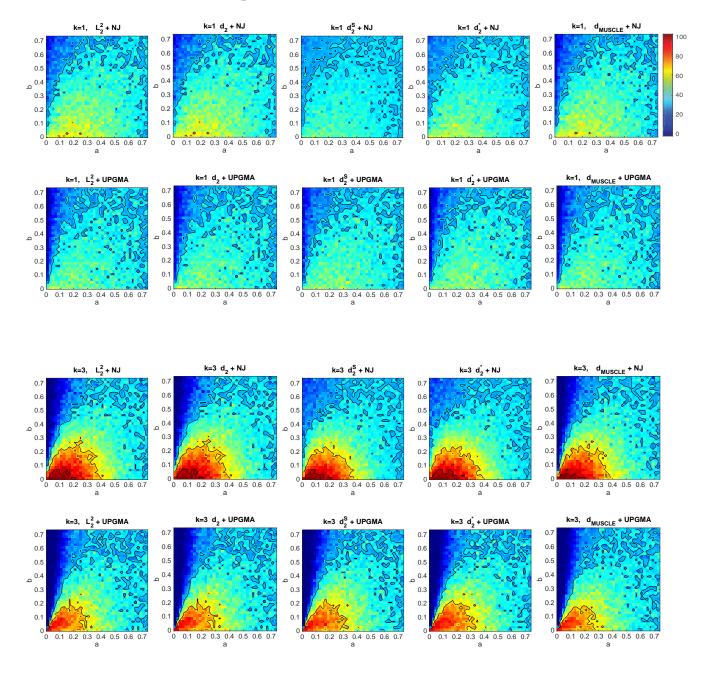
2.8 JC with indel rate $\mu=0.10$. Lavalette parameters $a=1.8,\,M=100$.

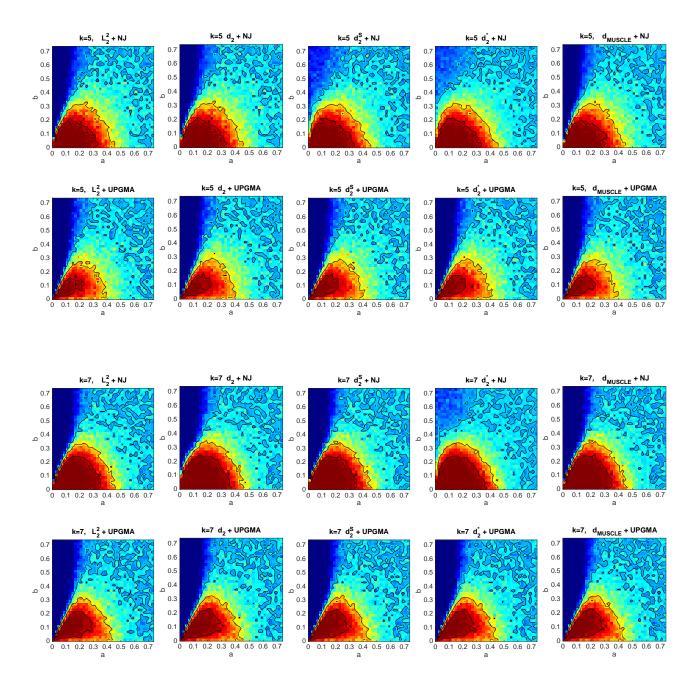


3 Simulation results using other k-mer distances + Neighbor Joining/UPGMA, 1000 bp

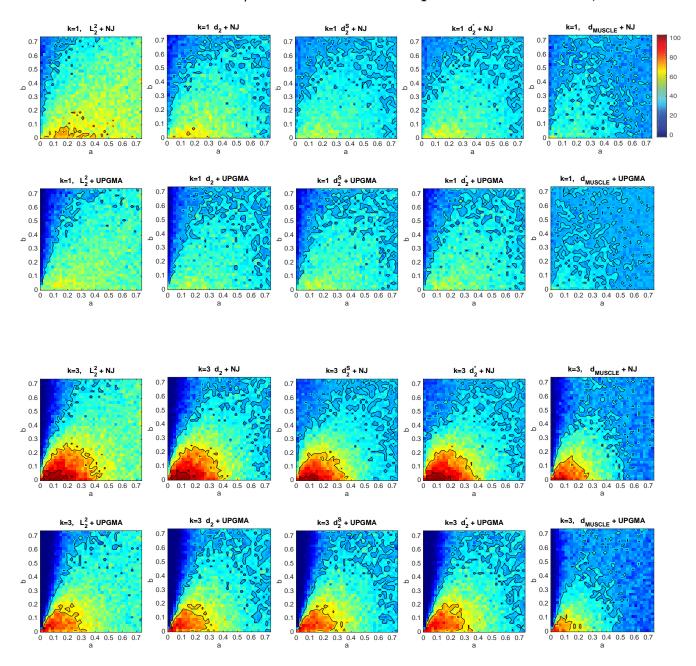
Each subgroup of figures corresponds to a fixed setting for the model parameters used to generate sequences. Titles indicate the value of k, the distance used, and whether tree construction was performed using NJ or UPGMA. Sequences have length 1000 bp.

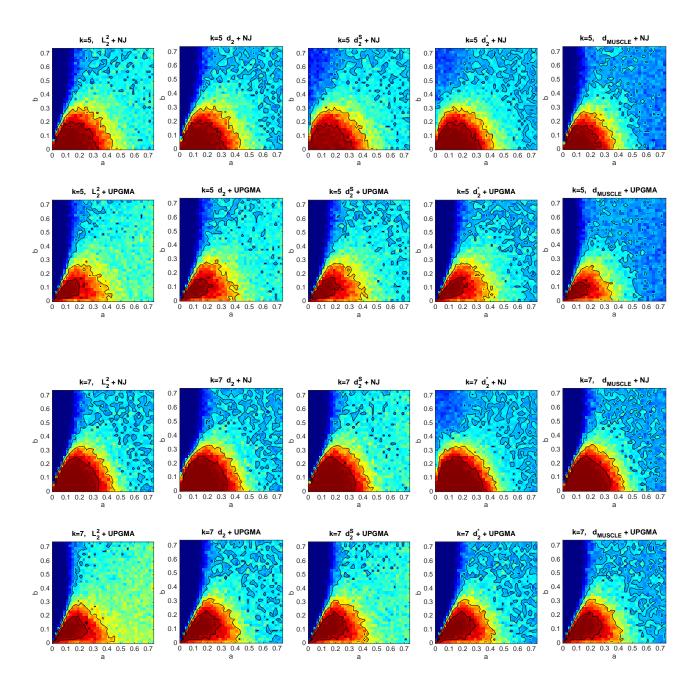
3.1 JC with no indel process.



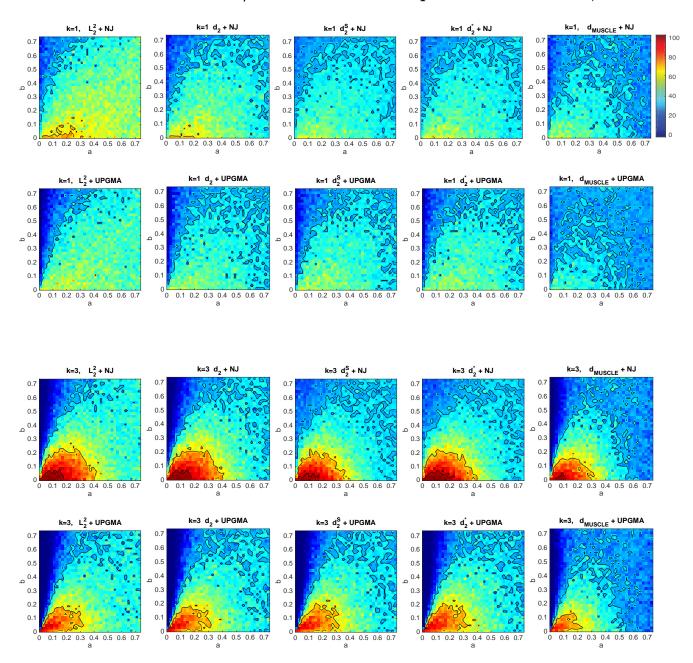


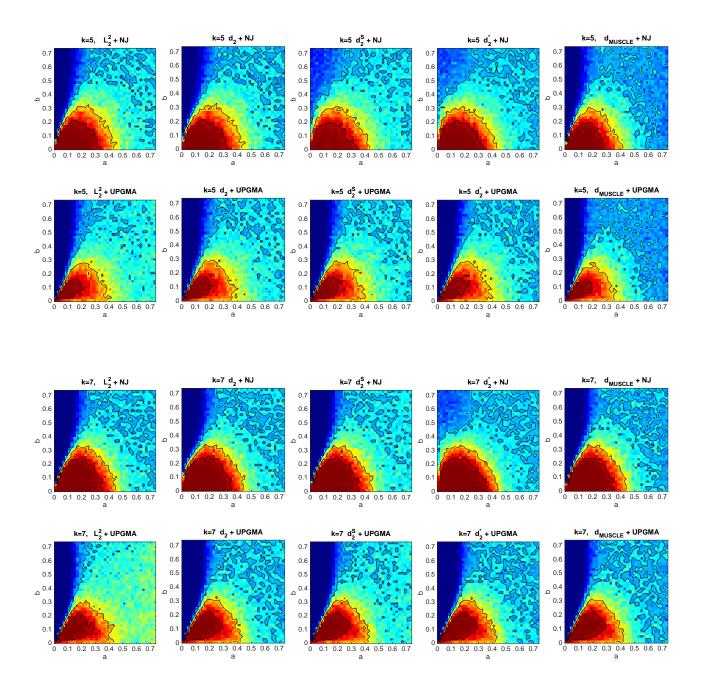
3.2 JC with indel rate $\mu=0.01$. Lavalette parameters $a=1.1,\,M=100$.



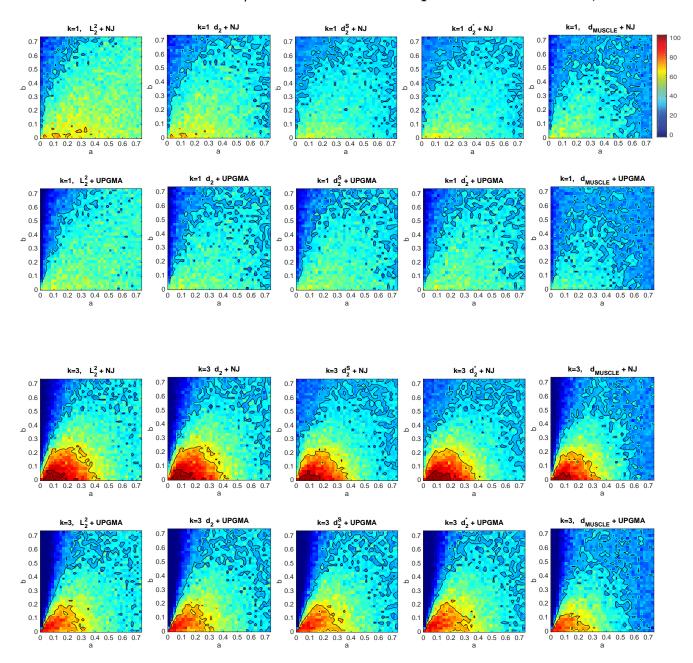


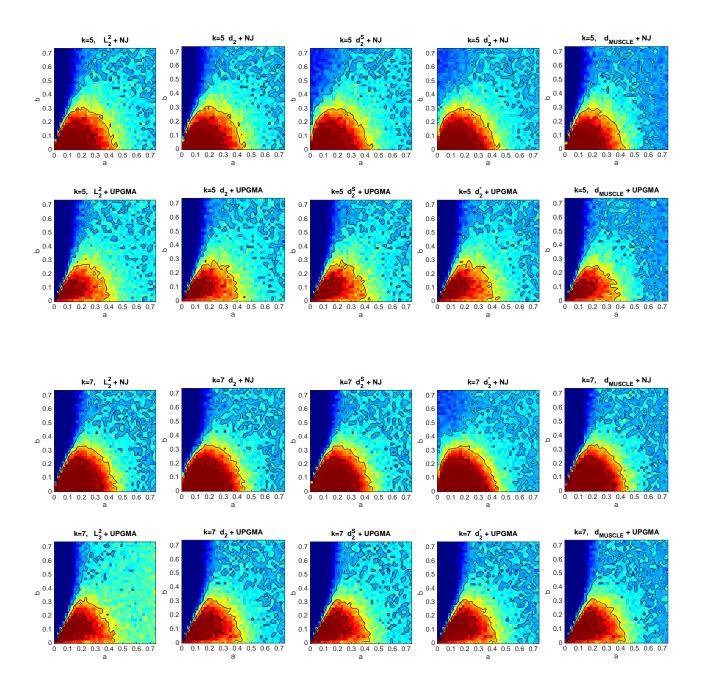
3.3 JC with indel rate $\mu=0.01$. Lavalette parameters $a=1.5,\,M=100$.



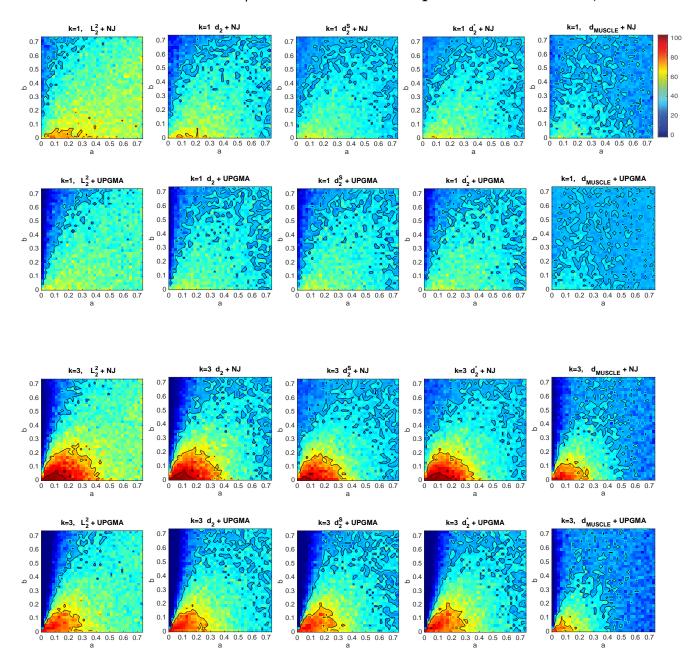


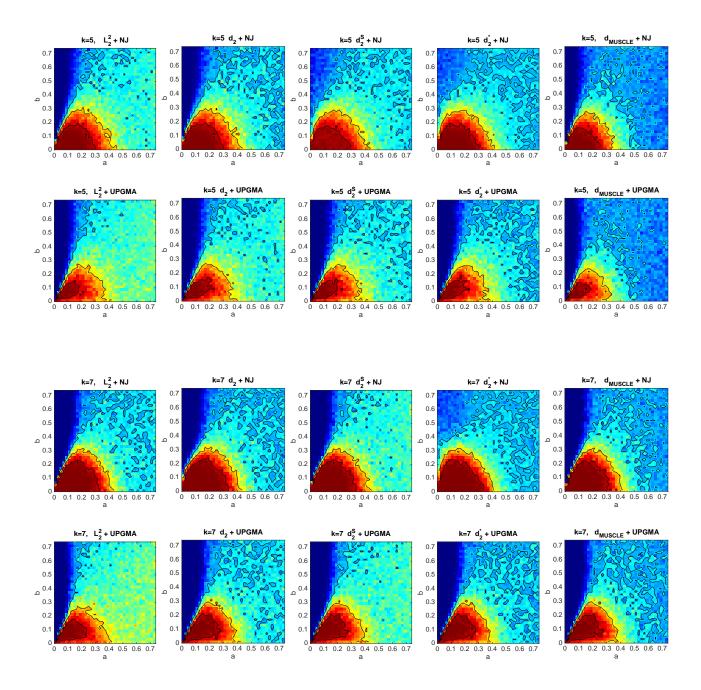
3.4 JC with indel rate $\mu=0.01$. Lavalette parameters $a=1.8,\,M=100$.



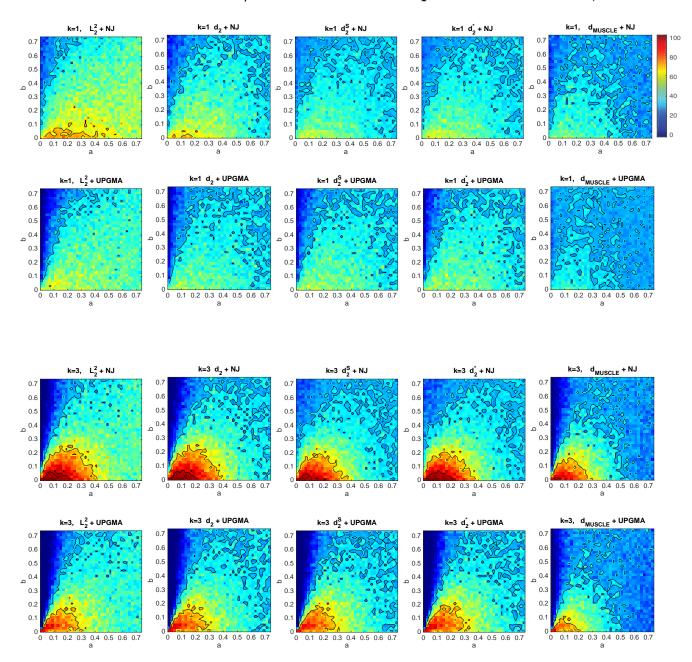


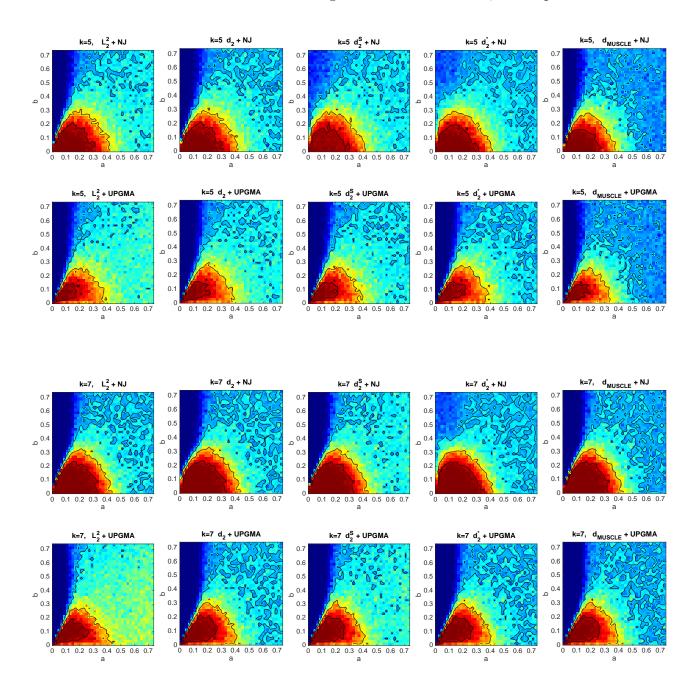
3.5 JC with indel rate $\mu=0.05$. Lavalette parameters $a=1.5,\,M=100$.



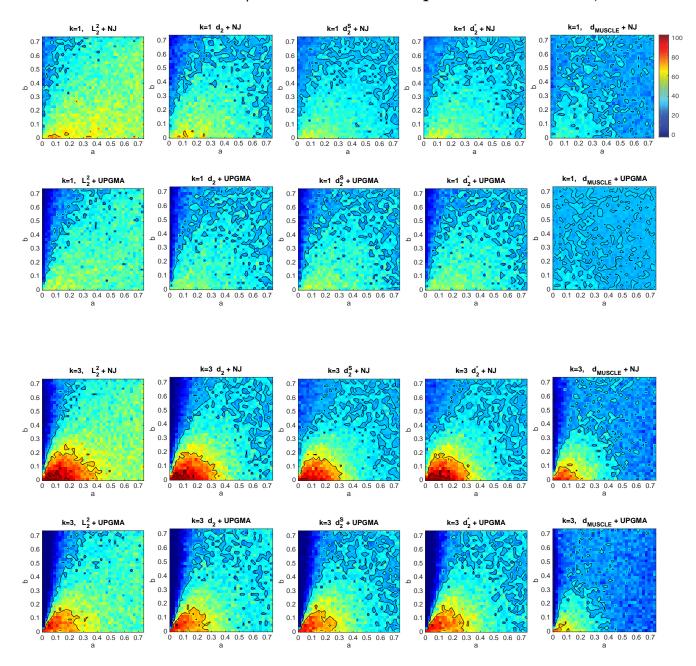


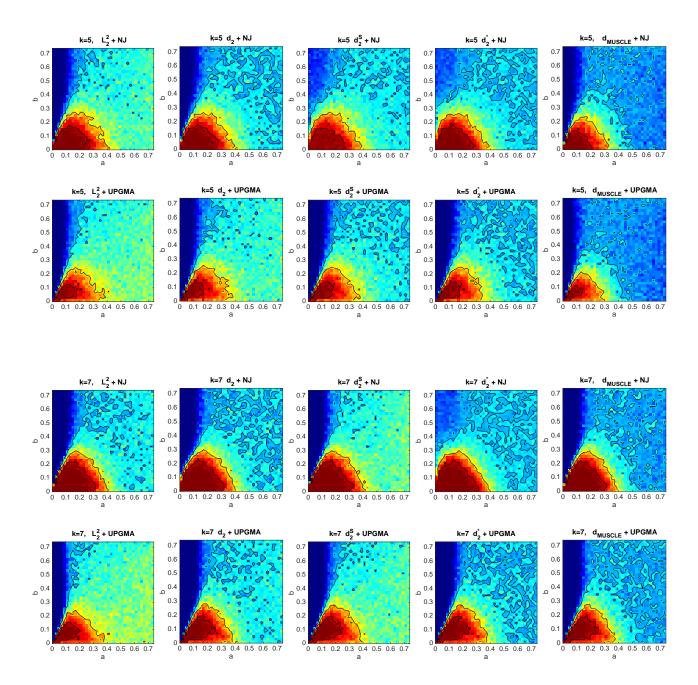
3.6 JC with indel rate $\mu=0.05$. Lavalette parameters $a=1.8,\,M=100$.



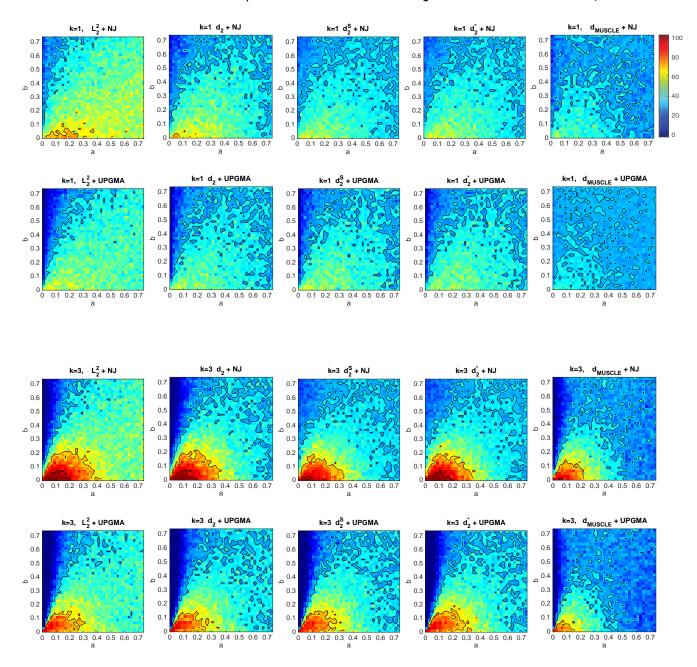


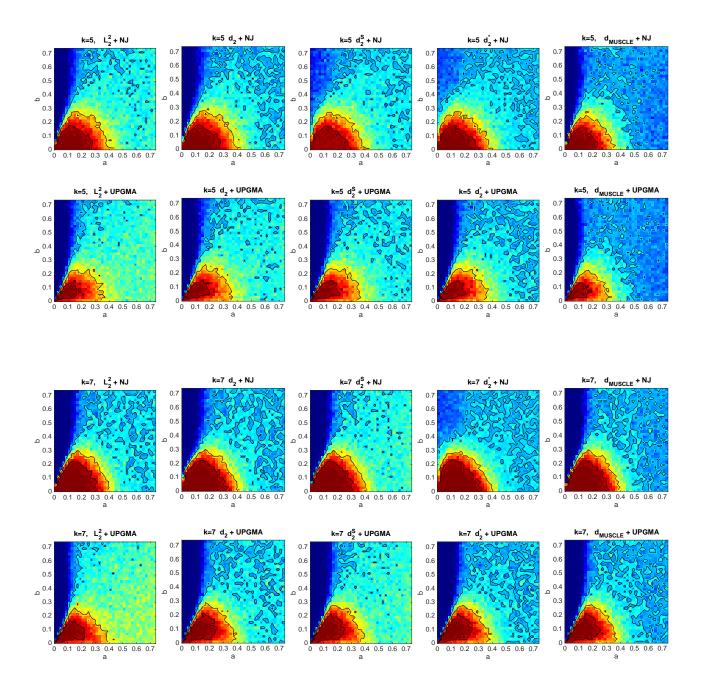
3.7 JC with indel rate $\mu=0.10$. Lavalette parameters $a=1.5,\,M=100$.





3.8 JC with indel rate $\mu=0.10$. Lavalette parameters $a=1.8,\,M=100$.

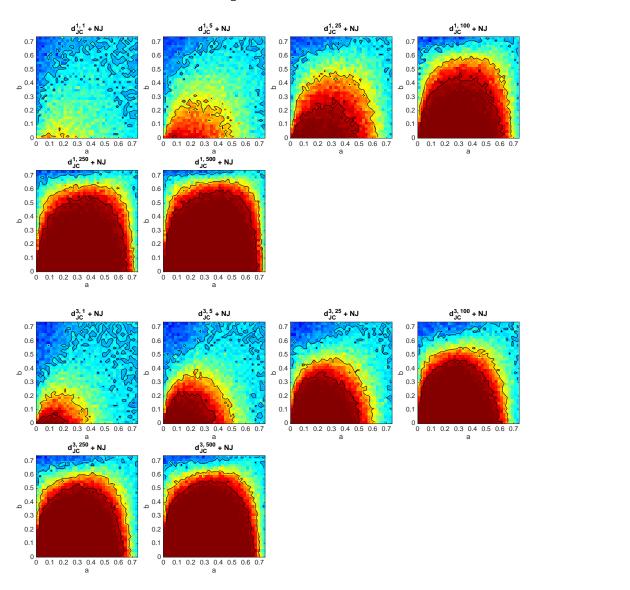


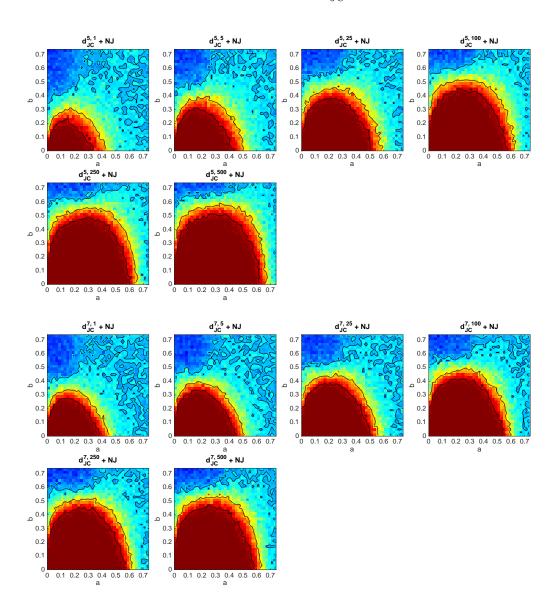


4 Simulation results using $d_{JC}^{k,B}$ + Neighbor Joining, 10,000 bp

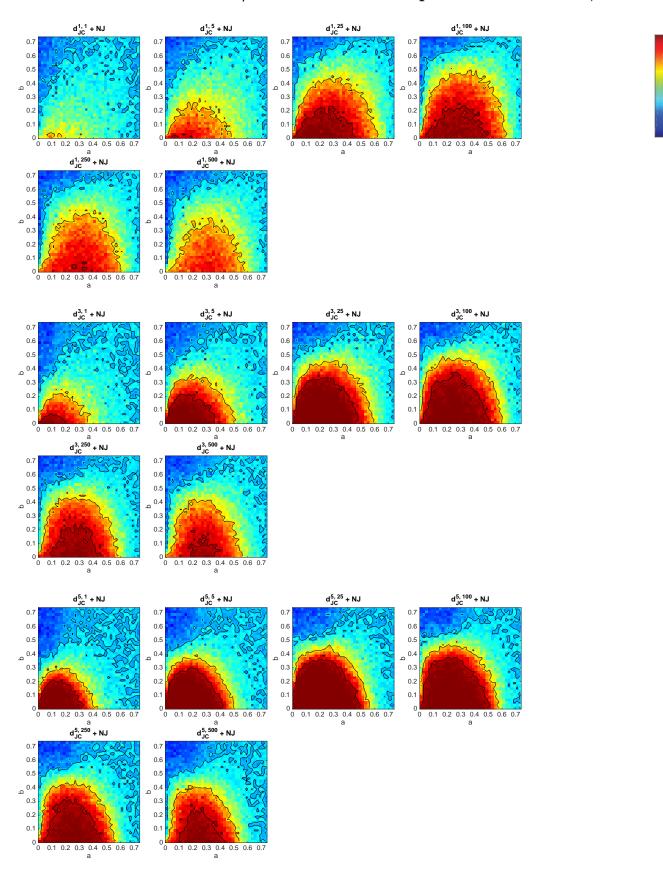
Each subgroup of figures corresponds to a fixed setting for the model parameters used to generate sequences. Titles indicate the value of k and the number of blocks used for computing $d_{JC}^{k,B}$. Sequences have length 10,000 bp.

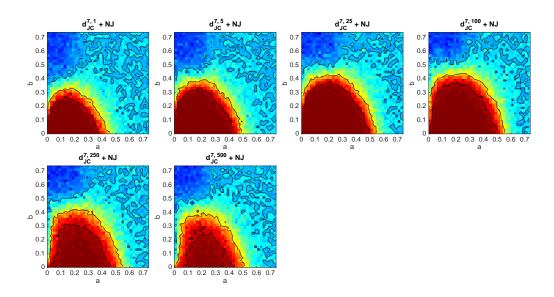
4.1 JC with no indel process.





4.2 JC with indel rate $\mu=0.01$. Lavalette parameters $a=1.5,\,M=100$.





4.3 JC with indel rate $\mu=0.05$. Lavalette parameters $a=1.8,\,M=100$.

