



# UNCOVERING THE DYNAMICS OF CRISPR ARRAY EVOLUTION WITH A SPACER ORDER RESPECTING MAXIMUM LIKELIHOOD – APPROACH

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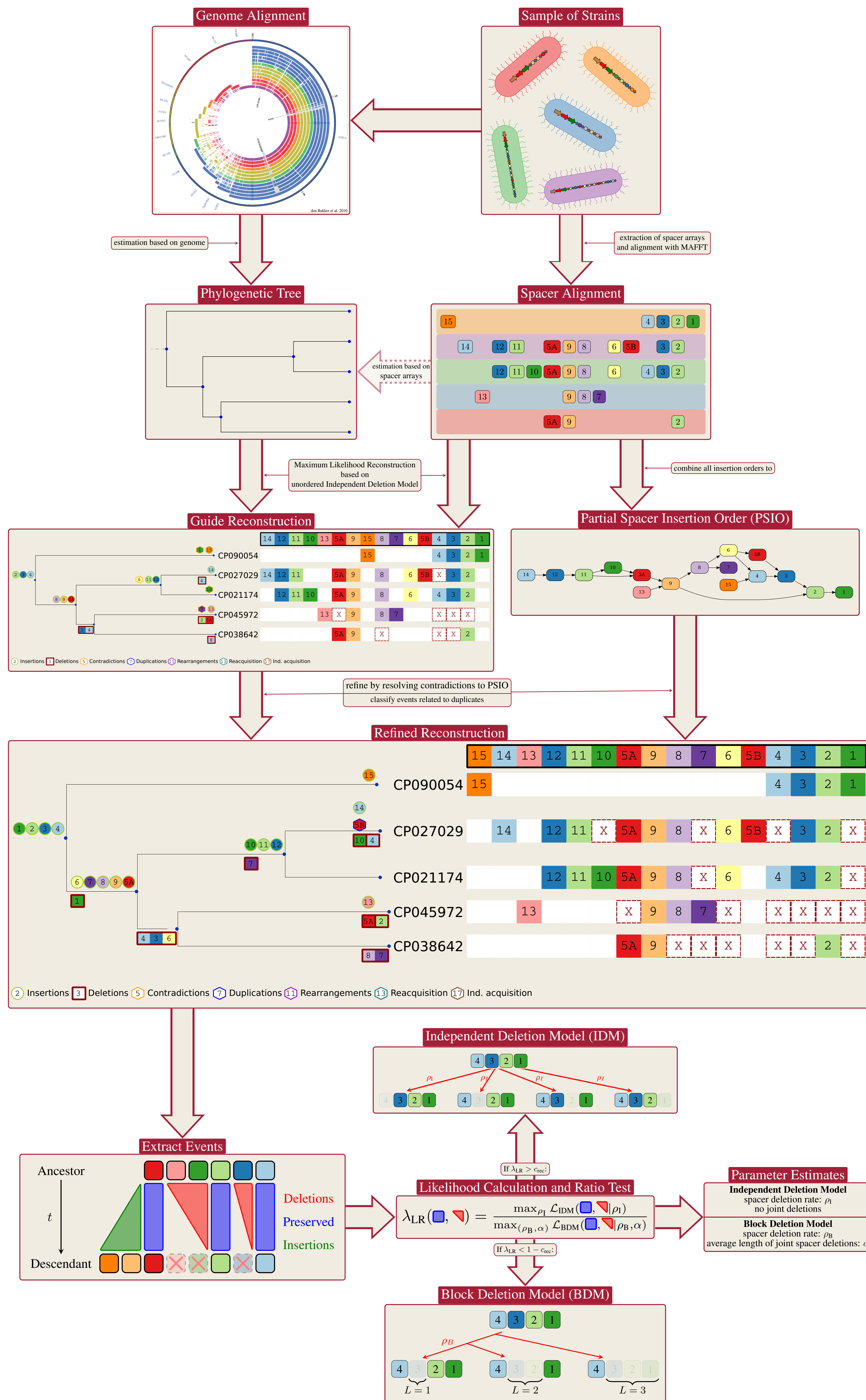
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## Overview

- CRISPR arrays provide a chronological history of acquired spacers.
- We introduce **SpacerPlacer**, a ancestral reconstruction tool that employs evolutionary models and enforces spacer insertion order to reconstruct ancestral arrays.
- With **SpacerPlacer** we investigate, if spacers are deleted in blocks, and compare estimated model parameters between CRISPR-Cas types, genus and more.

## Placing Spacers with SpacerPlacer: Ancestral Reconstruction Algorithm



## Data

- CRISPR array data extracted from *CRISPRdb* [1] (7352 repeats with 32624 arrays of highest evidence).
- Arrays were clustered by species, Cas type, overlap of spacers and spacer diversity into 337 groups with 5192 arrays (2327 are unique).

## Contact

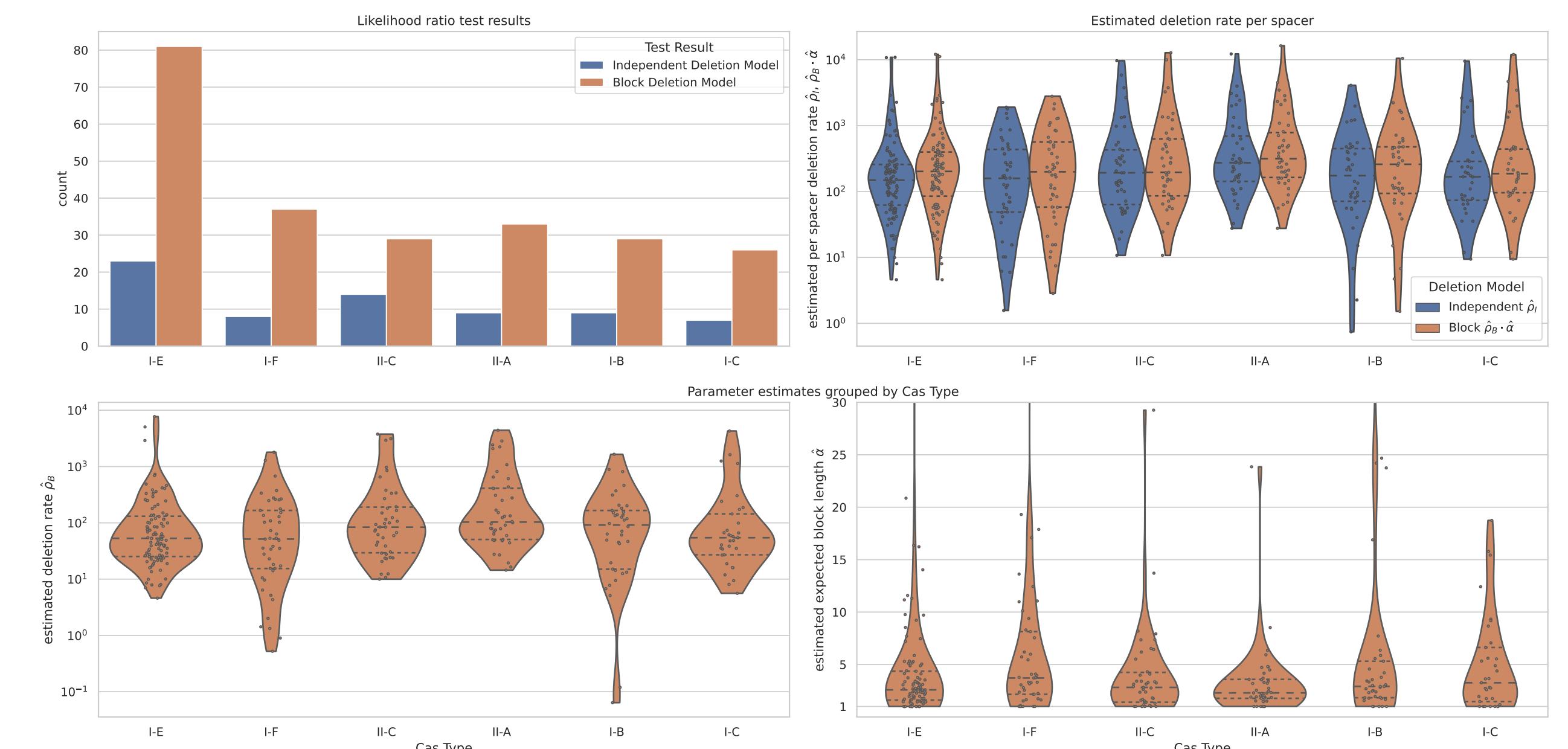
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<https://github.com/fbaumdicker/SpacerPlacer>

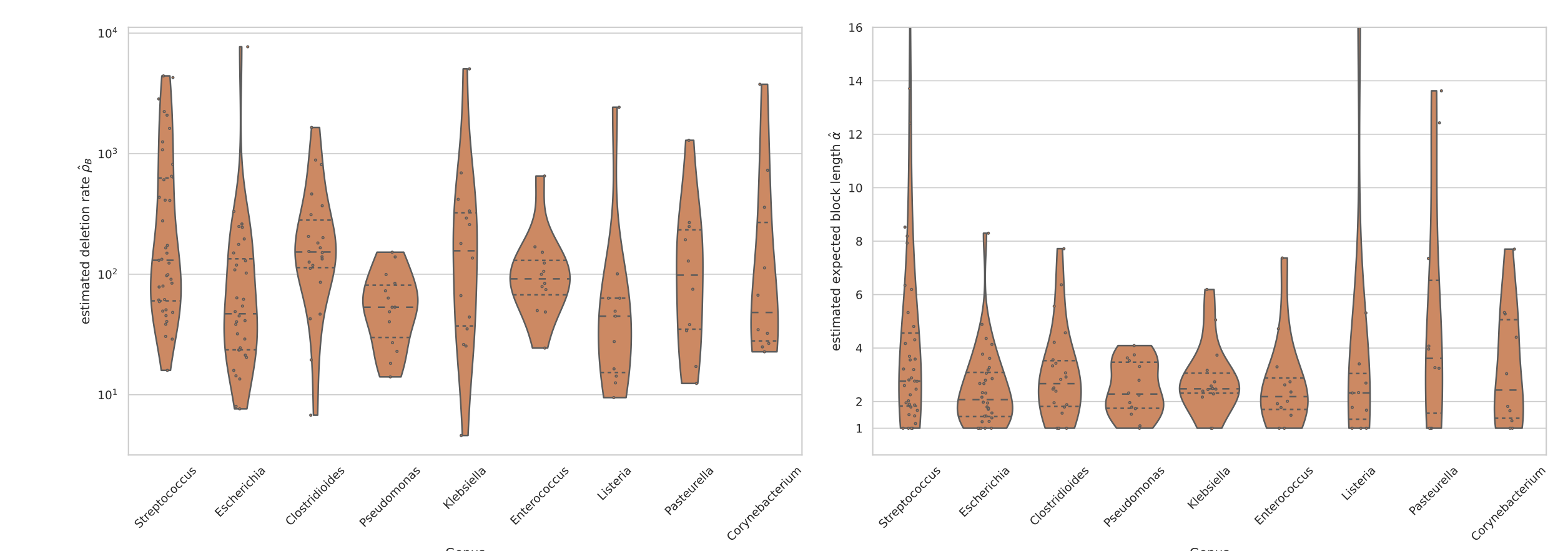


## Test Results, Parameter Estimates (Cas Type)

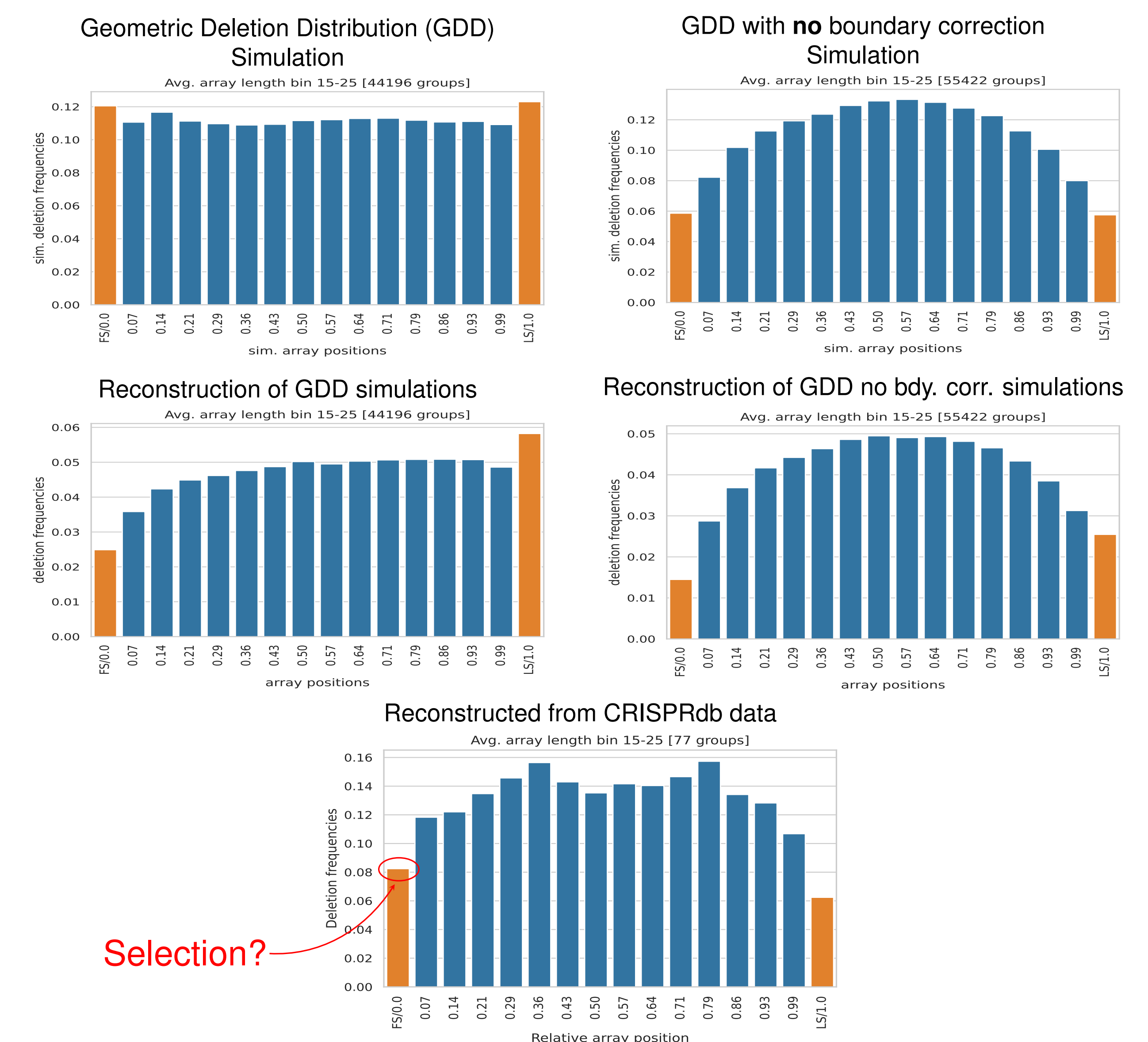


Mean of spacer deletion initiation rate  $\hat{\rho}_B \sim 300$  times higher than per site mutation rate.  
Mean of average length of block deletions  $\hat{\alpha} \approx 4.7$ .

## Parameter Estimates (Genus)



## Deletion Boundary Behavior → Selection?



## Conclusions and Applications

- Test results strongly suggest that spacers are lost in blocks.
- Marginal differences of deletion rates between Cas types. Larger differences between genera.
- First and last spacer are less likely to be deleted. Indication of selection at array insertion end.
- SpacerPlacer** serves as stepping stone for further research, e.g.:

### CRISPR - evo-inator

CRISPR evolution based inference of array transcription orientation

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### Relevant Publications

- Christine Pourcel et al. "CRISPRCasdb a successor of CRISPRdb containing CRISPR arrays and cas genes from complete genome sequences, and tools to download and query lists of repeats and spacers". In: *Nucleic acids research* 48.D1 (2020), pp. D535–D544.
- John Rozewicki et al. "MAFFT-DASH: integrated protein sequence and structural alignment". In: *Nucleic acids research* 47.W1 (2019), W5–W10.