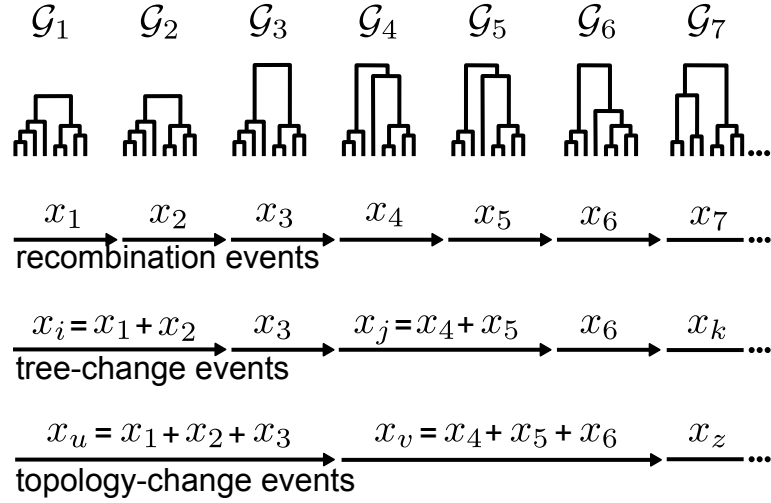


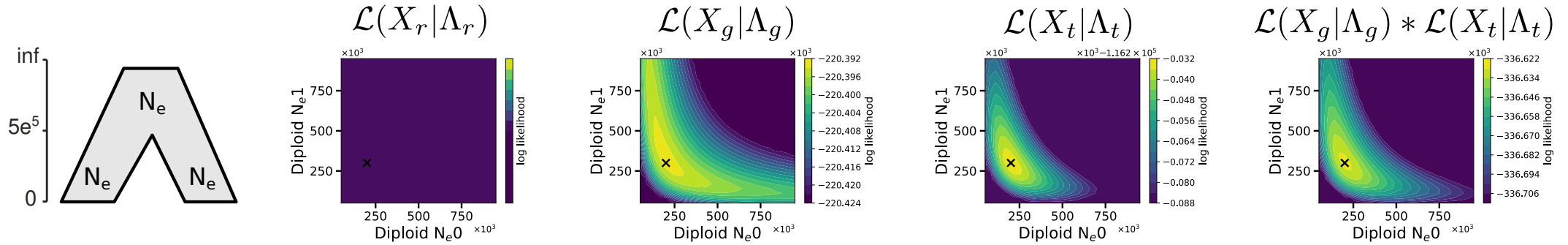
### (A) Proposed ARG for a genome region



### (B) Calculate MS-SMC waiting distance rate parameters ( $\lambda$ ) for each event given a parameterized demographic model:

Trees between events	Calculated rates of events	Interval lengths of events
$G_r = [\mathcal{G}_1, \mathcal{G}_2, \mathcal{G}_3, \dots]$	$\Lambda_r = [\lambda_{r1}, \lambda_{r2}, \lambda_{r3}, \dots]$	$X_r = [x_1, x_2, x_3, \dots]$
$G_g = [\mathcal{G}_1, \mathcal{G}_3, \mathcal{G}_4, \dots]$	$\Lambda_g = [\lambda_{g1}, \lambda_{g3}, \lambda_{g4}, \dots]$	$X_g = [x_i, x_3, x_j, \dots]$
$G_t = [\mathcal{G}_1, \mathcal{G}_4, \mathcal{G}_7, \dots]$	$\Lambda_t = [\lambda_{t1}, \lambda_{t4}, \lambda_{t7}, \dots]$	$X_t = [x_u, x_v, x_z, \dots]$

### (C) Likelihood surface of demographic model parameters inferred from waiting distances (MS-SMC):



### (D) Likelihood surface of demographic model parameters inferred from coalescent waiting times (MSC):

