Target Flipping on the RNA ND GP map

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Initial conditions: target T0 and seqs at seqscommon with max prob in T1

Each point is averaged over 100 simulations with the same parameters

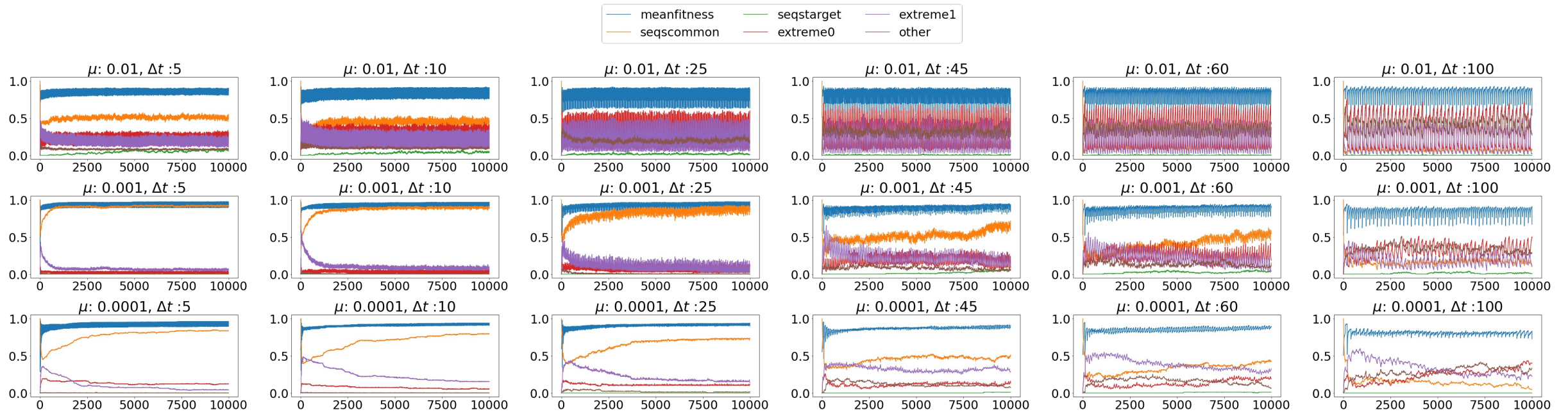(seqstarget increase present)
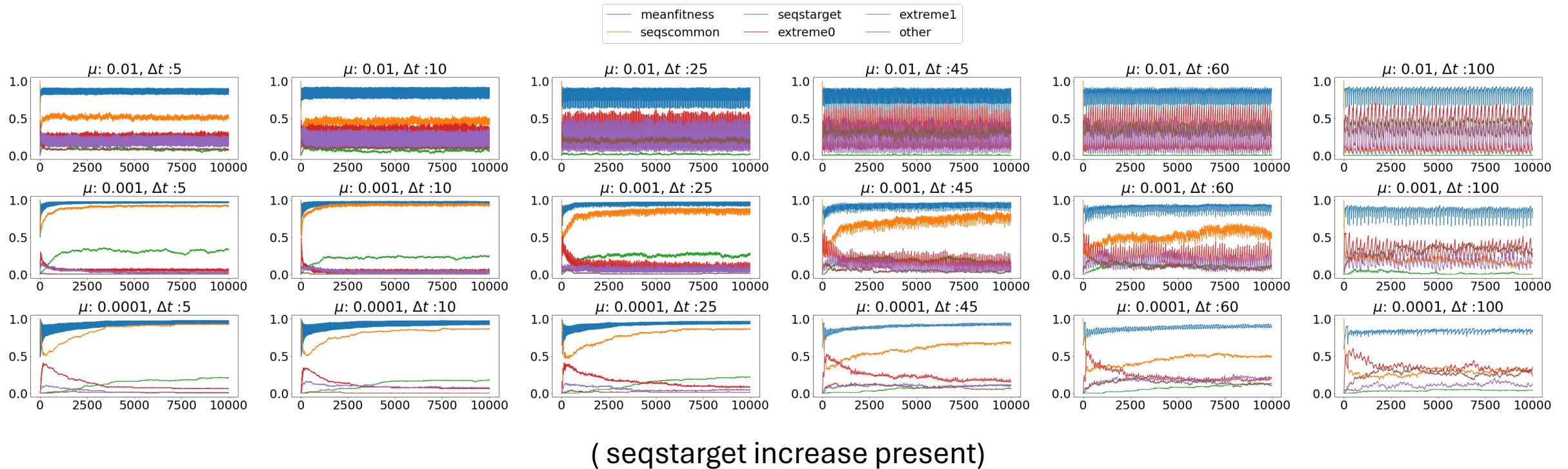
Simulation params:
N sample for fitness max = 10
N pop = 100
Fitness landscape = hamming

Initial conditions: target T1 and seqs at seqscommon with max prob in T0

Each point is averaged over 100 simulations with the same parameters

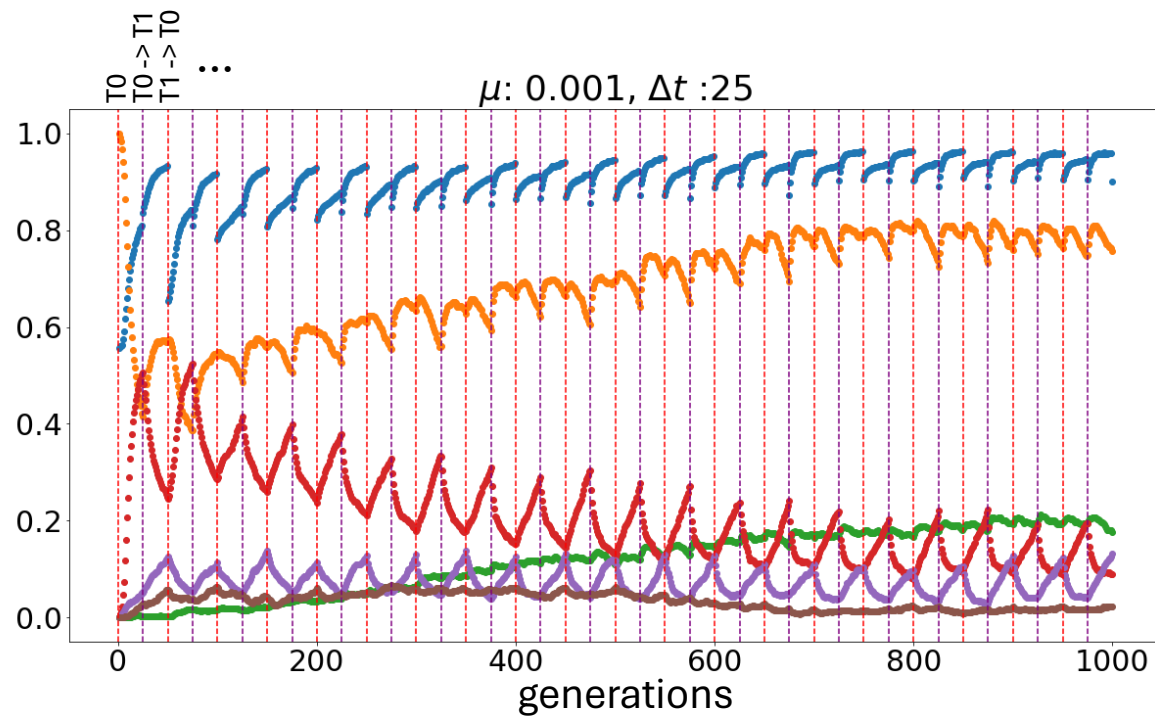(no seqstarget increase in this case)

Simulation params:
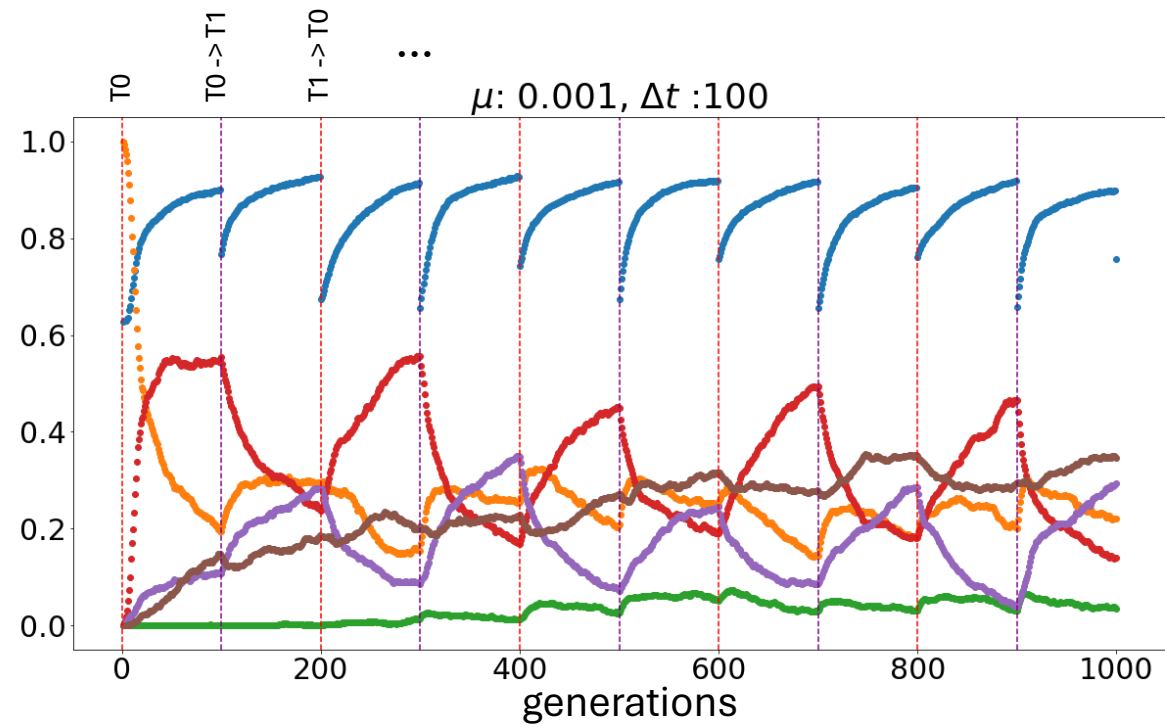N sample for fitness max = 10
N pop = 100
Fitness landscape = hamming

Special close-up examples
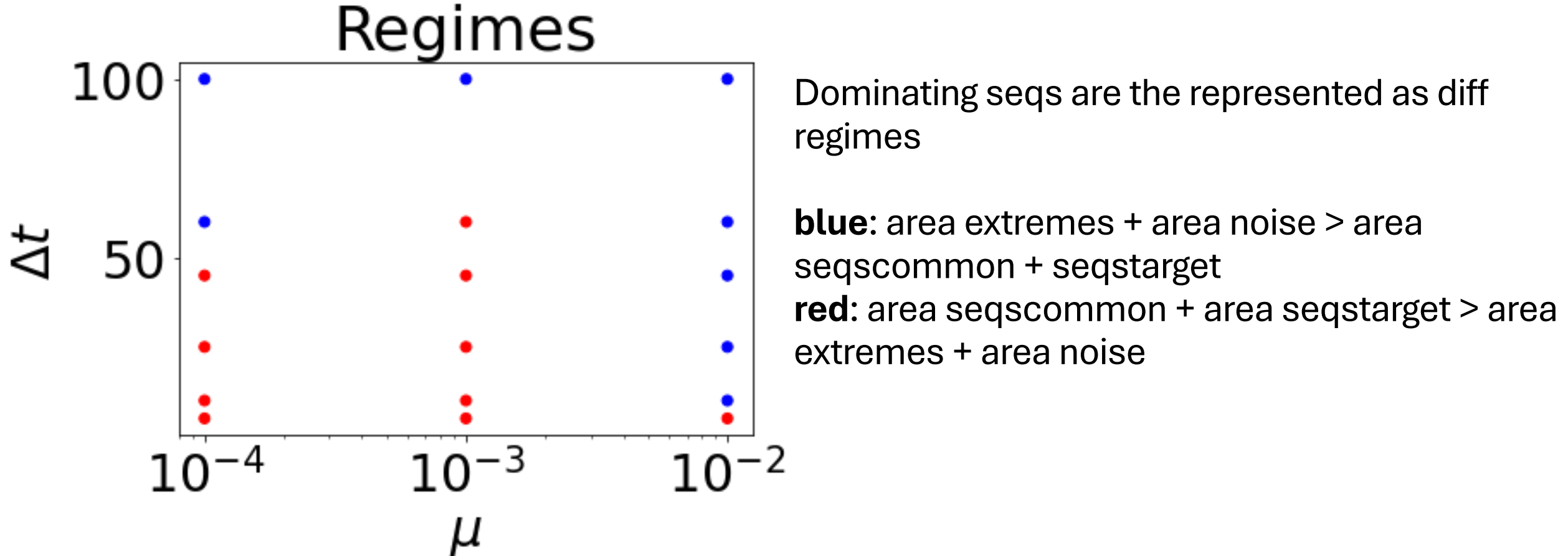
(Vertical lines are target flips)

Initial conditions: target T0 and seqs at seqscommon with max prob in T1

Integral over the curve for each type of seq and compare the areas to see which one dominates over the tot evolutionary sim

Dominating seqs are the represented as diff regimes

blue: area extremes + area noise > area seqscommon + seqstarget
red: area seqscommon + area seqstarget > area extremes + area noise

In progress... collecting more points now.