Nucleotide substitution variant count distributions (input samples) input2 input1 input3 1.2 -0.8 -0.4 0.0 15 10 5 · 20 Hamming_distance 10 Density 20 15 10 5 · 15 10 5 12 8 100 1000 10000 10 100 1000 10000 1e+01 1e+03 1e+05 10 variant count + 1 (log scale)