Nucleotide substitution variant count distributions (input samples) input1 input2 input3 0.8 0.6 0.4 0.2 0.0 1.0 0.5 0.0 15 -Hamming_distance 10 5 Density 15 10 5 10 -5 10.0 7.5 5.0 2.5 0.0 1e+05 1e+03 1e+05 1e+05 1e+01 1e+03 1e+01 1e+01 1e+03 variant count + 1 (log scale)