Nucleotide substitution variant count distributions (input samples) input1 input2 input3 1.00 0.75 0.50 0.25 0.00 0.9 0.6 0.3 0.0 20 -15 Hamming_distance 10 5 Density 15 10 -5 15 10 5 -9 6 3 1e+05 1e+03 1e+05 1e+05 1e+01 1e+03 1e+01 1e+01 1e+03 variant count + 1 (log scale)