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