Nucleotide substitution variant count distributions (input samples) input2 input1 input3 0.4 0.2 0.0 7.5 5.0 -2.5 0.0 9 Hamming_distance 6 · 3. Density 20 15 10 5 -15 10 5 -10 5 · 1e+03 1e+01 1e+03 1e+05 1e+01 1e+05 1e+01 1e+05 1e+03 variant count + 1 (log scale)