Nucleotide substitution variant count distributions (input samples) input1 input2 input3 0.5 -0.4 0.3 0.2 0.1 3. 2 · 8 -6 · Hamming_distance Density 15 10 5. 20 15 -10 5 -15 10 5 · 1e+05 1e+01 1e+03 1e+05 1e+05 1e+01 1e+03 1e+01 1e+03 variant count + 1 (log scale)