Fig. 3:

cin\_freq\_canc.csv – CIN mutator frequency at the end of simulation

cin\_time\_to\_canc.csv – time to cancer

cin\_time\_to\_mut.csv – time to CIN establishment

Order of rows in each dataset:

1. No CIN
2. No clustering
3. Low clustering of beneficial mutations
4. Medium clustering of beneficial mutations
5. High clustering of beneficial mutations
6. Low clustering of deleterious mutations
7. Medium clustering of deleterious mutations
8. High clustering of deleterious mutations

Fig. 4:

cin\_freq\_canc.csv – CIN mutator frequency at the end of simulation (betabinomial/geometric refers to clustering of beneficial mutations)

cin\_time\_to\_canc.csv – time to cancer (betabinomial/geometric refers to clustering of beneficial mutations)

cin\_time\_to\_mut.csv – time to CIN establishment (betabinomial/geometric refers to clustering of beneficial mutations)

Order of rows in each dataset:

1. Default parameter values
2. 10-fold higher CIN rate
3. 100-fold higher CIN rate
4. 5-fold higher *sdel*
5. 10-fold higher *sdel*