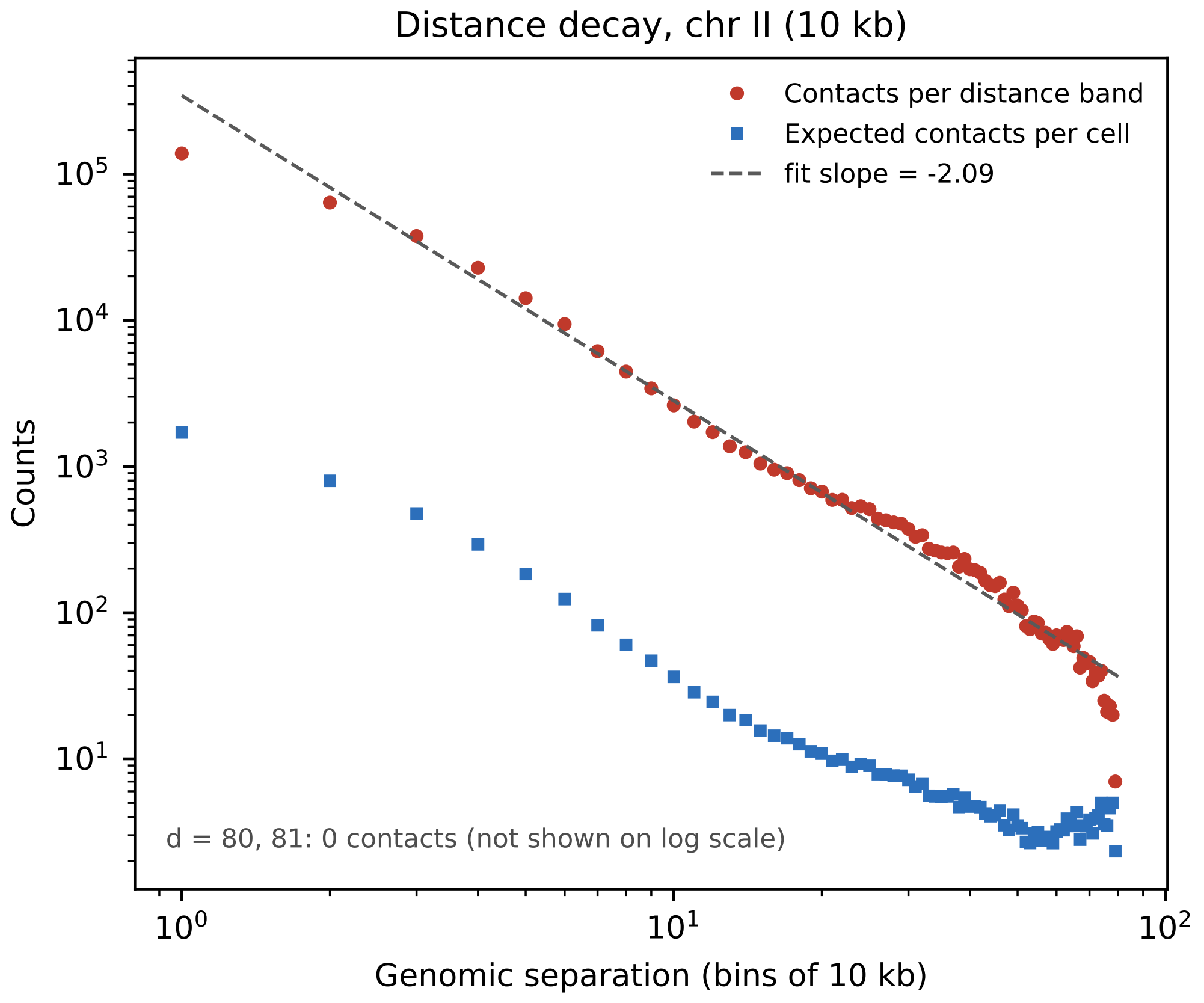
Distance decay, chr II (10 kb)
Contacts per distance band
Expected contacts per cell
fit slope = -2.09
Counts
10^5
10^4
10^3
10^2
10^1
d = 80, 81: 0 contacts (not shown on log scale)
10^0
10^1
10^2
Genomic separation (bins of 10 kb)