Supplementary Material to:
The influence of TF competition on the relationship between occupancy and affinity
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Table S1. TF species default parameters

| parameter                                           | lacI | non-cognate | notation          |
|-----------------------------------------------------|------|-------------|-------------------|
| copy number                                         | see main manuscript |  | $\text{TF}_x$ |
| motif sequence                                      | see Table S2 | - |                  |
| energetic penalty for mismatch                      | $1 \ K_B T$ | $13 \ K_B T$ | $\epsilon_x$ |
| nucleotides covered on left                         | 0 bp | 23 bp       | $\text{TF}^{\text{left}}_x$ |
| nucleotides covered on right                        | 0 bp | 23 bp       | $\text{TF}^{\text{right}}_x$ |
| association rate to the DNA                         | see main manuscript | - | $k^{\text{assoc}}_x$ |
| unbinding probability                               | 0.001474111 | 0.001474111 | $p^{\text{unbind}}_x$ |
| probability to slide left                           | 0.4992629 | 0.4992629 | $p^{\text{left}}_x$ |
| probability to slide right                          | 0.4992629 | 0.4992629 | $p^{\text{right}}_x$ |
| probability to dissociate completely when unbinding | 0.1675 | 0.1675 | $p^{\text{jump}}_x$ |
| time bound at the target site                       | $1.18E \ - \ 6 \ s$ | $0.3314193 \ s$ | $\tau^{\text{th}}_x$ |
| the size of a step to left                          | 1 bp | 1 bp        | $\sigma^{\text{hop}}_x$ |
| the size of a step to right                         | 1 bp | 1 bp        | $d^{\text{jump}}_x$ |
| variance of repositioning distance after a hop      | 1 bp | 1 bp        | $d^{\text{jump}}_x$ |
| the distance over which a hop becomes a jump        | 100 bp | 100 bp | $d^{\text{jump}}_x$ |
| the proportion of prebound molecules                | 0.0 | 0.9        |                   |
| affinity landscape roughness                        | - | $1.0 \ K_B T$ |
Table S2. lacI PWM

| Position | A     | C     | G     | T     |
|----------|-------|-------|-------|-------|
| 1        | 0.6200| -0.6900| 0.1400| -0.6900|
| 2        | 0.6200| -0.6900| 0.1400| -0.6900|
| 3        | 0.1600| 0.1400| -0.6900| 0.1800|
| 4        | 0.1600| -0.6900| -0.6900| 0.6200|
| 5        | -0.7000| -0.7000| 0.9000| -0.7000|
| 6        | -0.6900| -0.6900| -0.6900| 0.9300|
| 7        | 0.0077| -0.0084| -0.0073| 0.0083|
| 8        | 0.0077| -0.0084| -0.0073| 0.0083|
| 9        | 0.0077| -0.0084| -0.0073| 0.0083|
| 10       | 0.0077| -0.0084| -0.0073| 0.0083|
| 11       | 0.0077| -0.0084| -0.0073| 0.0083|
| 12       | 0.0077| -0.0084| -0.0073| 0.0083|
| 13       | 0.0077| -0.0084| -0.0073| 0.0083|
| 14       | 0.0077| -0.0084| -0.0073| 0.0083|
| 15       | 0.0077| -0.0084| -0.0073| 0.0083|
| 16       | 0.6200| -0.6900| 0.1400| -0.6900|
| 17       | -0.7000| 0.9000| -0.7000| -0.7000|
| 18       | 0.9300| -0.6900| -0.6900| -0.6900|
| 19       | 0.9300| -0.6900| -0.6900| -0.6900|
| 20       | -0.6900| 0.1400| -0.6900| 0.6200|
| 21       | -0.6900| 0.1400| -0.6900| 0.6200|
Generating the *in silico* ChIP profile

```r
generateChIPProfile <- function(input.vec, mean, sd, smooth = NULL) {
  var = sd^2
  shp = mean^2/var
  scl = var/mean
  l = length(input.vec)

  f = dgamma(0:length(input.vec), shape = shp, scale = scl)
  F = rev(cumsum(rev(f)))

  peak.centres = which(input.vec > mean(input.vec))
  peaks = vector("numeric", l)

  for(pc in peak.centres) {
    this.peak = vector("numeric", l)
    this.peak[pc:l] = F[1:(l-pc+1)]
    this.peak[1:(pc-1)] = F[pc:2]
    peaks = peaks + this.peak * input.vec[pc]
  }

  if(!is.null(smooth)){
    if((smooth %% 2) == 0){smooth = smooth - 1}
    mid = round(smooth/2,0) + 1
    d = smooth - mid
    for(i in mid:(length(peaks) - d)) {
      peaks[i] = mean(peaks[max(0,(i-d)):min(length(input.vec),(i+d))])
    }
  }

  return(peaks)
}
```