

# Bayesian analysis

Identifying essential genes by mutagenesis

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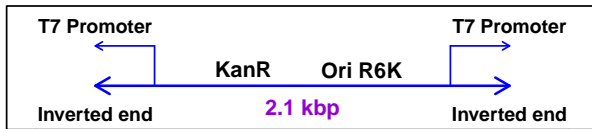
# Mycobacterium tuberculosis

- ▶ The organism that causes tuberculosis.
  - Cost for treatment: ~\$15,000
  - Other bacterial pneumonias: ~\$35
- ▶ 4.4 Mbp circular genome, completely sequenced
- ▶ 4250 known or inferred genes

Goal: identify the essential genes

Method: random transposon mutagenesis

# Himar1 transposon



5'-TCGAAGCCTGCGACTAACGTTTAAAGTTTG-3'  
3'-AGCTTCGGACGCTGATTGCAAATTTCAAAC-5'

Note:  $\geq 30$  stop codons in each reading frame

# Sequence of the gene MT598

... TCAATATGAAGCGCGCGGGCCCGGCCGCCATCGGCCCCGTCGATCCG

start      10      20      30      40

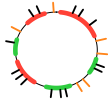
AGTGCGCACGGCCGAAGTGAGCCACCACCGTAGCGCCGCCG

50      60      70      80

AGTTCGCTTCCGCGGACGCAAGCCCGGGATTTGCGGAGTAGCGTAC ...

90      100      110      stop

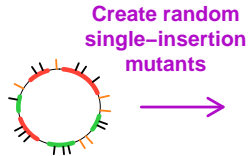
# Random transposon mutagenesis



**Red = essential**

**Green = non-essential**

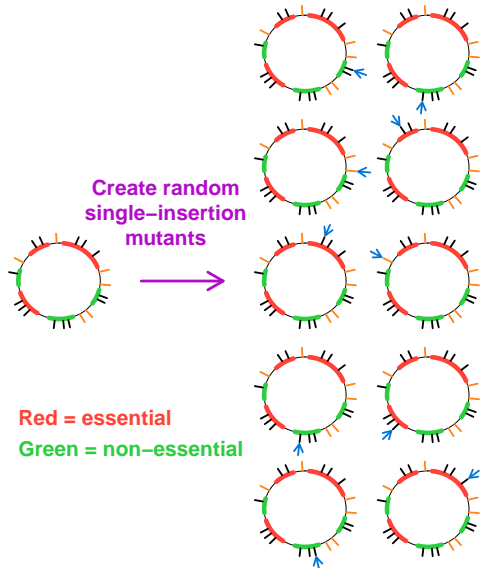
# Random transposon mutagenesis



Red = essential

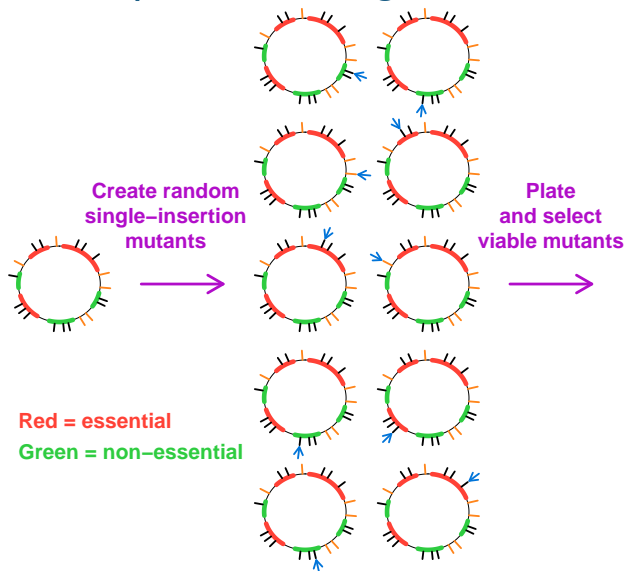
Green = non-essential

# Random transposon mutagenesis

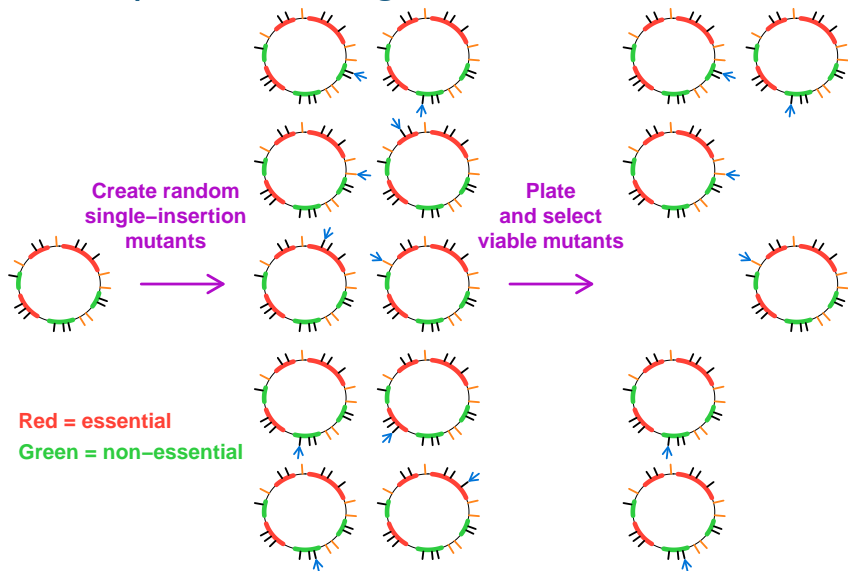




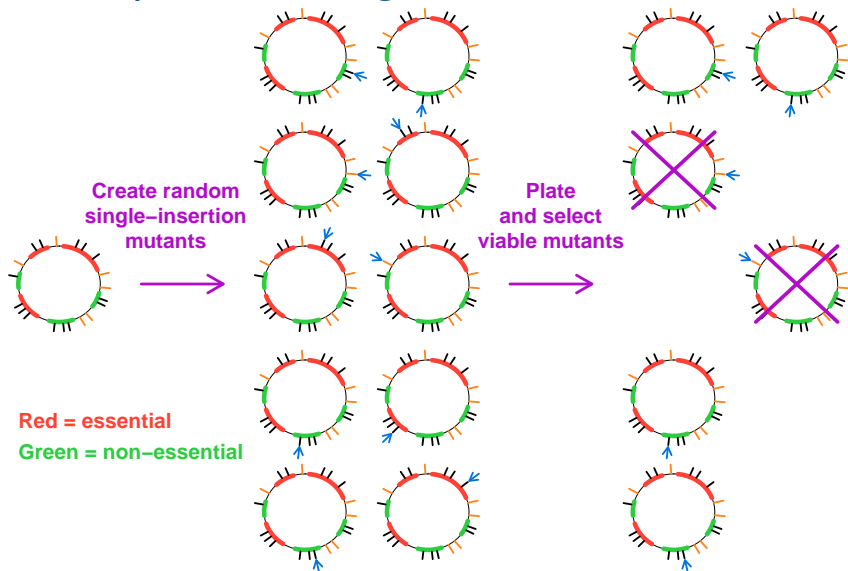
# Random transposon mutagenesis



# Random transposon mutagenesis



# Random transposon mutagenesis



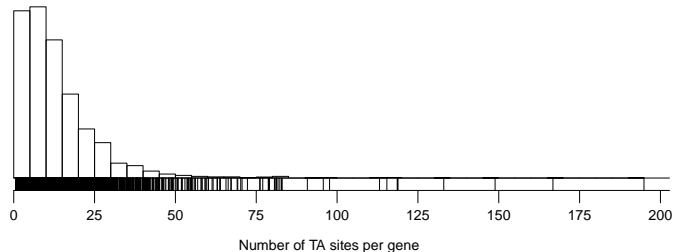
# Random transposon mutagenesis

- ▶ Location of transposon insertion determined by sequencing across junctions
- ▶ Viable insertion within a gene  $\implies$  gene is non-essential
- ▶ Essential genes: we will never see a viable insertion
- ▶ **Complication:** Insertions in the very distal portion of an essential gene may not be sufficiently disruptive.  
Thus, we omit from consideration insertions sites within the last 20% and last 100 bp of a gene.

# The data

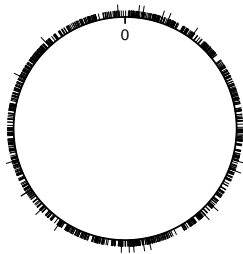
- ▶ Number, locations of genes
- ▶ Number of insertion sites in each gene
- ▶  $n$  viable mutants with exactly one transposon insertion
- ▶ Location of the transposon insertion in each mutant

# TA sites in *M. tuberculosis*



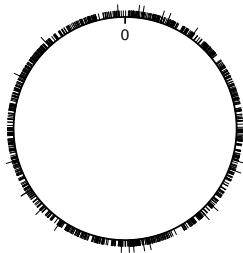
- ▶ 74,403 sites
- ▶ 65,649 sites within a gene
- ▶ 57,934 sites within proximal portion of a gene
- ▶ 4204/4250 genes with at least one TA site

# 1425 insertion mutants



- ▶ 1425 insertion mutants
- ▶ 1025 within proximal portion of a gene
- ▶ 21 double-hits
- ▶ 770 unique genes hit

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Questions: Proportion of essential genes in *M. tuberculosis*?

Which genes are likely essential?



# Model

Transposon inserts completely at random

- ▶ Each TA site equally likely
- ▶ Genes are either completely essential or completely non-essential

# Model

N genes       $x_i$  = no. TA sites in gene  $i$

n mutants       $y_i$  = no. mutants with insertion in gene  $i$

$$\theta_i = \begin{cases} 1 & \text{if gene } i \text{ is non-essential} \\ 0 & \text{essential} \end{cases}$$

**Model:**  $\mathbf{y} \sim \text{multinomial}(n, \mathbf{p})$       where  $p_i = x_i \theta_i / \sum_j x_j \theta_j$

**Goal:** Estimate  $\theta_+ = \sum_i \theta_i$       or       $1 - \theta_+ / N$

# The likelihood

$$L(\boldsymbol{\theta} \mid \mathbf{y}) = \binom{n}{\mathbf{y}} \prod_i (x_i \theta_i)^{y_i} / \sum_j (x_j \theta_j)^n$$
$$\propto \begin{cases} (\sum_i x_i \theta_i)^{-n} & \text{if } \theta_i = 1 \text{ whenever } y_i > 0 \\ 0 & \text{otherwise} \end{cases}$$

## Notes:

- ▶ Depends only on which  $y_i > 0$  and not on the specific values
- ▶ The MLE is  $\hat{\theta}_i = 1\{y_i > 0\}$

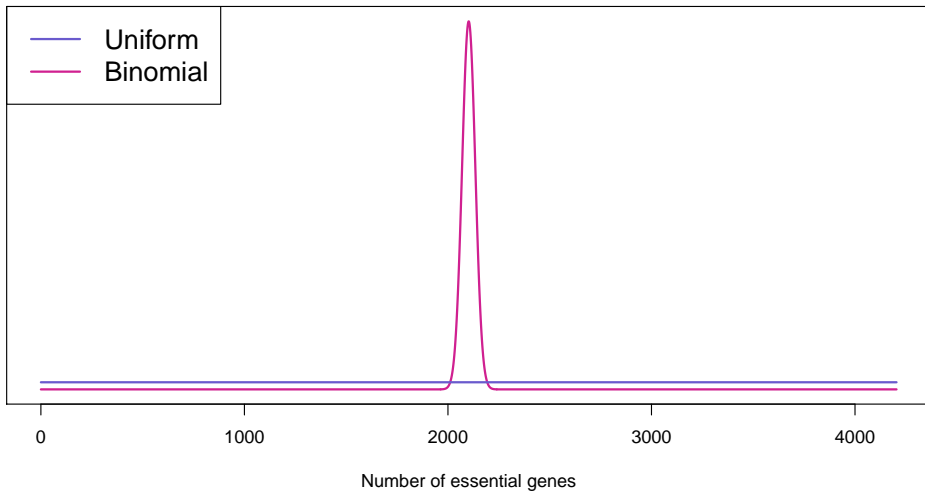
# The prior

$\theta_+ \sim \text{uniform on } \{ 0, 1, \dots, N \}$

$\theta \mid \theta_+ \sim \text{uniform over all sequences of 0's and 1's with } \theta_+ \text{ 1's}$

## Notes:

- ▶ We are assuming that  $\Pr(\theta_i = 1) = 1/2$
- ▶ This is quite different from taking  $\theta_i$  iid Bernoulli(1/2)
- ▶ We are assuming that  $\theta_i$  is independent of  $x_i$  and the length of the gene
- ▶ We could make use of information about the essential status of particular genes (e.g. known viable knock-outs)



# A Gibbs sampler

Goal: Estimate  $\Pr(\boldsymbol{\theta} \mid \mathbf{y})$

Gibbs sampler:

- ▶ Begin with some initial assignment  $\boldsymbol{\theta}^{(0)}$
- ▶ For iteration  $s$ , consider each gene one at a time
  - Let  $\boldsymbol{\theta}_{-i}^{(s)} = (\theta_1^{(s+1)}, \dots, \theta_{i-1}^{(s+1)}, \theta_{i+1}^{(s)}, \dots, \theta_N^{(s)})$
  - Calculate  $\Pr(\theta_i = 1 \mid \boldsymbol{\theta}_{-i}^{(s)}, \mathbf{y})$
  - Assign  $\theta_i^{(s)} = 1$  at random with that probability
- ▶ Repeat many times

This is an example of **Markov chain Monte Carlo (MCMC)**.

# MCMC in action



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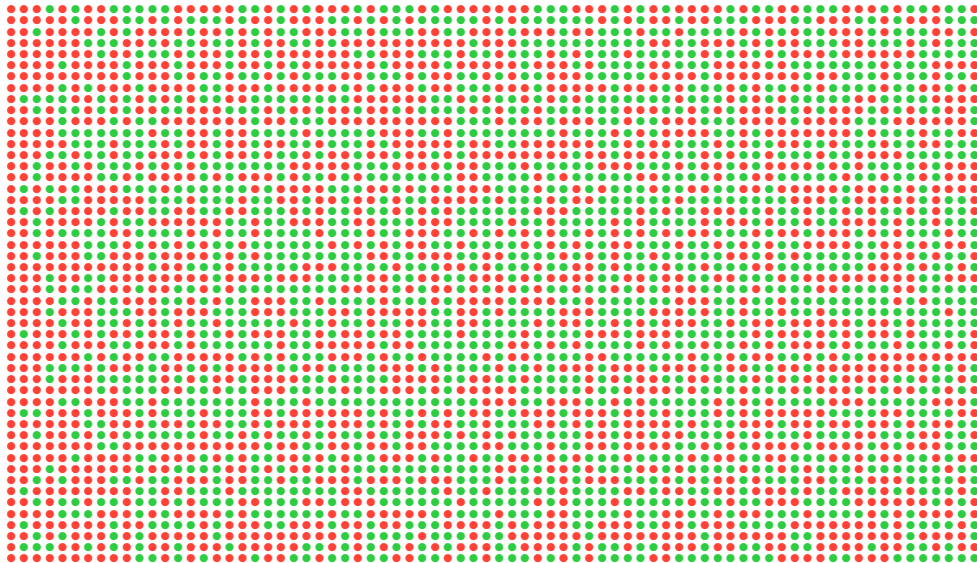




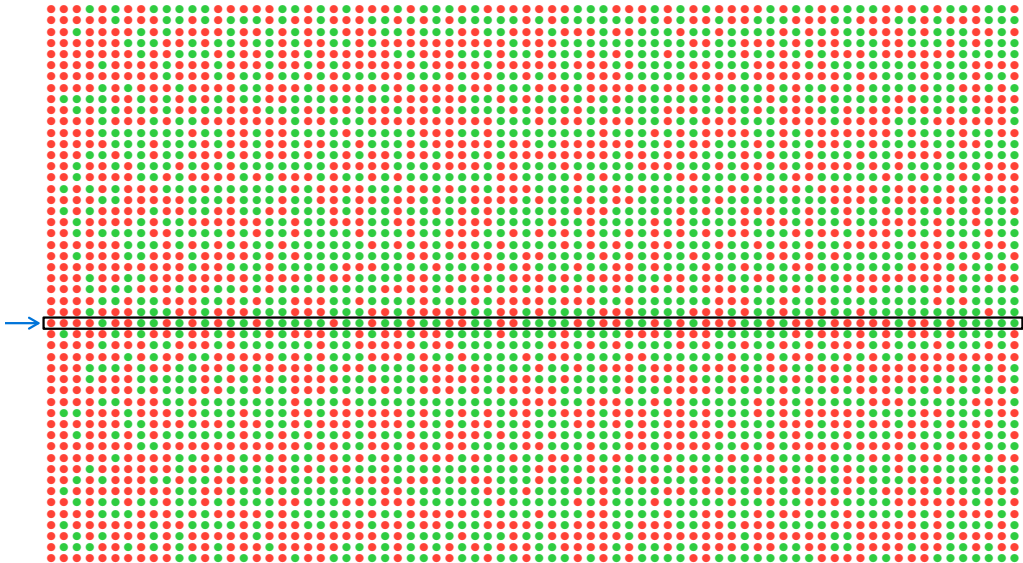
# MCMC in action



# MCMC in action



# MCMC in action



# The conditional probabilities

If  $y_i > 0$ , then  $\Pr(\theta_i = 1 \mid \mathbf{y}, \boldsymbol{\theta}_{-i}^{(s)}) = 1$

$$\begin{aligned}\text{If } y_i = 0, \quad \text{Let } A &= \sum_{j < i} \theta_j^{(s+1)} + \sum_{j > i} \theta_j^{(s)} \\ B &= \sum_{j < i} x_j \theta_j^{(s+1)} + \sum_{j > i} x_j \theta_j^{(s)}\end{aligned}$$

$$\text{Then } \Pr(\boldsymbol{\theta}_{-i}^{(s)}, \theta_i = k) = \binom{n}{A+k} / n$$

$$\Pr(\mathbf{y} \mid \boldsymbol{\theta}_{-i}^{(s)}, \theta_i = k) = (B + k x_i)^{-n}$$

$$\begin{aligned}\text{And so } \Pr(\theta_i = 1 \mid \mathbf{y}, \boldsymbol{\theta}_{-i}^{(s)}) &= \dots \\ &= \frac{(1 + x_i/B)^{-n}}{(1 + x_i/B)^{-n} + (n - A)/(A + 1)}\end{aligned}$$

# Estimators

The Gibbs sampler produces  $\theta^{(0)}, \theta^{(1)}, \dots, \theta^{(S)}$

We discard the first 200 or so samples (“burn-in”).

Estimated number of non-essential genes:  $E(\theta_+ | \mathbf{y})$

$$\theta_+^{(s)} = \sum_i \theta_i^{(s)} \quad \longrightarrow \quad \hat{\theta}_+ = \frac{1}{S-200} \sum_{s=201}^S \theta_+^{(s)}$$

Probability that gene  $i$  is non-essential:  $E(\theta_i | \mathbf{y}) = \Pr(\theta_i = 1 | \mathbf{y})$

$$\hat{\theta}_i = \frac{1}{S-200} \sum_{s=201}^S \theta_i^{(s)}$$

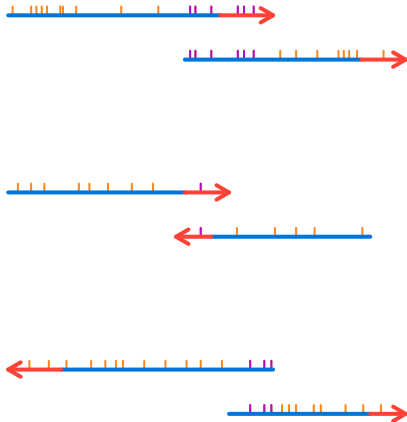
or Rao-Blackwellize:

$$\hat{\theta}_i^* = \frac{1}{S-200} \sum_{s=201}^S \Pr(\theta_i = 1 | \mathbf{y}, \theta_{-i}^{(s)})$$

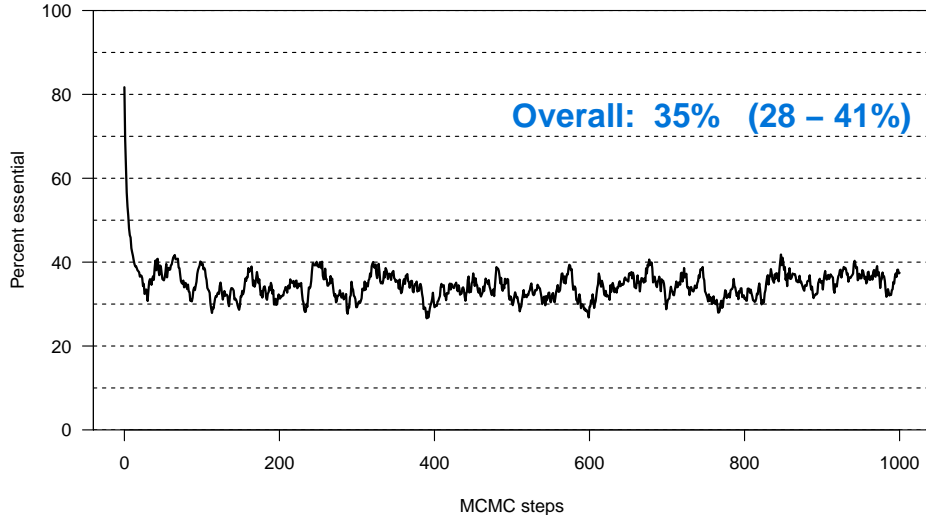
# A further complication

## Many genes overlap

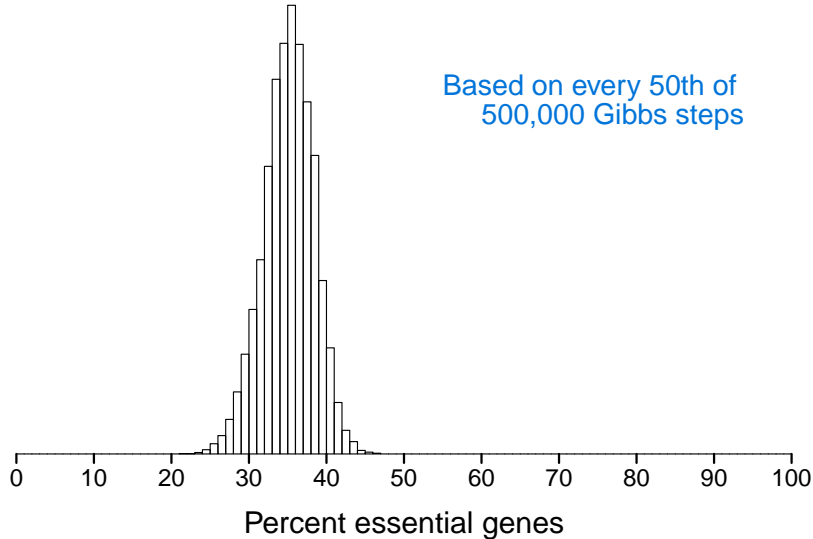
- ▶ Of 4250 genes, 1005 pairs overlap (mostly by exactly 4 bp).
- ▶ The overlapping regions contain 547 insertion sites.
- ▶ Omit TA sites in overlapping regions, unless in the proximal portion of *both* genes.
- ▶ The algebra gets a bit more complicated.



# Percent essential genes in *M. tb.*

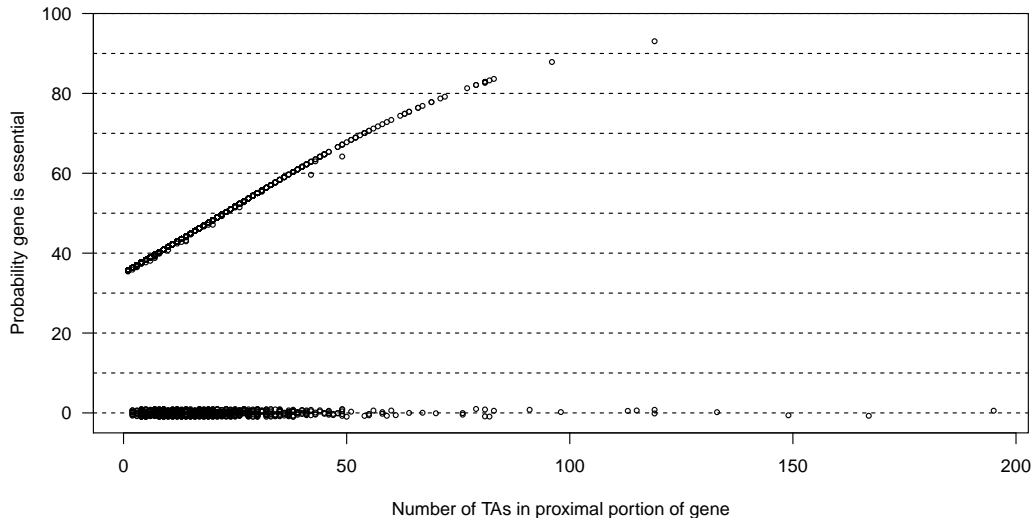


# Percent essential genes in *M. tb.*





# Probability each gene is essential



# Yet another complication

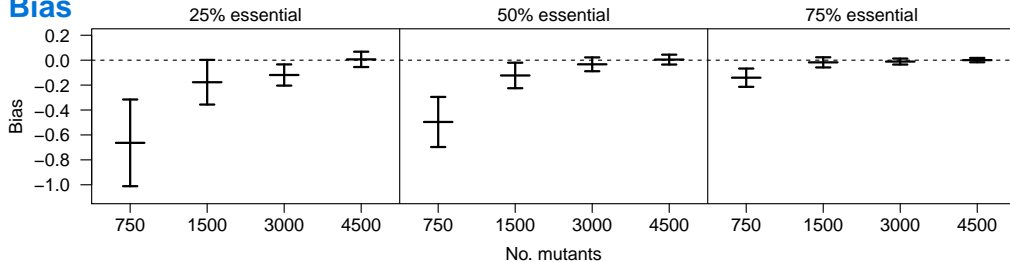
**Operon:** A group of adjacent genes that are transcribed together as a single unit.



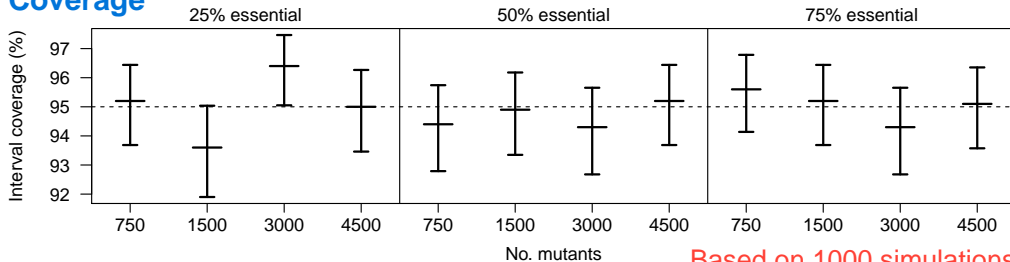
- ▶ Insertion at a TA site could disrupt all downstream genes
- ▶ If a gene is essential, insertion in any upstream gene would be non-viable
- ▶ Re-define the meaning of “essential gene”.
- ▶ If operons were known, one could get an improved estimate of the proportion of essential genes.
- ▶ If one ignores the presence of operons, estimates should still be unbiased.

# Frequentist properties

## Bias



## Coverage



Based on 1000 simulations

# Summary

- ▶ Bayesian method, using MCMC, to estimate the proportion of essential genes in a genome with data from random transposon mutagenesis.
- ▶ Crucial assumptions:
  - Randomness of transposon insertion.
  - Essentiality is an all-or-none quality.
  - No relationship between essentiality and no. insertion sites.
  - The 80% rule.
- ▶ For *M. tuberculosis*, with data on 1400 mutants:
  - 28 – 41% of genes are essential
  - 20 genes which have  $\geq 64$  TA sites and for which no mutant has been observed, have  $> 75\%$  chance of being essential.

# References

- ▶ Lamichhane et al. (2003) Proc Natl Acad Sci USA 100:7213-7218  
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- ▶ Blades and Broman (2002) Tech Report MS02-20  
[bit.ly/ms0220](https://bit.ly/ms0220)
- ▶ R/negenes package  
[cran.r-project.org/package=negenes](https://cran.r-project.org/package=negenes)