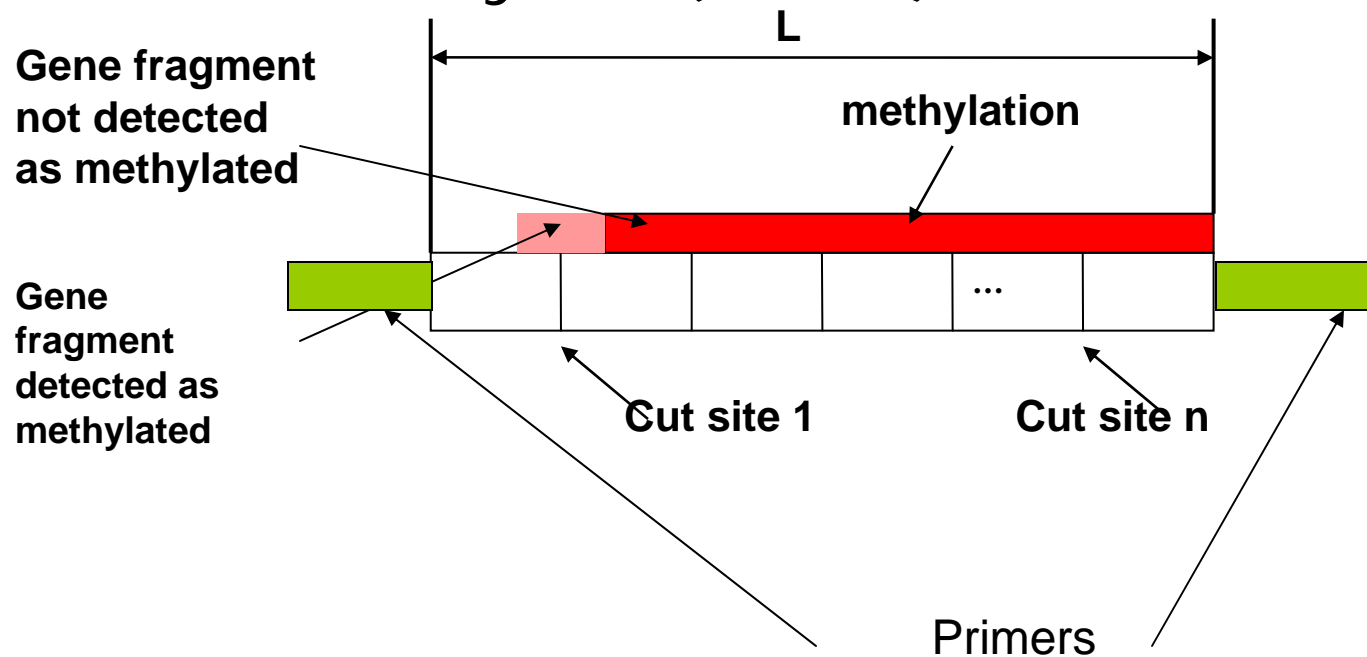
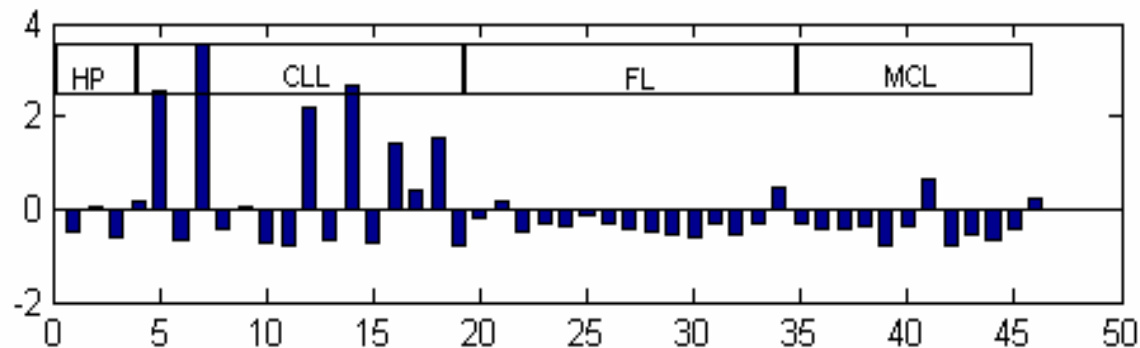


Methylation cDNA microarray

- **Technique:** Differential methylation hybridization (DMH) : methylation sensitive restriction enzyme (BstUI)



Problem 1: The observed methylation is a random variable



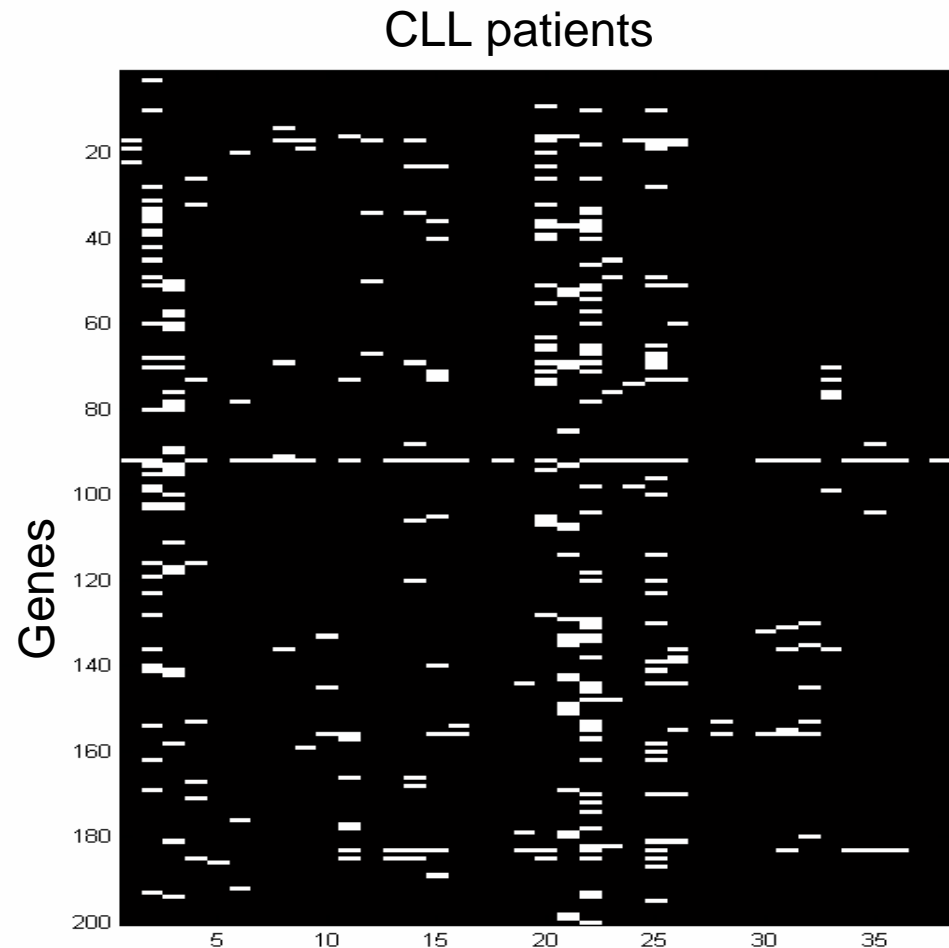
- The probability of a methylated gene to be found methylated on the chip is:

$$p = \frac{\text{number of favorable cases, } L/(n + 1)}{\text{all the possible cases, } L} = \frac{1}{n + 1}$$

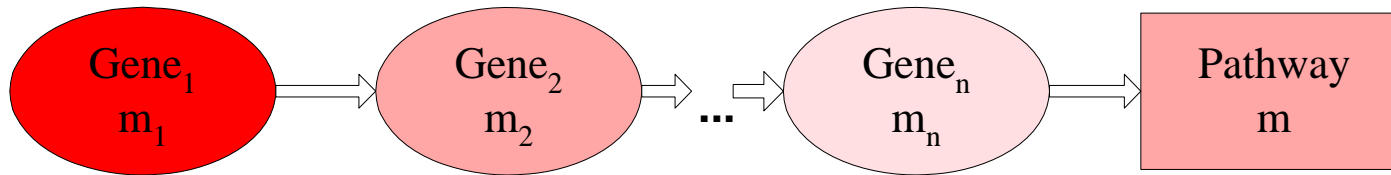
- The probability of a methylation pattern (binomial distribution) : $p^m(1-p)^n$

Problem 2: There is no such thing as “co-methylation”

- The genes vs patients matrix has “lines” rather than “blocks” →
clustering or co-clustering are not useful
- **Rare event**



Solution: cumulative pathway methylation



$$m_i = \begin{cases} 0 & \text{if } \text{logratio}_i \leq 0 \\ 1 & \text{if } \text{logratio}_i > T \\ \text{logratio}_i / T & \text{else} \end{cases}$$

$$m = \max \left\{ 1, \sum_1^n m_i \right\}$$

$$T=2$$

