

CANCER GENOMICS

Lecture 3:

Probabilistic Methods for Profiling Copy Number Alterations

GENOME 541
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Outline

1. Detecting Copy Number Alterations in Cancer Genomes

- Predicting copy number features from sequence data
- Copy number analysis workflow
- Data normalization

2. Continuous Hidden Markov Model (HMM)

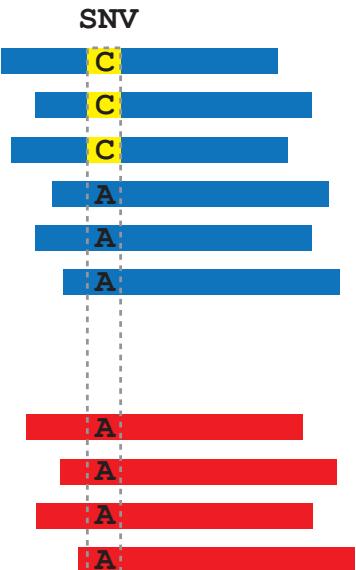
- Graphical model representation
- Components of a continuous HMM
- Inference & parameter estimation using expectation-maximization (EM)

3. Copy Number Profiling using a Hidden Markov Model

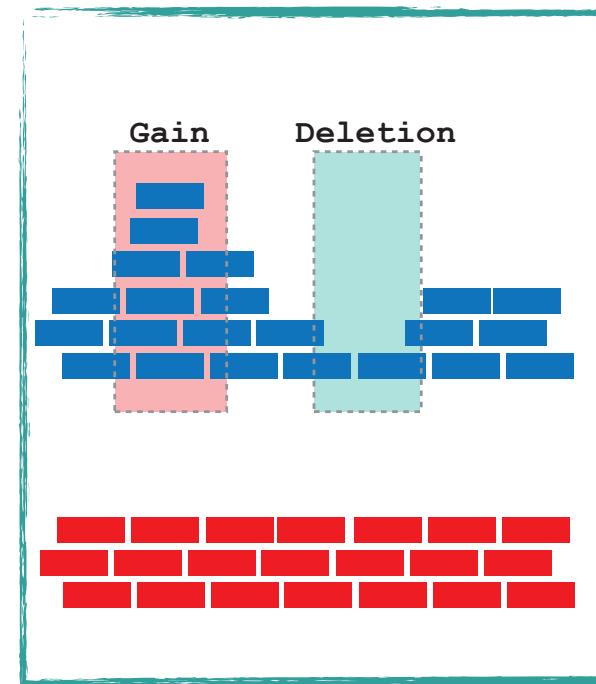
- Probabilistic model for copy number analysis
- Predicting copy number segments using the Viterbi algorithm

1. Detecting Copy Number Alterations in Cancer Genomes

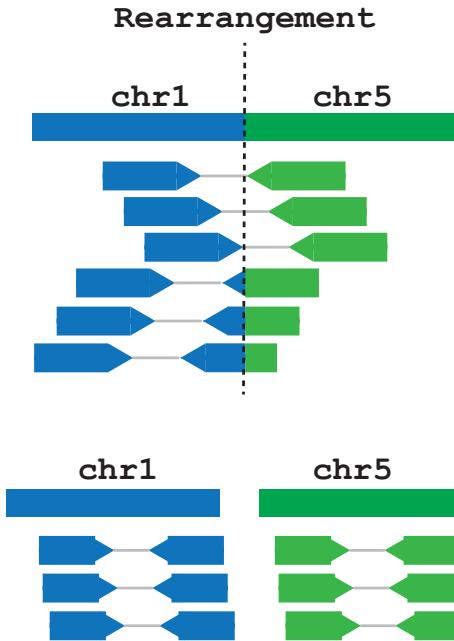
Mutations (SNV, INDEL)



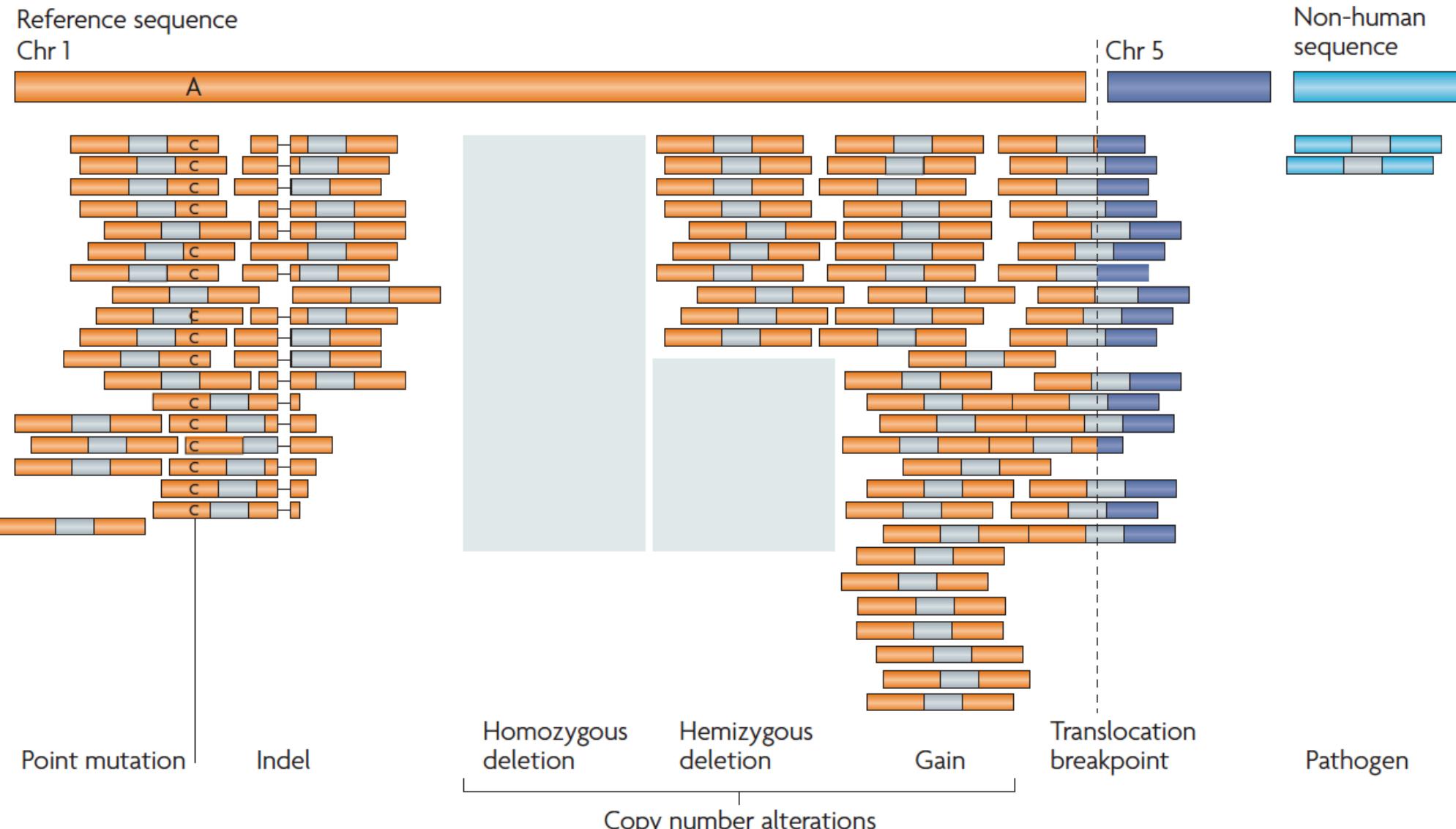
Copy Number Alterations



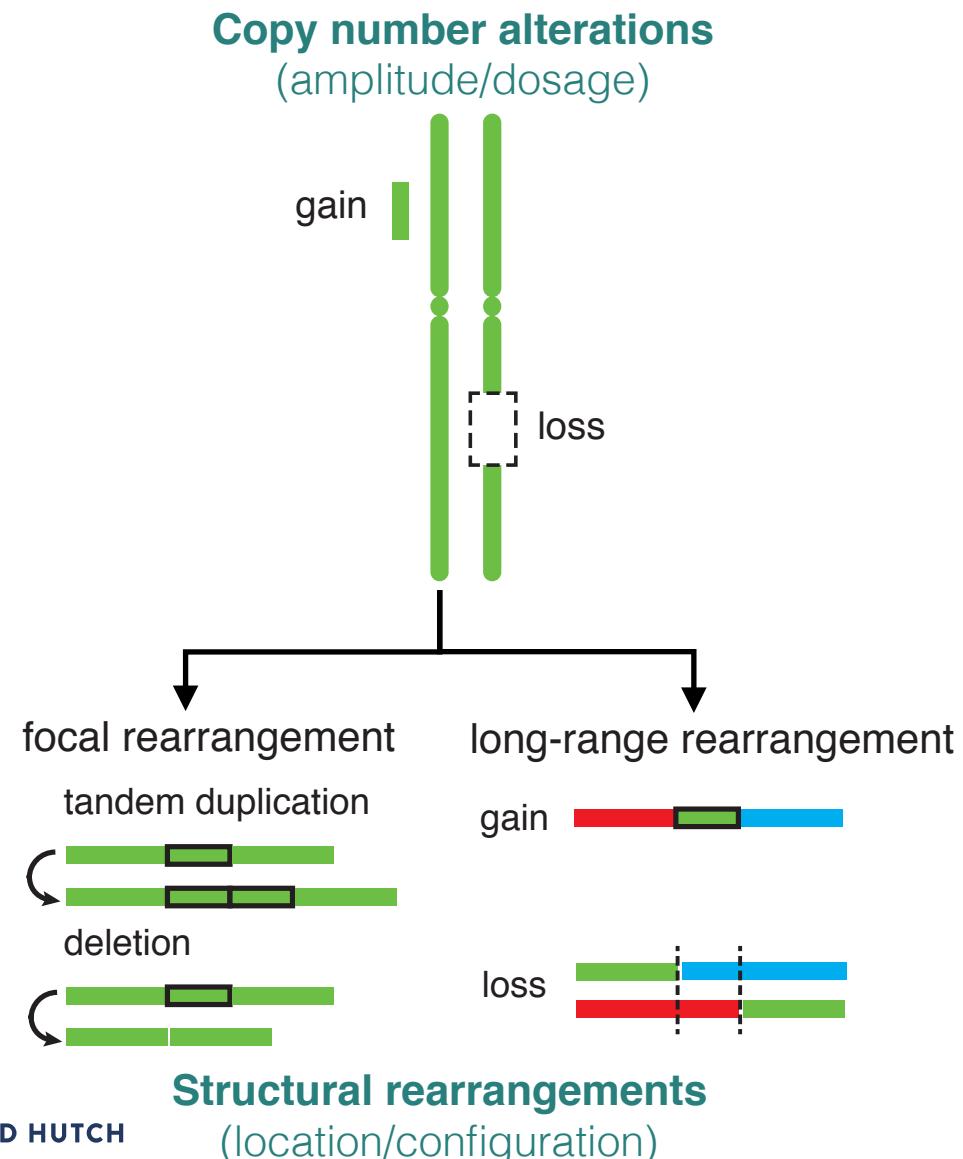
Structural Variants



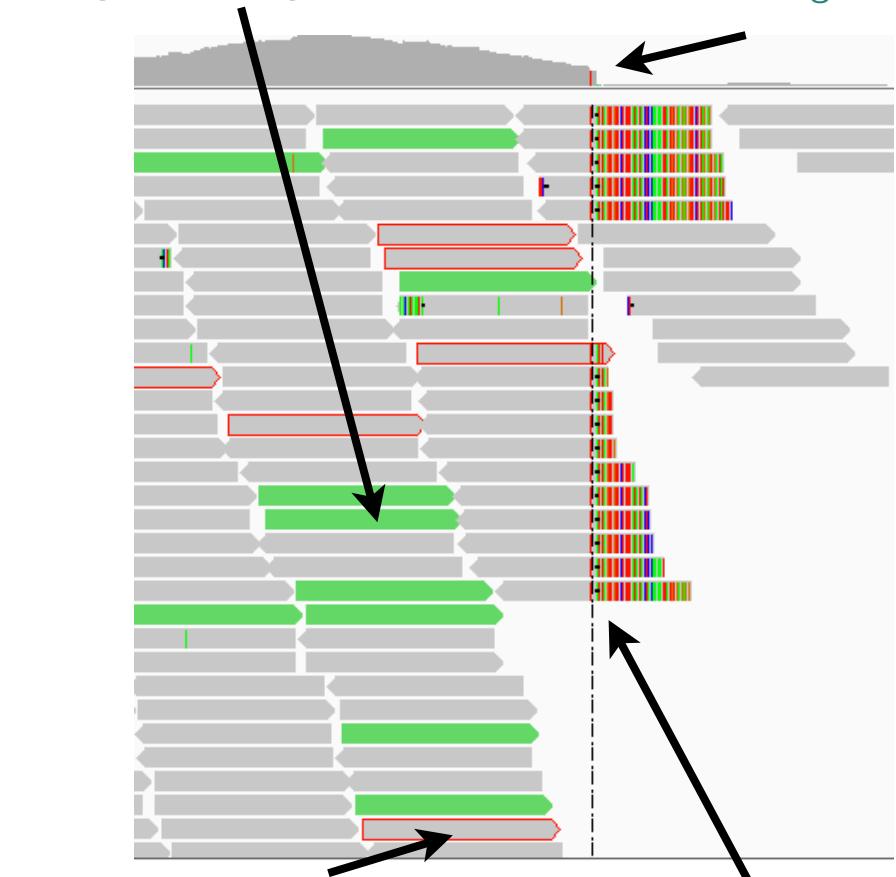
Predicting genomic alterations from sequence data



Predicting genomic alterations from sequence data



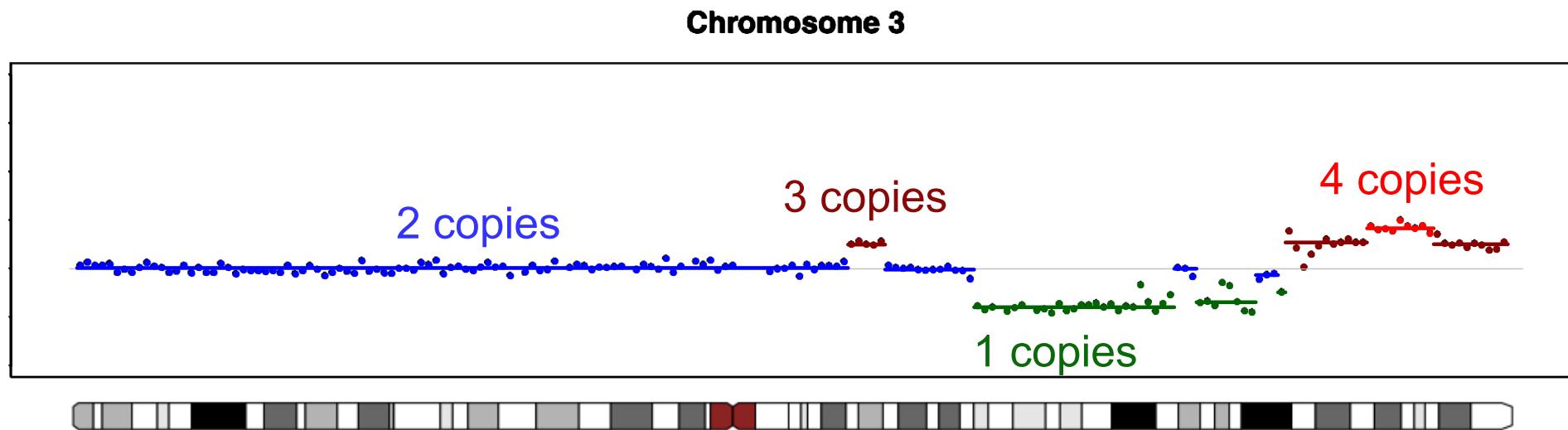
"discordant read pair"
read pairs with aberrant inferred fragment length



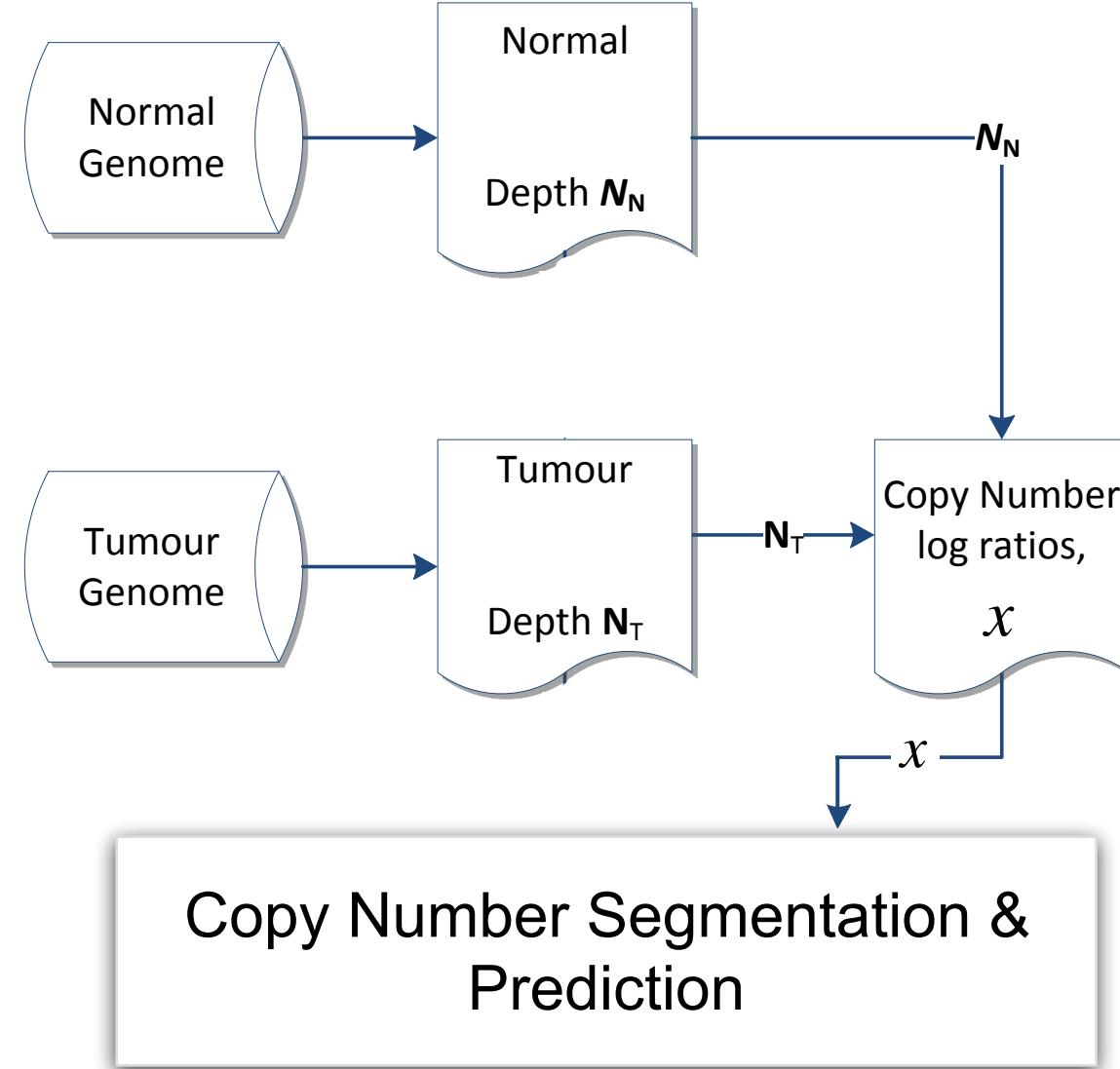
"copy number change"
abrupt change in read coverage

Tumor DNA Copy Number Analysis Strategy

1. Using sequencing read coverage as a measure for DNA copy number
2. Identifying segments of coverage changes
3. Predicting the number of copies for each segment

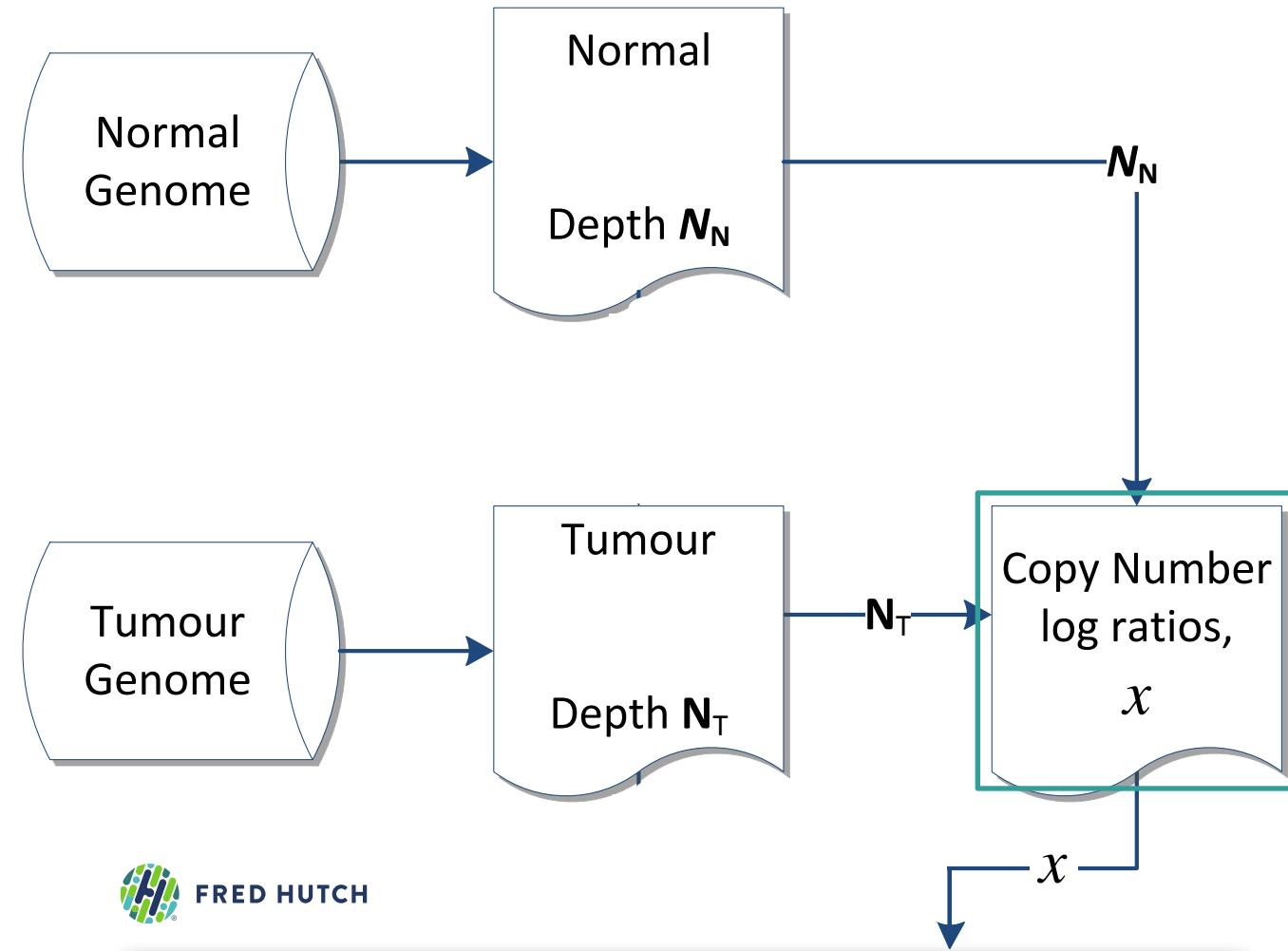


Cancer Genome Copy Number Analysis Workflow



Copy Number Analysis Workflow: Normalization

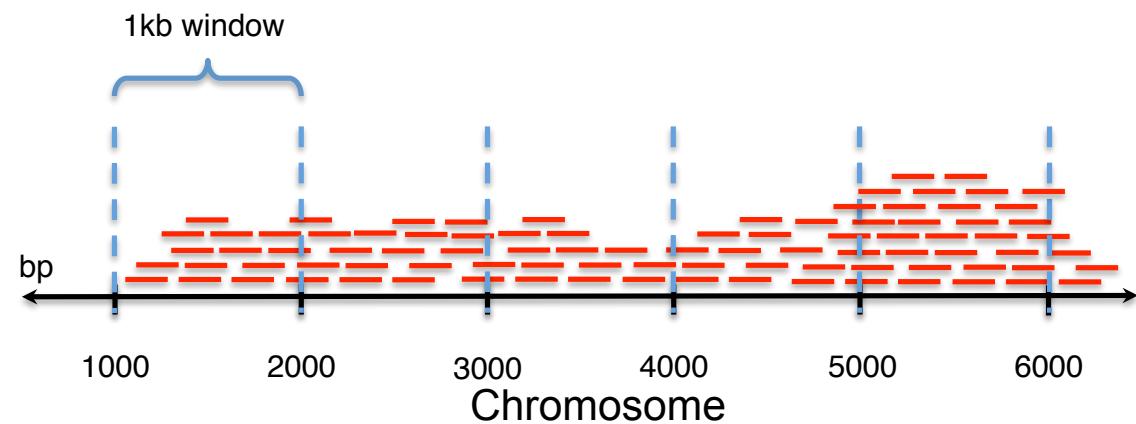
1. Correct GC/mappability biases for tumor read depth



N^{normal} = normal read depth

N^{tumor} = tumor read depth

$$\frac{N^{tumor}}{N^{normal}} = \text{copyratio}$$



Copy Number Analysis Workflow: GC content bias

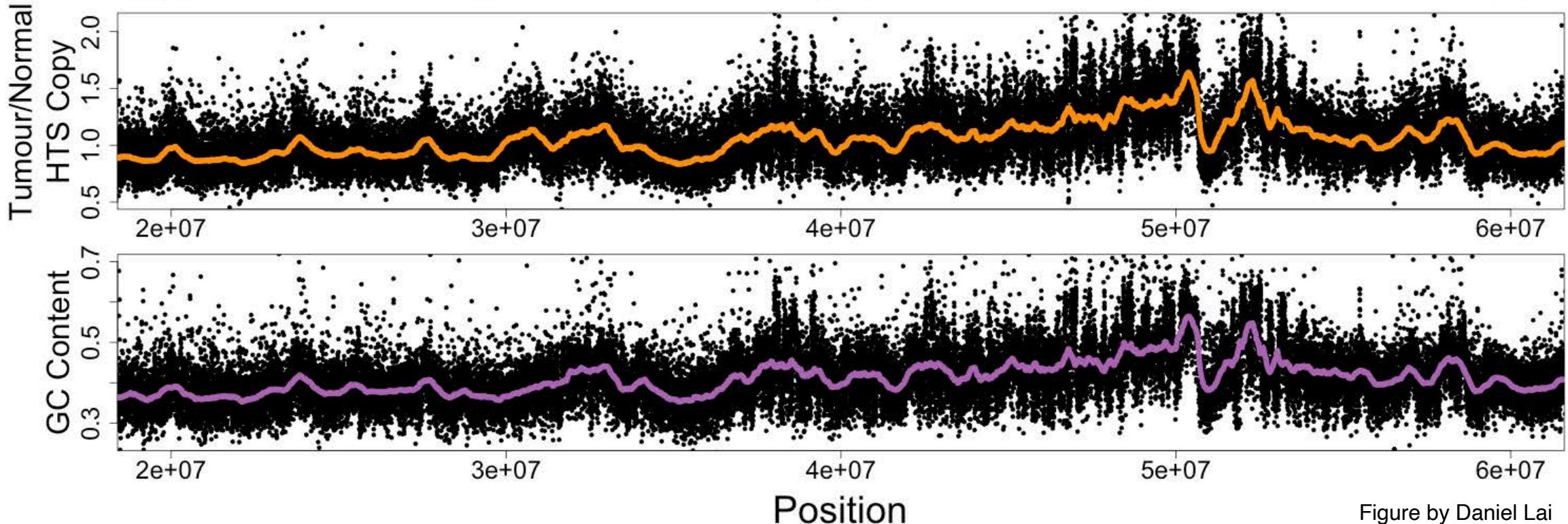


Figure by Daniel Lai

Benjamini and Speed. *Nucleic Acids Research* **40**:e72-86 (2012)

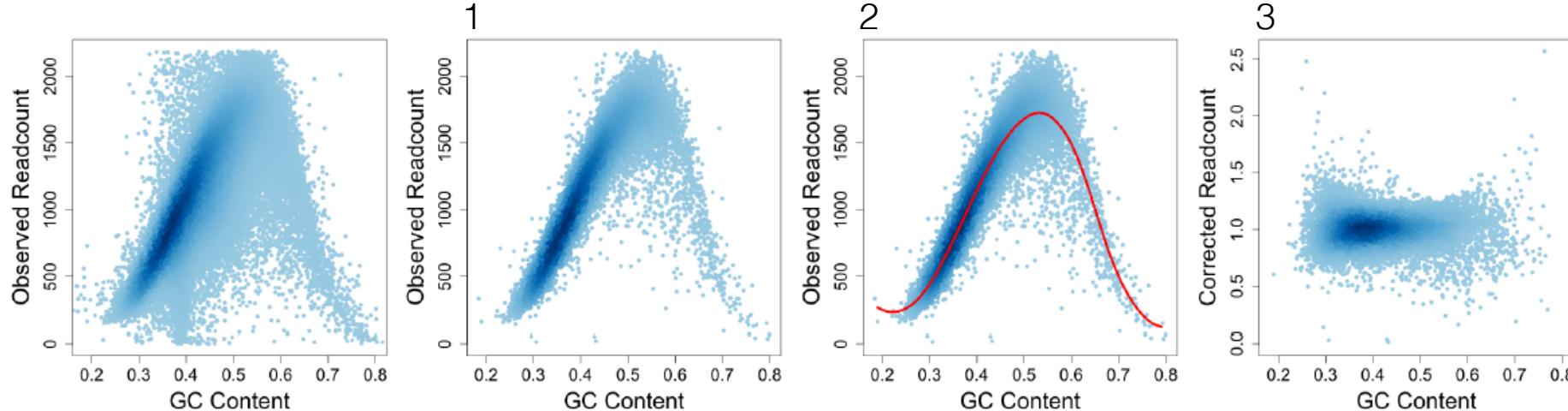
Boeva et al. *Bioinformatics* **29**(3):423-5 (2012)

Ha et al. *Genome Research* **22**:1995-2007 (2012).

Adalsteinsson*, Ha* Freeman* et al. *Nature Communications* **8**:1324 (2017)

Copy Number Analysis Workflow: GC correction (1)

1. Randomly select 50k bins and filter outliers (bottom & top 1%)
2. Fit `loess()` curve
 - local nonlinear regression
 - smoothing parameter (bandwidth): amount of local data to fit
3. $\text{corrected read count} = \frac{\text{observed read count (blue dot)}}{\text{expected read count (red line)}}$
 - relative differences between observed and predicted read counts



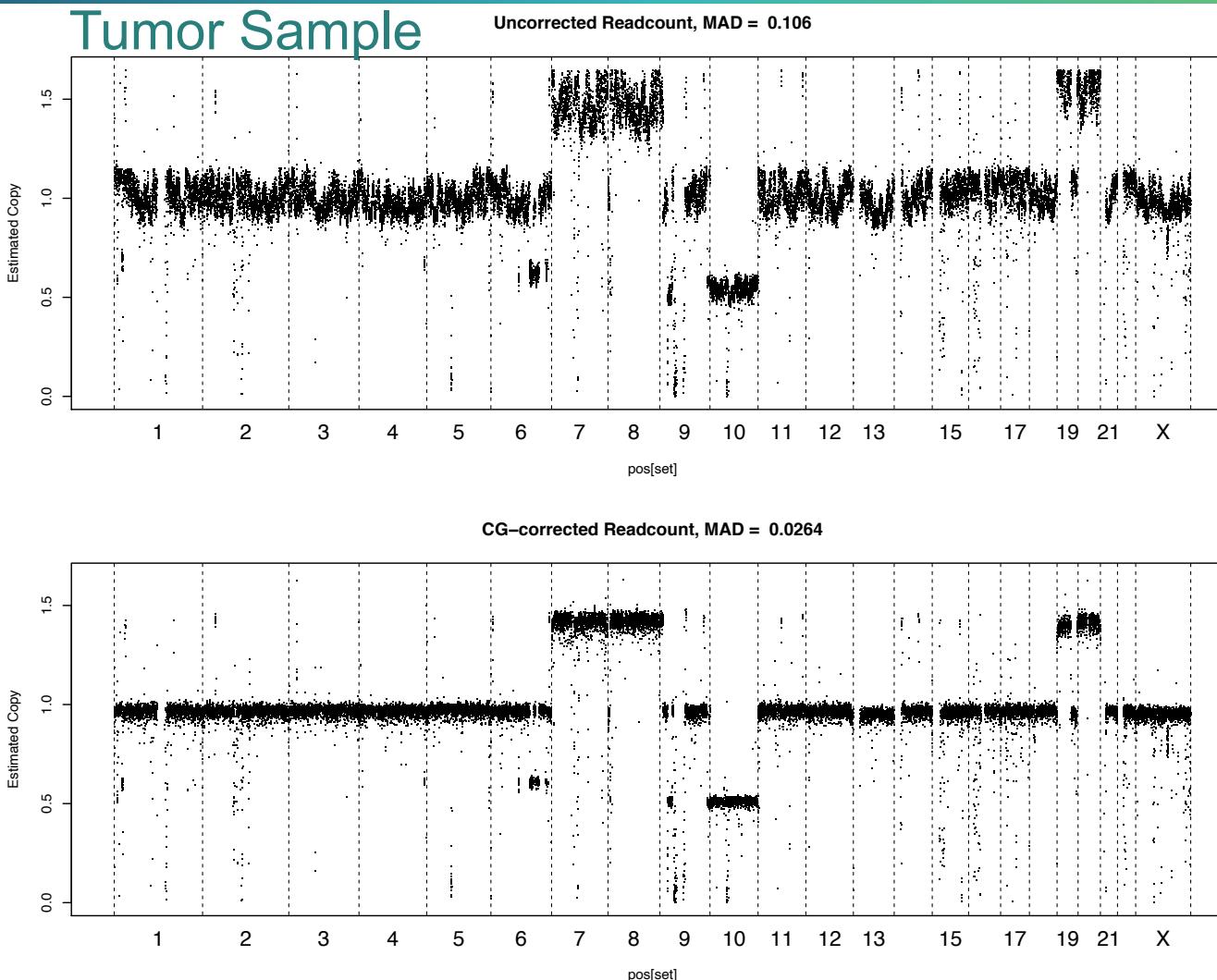
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Adalsteinsson*, Ha* Freeman* et al. *Nature Communications* **8**:1324 (2017) 10

Copy Number Analysis Workflow: GC correction (2)



Un-corrected
read counts



GC-corrected
read counts

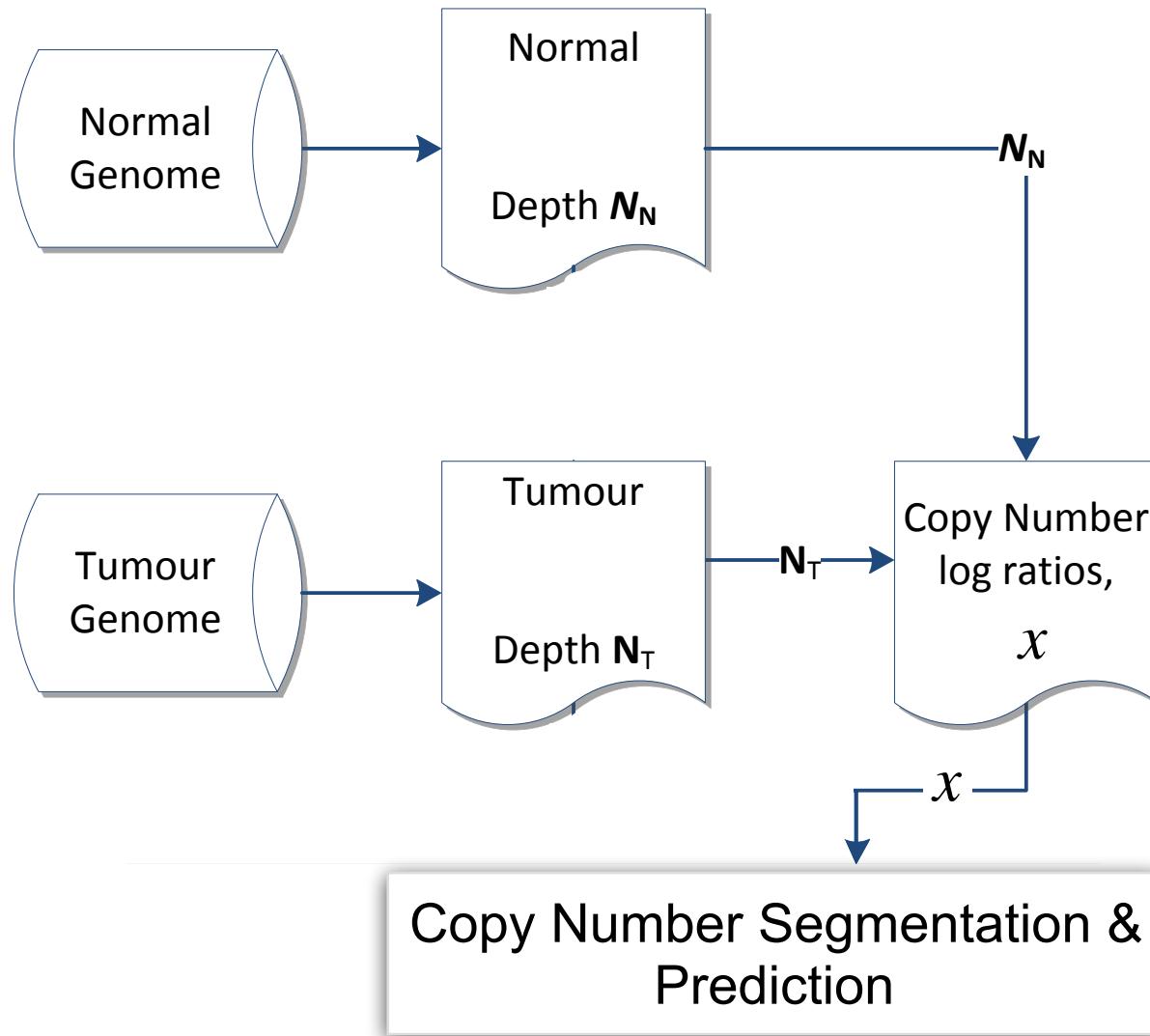
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Ha et al. *Genome Research* **22**:1995-2007 (2012).

Adalsteinsson*, Ha* Freeman* et al. *Nature Communications* **8**:1324 (2017) 11

Copy Number Analysis Workflow: Normalization



1. Correct GC/mappability biases for tumor read depth

N^{normal} = normal read depth

N^{tumor} = tumor read depth

\hat{N}^{normal} = corrected normal read depth

\hat{N}^{tumor} = corrected tumor read depth

$$\log_2 \left(\frac{\hat{N}^{tumor}}{\hat{N}^{normal}} \right) = \text{corrected log ratio}$$

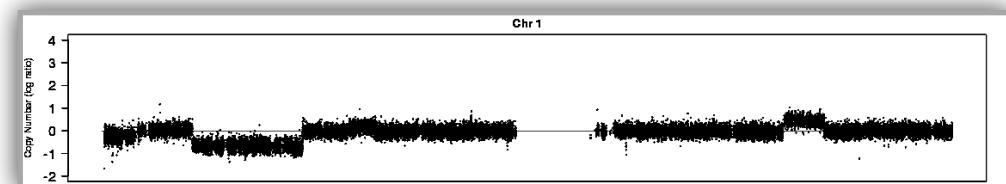
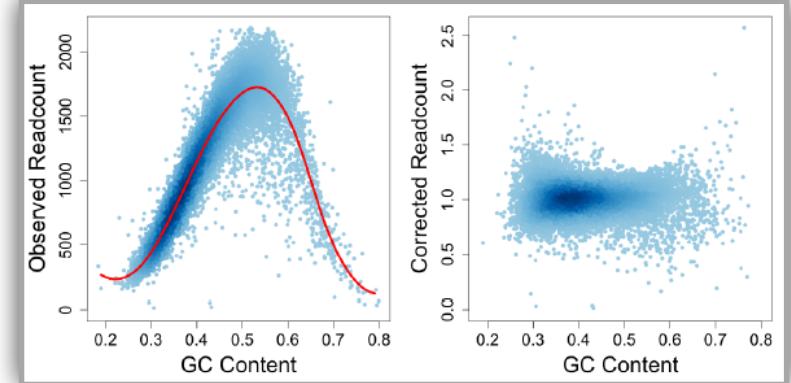
2. Perform segmentation and copy number prediction

Input Sequencing Data for Copy Number Analysis

Input Data After Normalization

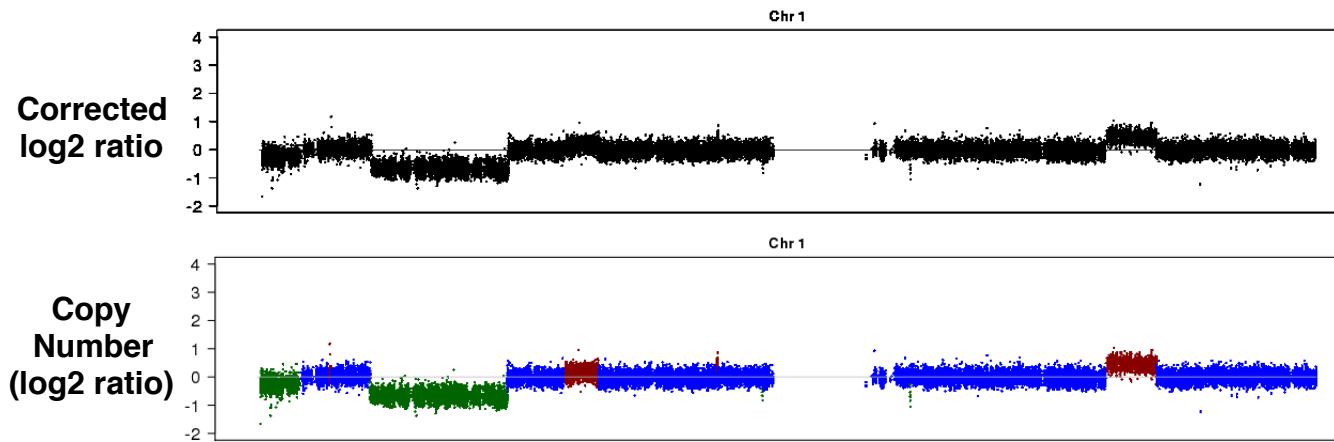
- GC-content bias correction applied to separately for
 - tumor sample reads $N_{1:T}^{Tumor}$
 - normal sample reads $N_{1:T}^{Normal}$
- Normalize tumor corrected read counts \hat{N}_i^{Tumor} with normal corrected read counts \hat{N}_i^{Normal} to obtain the log ratio for bin $t \in \{1, \dots, T\}$

$$x_t = \log_2 \left(\frac{\hat{N}_t^{Tumor}}{\hat{N}_t^{Normal}} \right)$$



Benjamini and Speed. *Nucleic Acids Research* **40**:e72-86 (2012)
Boeva et al. *Bioinformatics* **29**(3):423-5 (2012)
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Copy Number Segmentation and Prediction



Data normalization

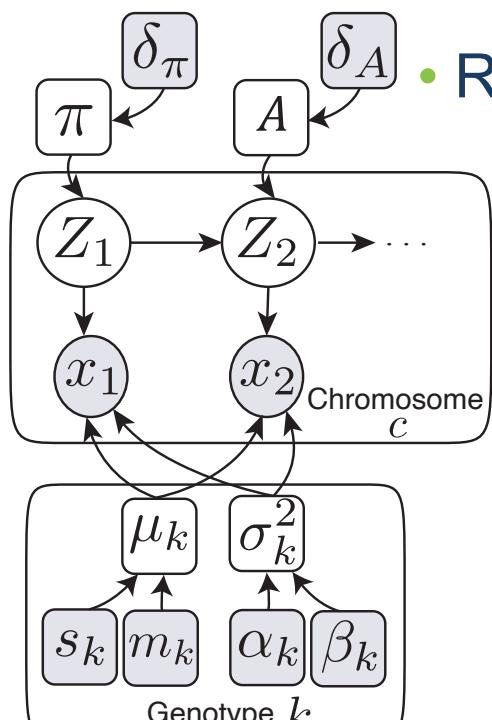
Copy Number Segmentation

- What are the genomic segments of copy number alterations?
- What is the copy number value for each segment?
- How do we account for variability/noise in the data?

Continuous hidden Markov model (HMM)

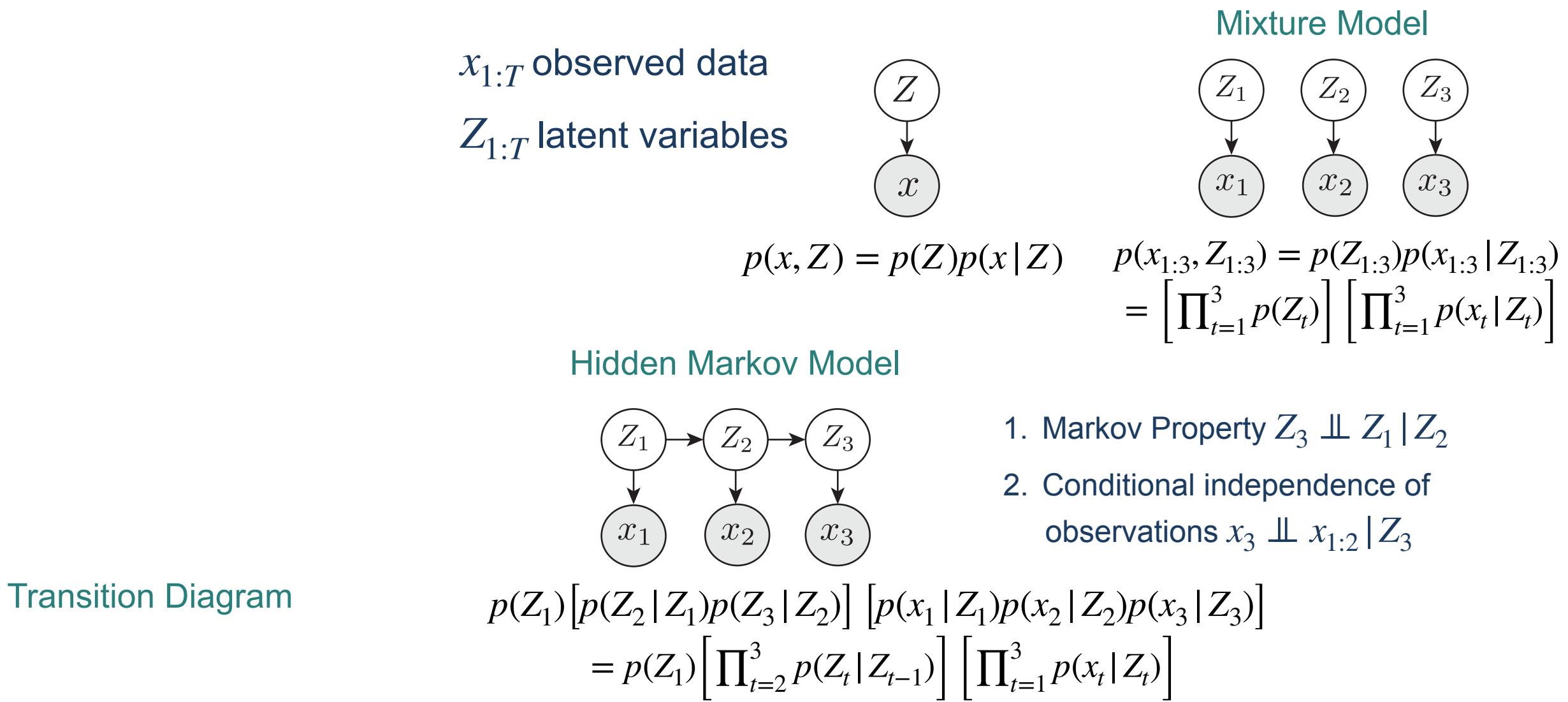
2. Continuous hidden Markov model

- Hidden Markov Models vs Mixture Models
- Components of a Continuous HMM
- Inference and Parameter Learning using EM



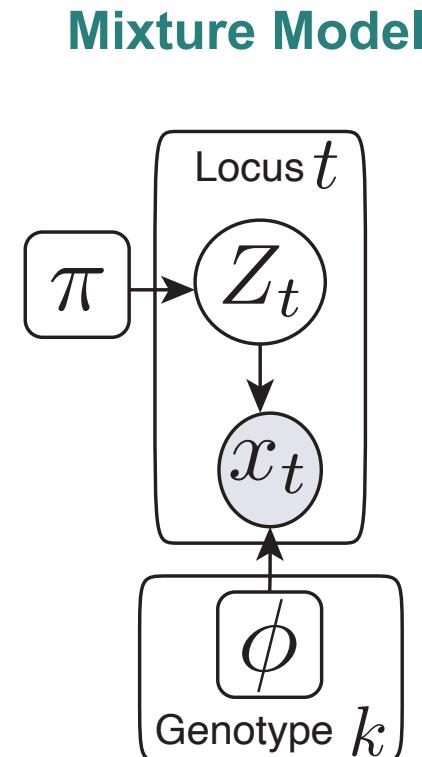
- References:
- **HMMcopy** - Ha et al. *Genome Research* **22**:1995-2007 (2012).
- **ichorCNA** - Adalsteinsson*, Ha* Freeman* et al. *Nature Communications* **8**:1324 (2017).
- **TitanCNA** - Ha et al. TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequencing data. *Genome Research* **24**:1881-1893 (2014).
- Murphy, K. (2012). Machine Learning: A Probabilistic Perspective. MIT Press. ISBN: 9780262018029
- Bishop, C. M. (2006). Pattern Recognition and Machine Learning (Information Science and Statistics). Springer. ISBN: 0387310738

Probabilistic Graphical Model for HMMs



From Mixture Models to Hidden Markov Models

- Mixture model for iid data is a special case of the HMM



$$p(x_{1:T}, Z_{1:T}) = p(Z_{1:T})p(x_{1:T} | Z_{1:T})$$

**Joint Probability Distribution
(Complete data likelihood)**

$x_{1:T}$ observed data

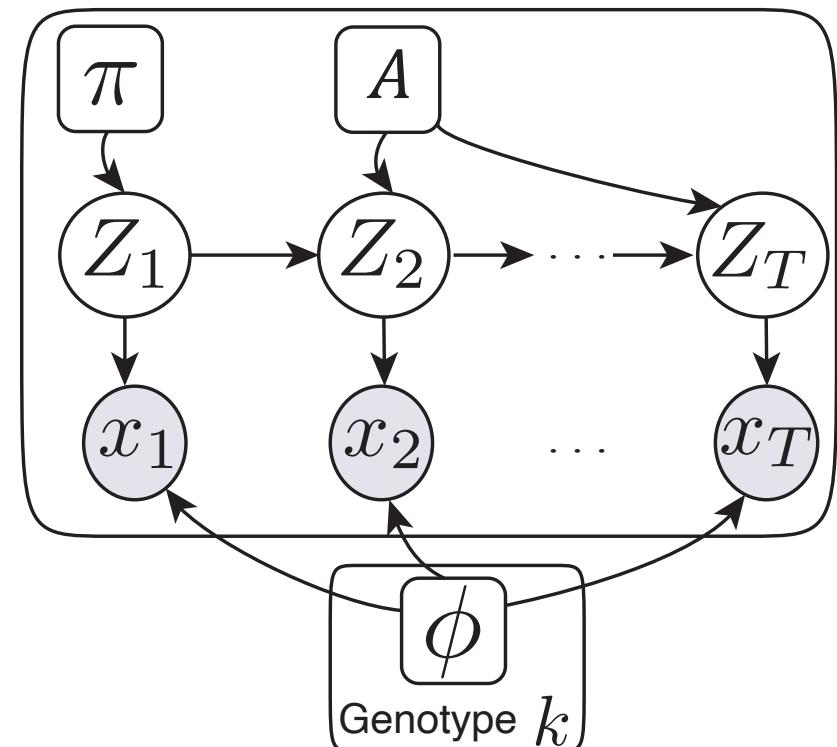
$Z_{1:T}$ latent variables

π mixture weights

ϕ observation parameters

$$p(x_{1:T}, Z_{1:T} | \theta) = \left[\prod_{t=1}^T p(Z_t | \pi) \right] \prod_{t=1}^T p(x_t | Z_t, \phi)$$

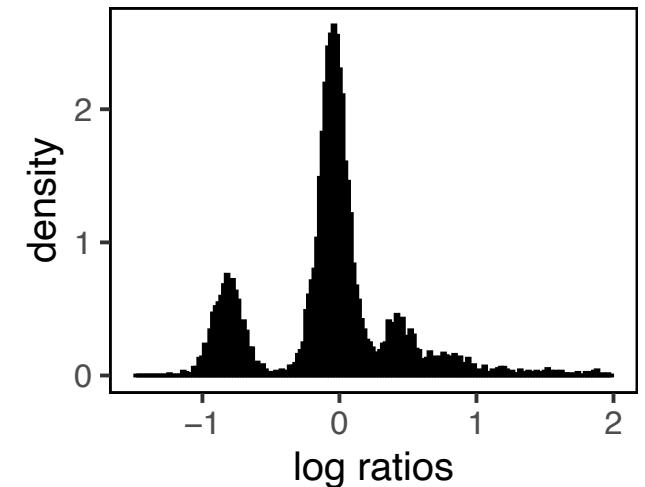
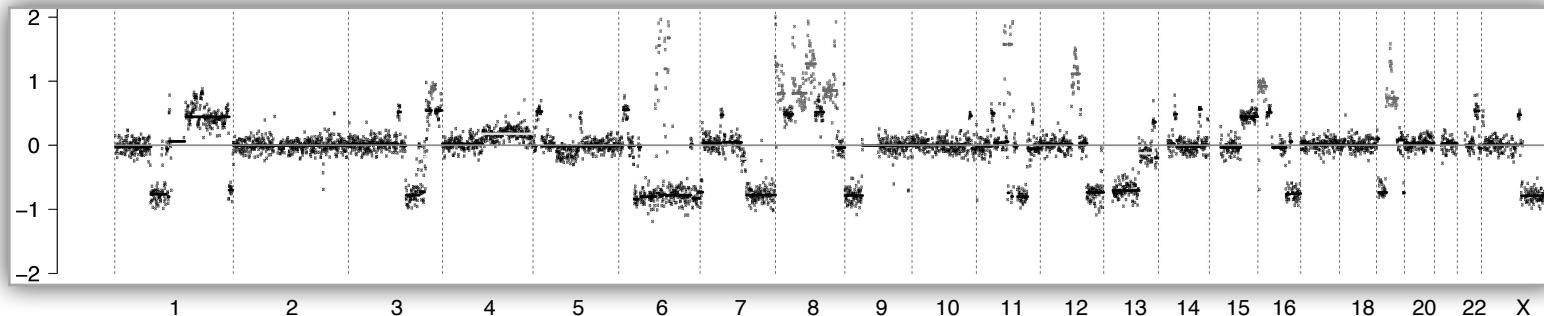
Hidden Markov Model



$$p(x_{1:T}, Z_{1:T} | \theta) = \left[p(Z_1 | \pi) \prod_{t=2}^T p(Z_t | Z_{t-1}, A) \right] \prod_{t=1}^T p(x_t | Z_t, \phi)$$

Gaussian Mixture Model for Log Ratio Data

Corrected
(log2 ratio)



The ratios $\frac{\hat{r}_t^{Tumor}}{\hat{r}_t^{Normal}}$, for all t loci are log-normal distributed, so the log ratios $x_{1:T}$ follow a normal distribution.

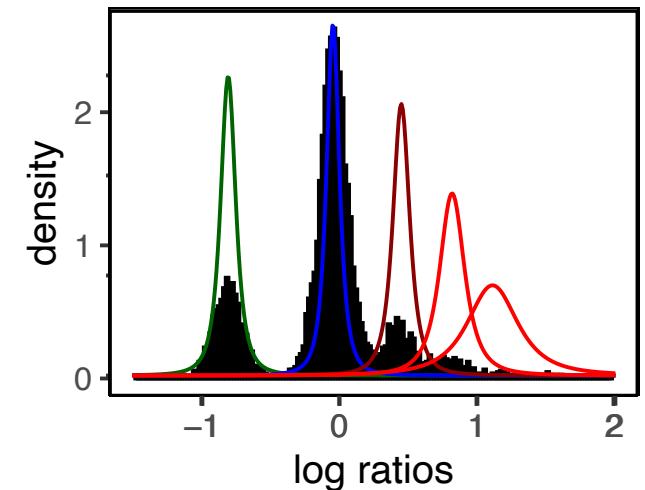
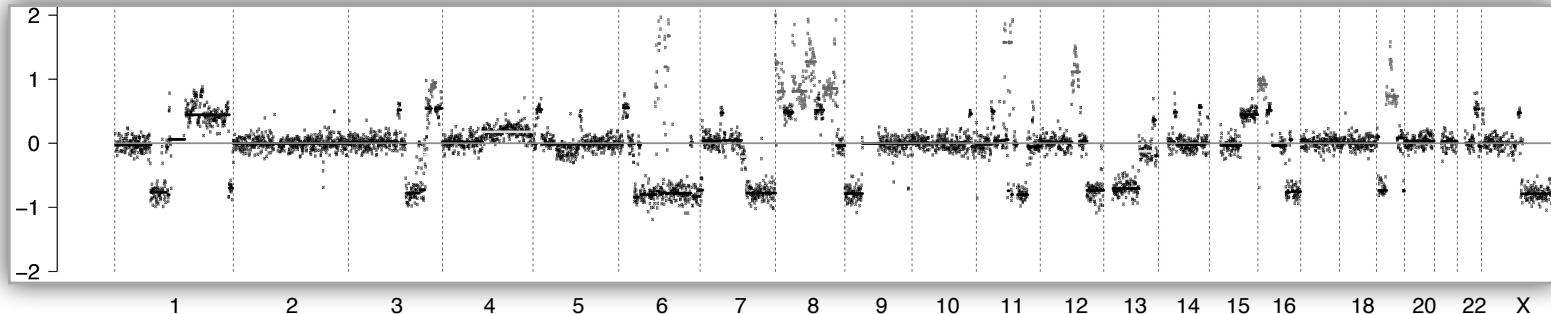
The Gaussian Distribution

Let X be a continuous measurement with mean μ and variance σ^2 , then X has a Gaussian distribution,
 $X \sim \mathcal{N}(\mu, \sigma^2)$ or $p(X = x) = \mathcal{N}(x | \mu, \sigma^2)$ where

$$\mathcal{N}(x | \mu, \sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2\sigma^2}(x-\mu)^2}$$

Gaussian Mixture Model for Log Ratio Data

Corrected
(log2 ratio)



The ratios $\frac{\hat{r}_t^{Tumor}}{\hat{r}_t^{Normal}}$, for all t loci are log-normal distributed, so the log ratios $x_{1:T}$ follow a normal distribution.

The Gaussian Mixture Model

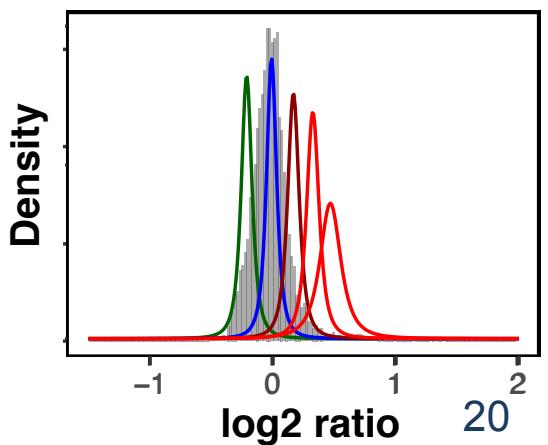
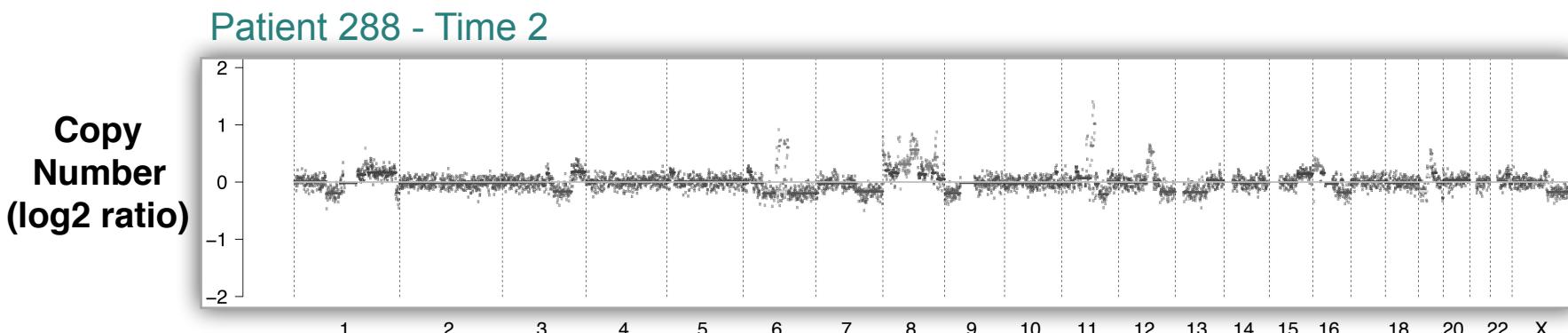
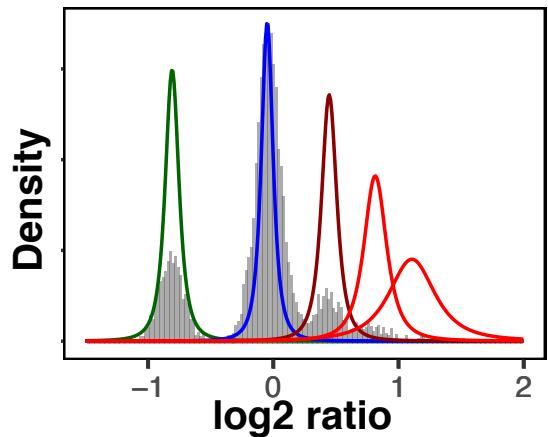
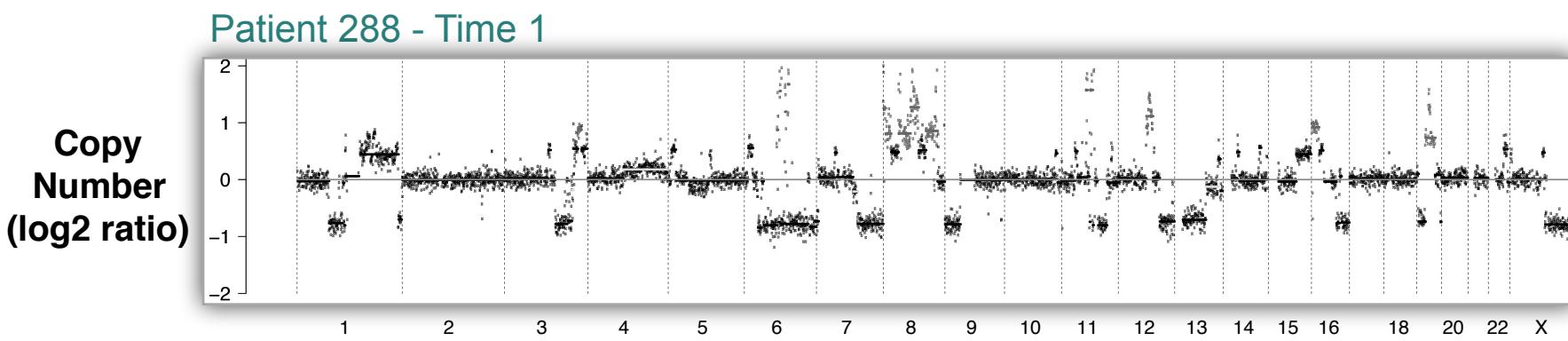
Define a likelihood for a ***K*-component mixture of Gaussians** with means $\mu = \{\mu_1, \dots, \mu_K\}$ and variance $\sigma^2 = \{\sigma_1^2, \dots, \sigma_K^2\}$, where the observation model is a conditional Gaussian

$$p(x_t | Z_i = k, \mu, \sigma^2) = \mathcal{N}(x_t | \mu_k, \sigma_k^2)$$

Rationale for Estimating Likelihood Parameters

Why are the data multi-modal?

Why should we estimate the mixture distribution parameters?



Components of a continuous HMM

Input Data: log ratios

There are T different data points with continuous values $x = \{x_1, \dots, x_T\}$.

Latent State Model

- The latent variables $Z = \{Z_1, \dots, Z_T\}$ can be assigned values from a set of K discrete states with probability

Initial state distribution

- The probabilities of the states for the first latent variable Z_1 is the parameter $\pi = \{\pi_1, \dots, \pi_K\}$
- π follows a prior distribution $p(\pi_k | \delta_k) = Dir(\pi_k | \delta_k)$

Transition Model (homogenous HMM)

- The conditional distribution between adjacent data i and j corresponds to a table A of transition probabilities

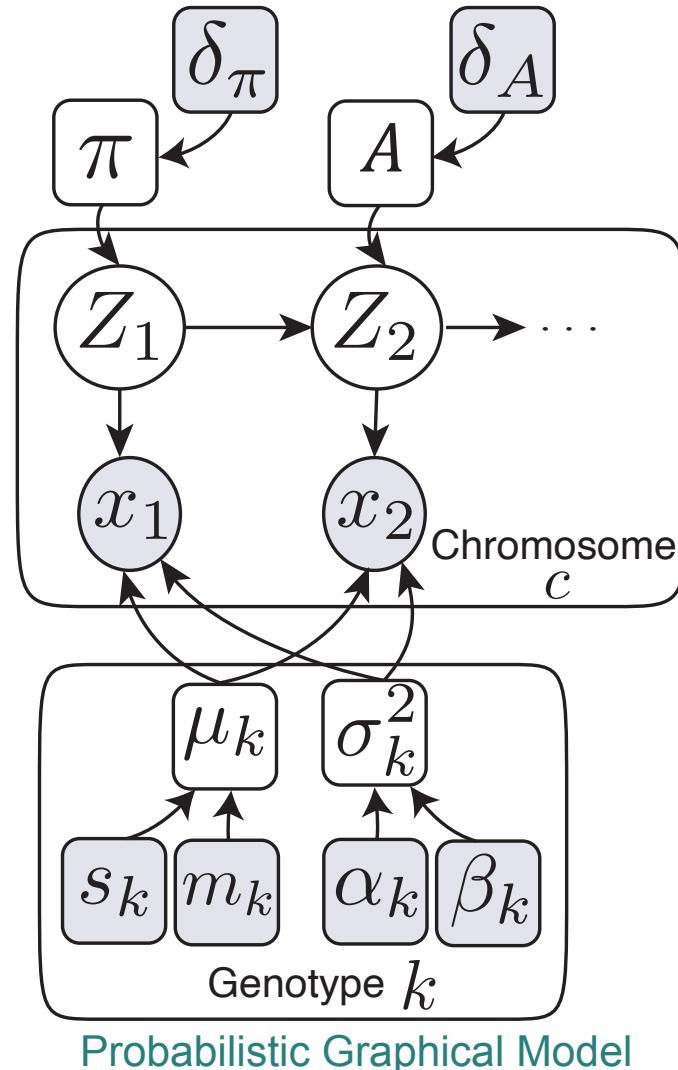
$$p(Z_t = j | Z_{t-1} = i) = A_{ij}$$

Emission Model (Continuous HMM)

- The emission is modeled using a mixture of Gaussians with the likelihood model

$$p(x_t | Z_t = k, \mu, \sigma^2) = \mathcal{N}(x_t | \mu_k, \sigma_k^2)$$

- μ is modeled with a prior $p(\mu_k | m_k, s_k) = \mathcal{N}(\mu_k | m_k, s_k)$
- σ^2 is modeled with prior $p(\sigma_k^2 | \alpha_k, \beta_k) = InvGamma(\sigma_k^2 | \alpha_k, \beta_k)$



Inference & parameter estimation using EM

Expectation-Maximization: Inference and parameter training

Initialize parameters: π, A, μ

E-Step: Inference using Forwards-Backwards Algorithm (Baum-Welch)

1. Compute “responsibilities” (Posterior of the latent states $\gamma(Z_{1:T})$)
 - State $Z_t = k$ is “responsible for generating observation x_t ”
2. Compute “2-slice marginals” (Posterior of state transitions $\xi(Z_{t-1}, Z_t)$)
 - Expected number of transitions from state k to j

M-Step: Update parameters (learning)

1. Initial state distribution, π
2. Transition probabilities, A
3. Emission likelihood parameters, μ

Iterate between E-Step and M-Step, check when log posterior likelihood, $\log \mathbb{P}$, stops increasing.

Inference & parameter estimation using EM (E-Step)

E-Step: Forwards-backwards Algorithm (Baum-Welch; Sum-Product)

- Forward, $\alpha(Z_t)$: joint prob. of observing all *past* data up to time t when given Z_t
- Backward, $\beta(Z_t)$: conditional prob. of all *future* data from time $t + 1$ to T when given Z_t

Forward Probabilities ($T \times K$) - Past

$$\alpha(Z_t = k) = \mathcal{N}(x_t | \mu_k, \sigma_k^2) \sum_{j=1}^K \left\{ A_{jk} \alpha(Z_{t-1} = j) \right\}$$

Backward Probabilities ($T \times K$) - Future

$$\beta(Z_t = k) = \sum_{j=1}^K \left\{ \mathcal{N}(x_{t+1} | \mu_j, \sigma_j^2) A_{kj} \beta(Z_{t+1} = j) \right\}$$

Inference & parameter estimation using EM (E-Step)

E-Step: Compute Responsibilities & 2-Slice Marginals

- Responsibilities, $\gamma(Z_t = k)$: is the posterior on the latent states

$$\gamma(Z_t = k) = \frac{\alpha(Z_t = k)\beta(Z_t = k)}{p(\mathbf{x})}$$

Responsibilities
Matrix $K \times T$

- 2-Slice Marginals, $\xi(Z_{t-1} = k, Z_t = j)$: is the expected number of transitions between k to j

$$\xi(Z_{t-1} = k, Z_t = j) = \frac{\alpha(Z_{t-1} = k)A_{kj}\mathcal{N}(x_t | \mu_j, \sigma_j^2)\beta(Z_t = j)}{p(\mathbf{x})}$$

2 Slice Marginals
Matrix $K \times K \times T$

- The likelihood $p(\mathbf{x}) = p(\mathbf{x} | \boldsymbol{\mu}, \boldsymbol{\sigma}^2, \boldsymbol{\pi})$ is computed in the forwards recursion

$$\ell = \log p(\mathbf{x}) = \sum_{t=1}^T \log \left(\sum_{k=1}^K \alpha(Z_t = k) \right)$$

Log likelihood

Inference & parameter estimation using EM (M-Step)

Expected complete data log likelihood

Initial State Dist	Transition	Emission
$Q = \sum_{k=1}^K \gamma(Z_1 = k) \log \pi_k + \sum_{t=2}^T \sum_{j=1}^K \sum_{k=1}^K \xi(Z_{t-1} = k, Z_t = j) \log A_{kj} + \sum_{t=1}^T \sum_{k=1}^K \gamma(Z_t = k) \log \mathcal{N}(x_t \mu_k, \sigma_k^2)$		

M-Step: update parameters, π, μ, σ^2

$$\hat{\pi}_k = \frac{\gamma(Z_1 = k) + \delta^\pi(k) - 1}{\sum_{j=1}^K \{\gamma(Z_1 = j) + \delta^\pi(j) - 1\}}$$

$$\hat{\mu}_k = \frac{s_k \sum_{t=1}^T \gamma(Z_t = k) x_t + m \sigma_k^2}{s_k \sum_{t=1}^T \gamma(Z_t = k) + \sigma_k^2}$$

$$\hat{\sigma}_k^2 = \frac{\sum_{t=1}^T \gamma(Z_t = k) (x_t - \bar{x}_k)^2 + 2\beta_k}{\sum_{t=1}^T \gamma(Z_t = k) + 2(\alpha_k + 1)}$$

Where $\bar{x} = \frac{\sum_{t=1}^T \gamma(Z_t = k) x_t}{\sum_{t=1}^T \gamma(Z_t = k)}$

MAP for initial state distribution

MAP for Gaussian means

MAP for Gaussian variance

Inference & parameter estimation using EM (M-Step)

M-Step: Update transition matrix, A

$$\hat{A}_{kj} = \frac{\sum_{t=2}^T \xi(Z_{t-1} = k, Z_t = j) + \delta^A(k)}{\sum_{l=1}^K \left\{ \sum_{t=2}^T \xi(Z_{t-1} = k, Z_t = l) + \delta^A(l) \right\}}$$

Expected number of transitions from k to j

Prior counts

“Pseudo-counts”

Expected number of transitions from k to any other state

Evaluate the log posterior

$$\log \mathbb{P} = \ell + \log Dir(\hat{\pi} | \delta) + \sum_{k=1}^K \left\{ \log \mathcal{N}(\hat{\mu}_k | m_k, s_k) + \log InvGamma(\hat{\sigma}_k^2 | \alpha_k, \beta_k) + \log Dir(A_{k,1:K}^{(0)} | \hat{A}_{k,1:K}) \right\}$$

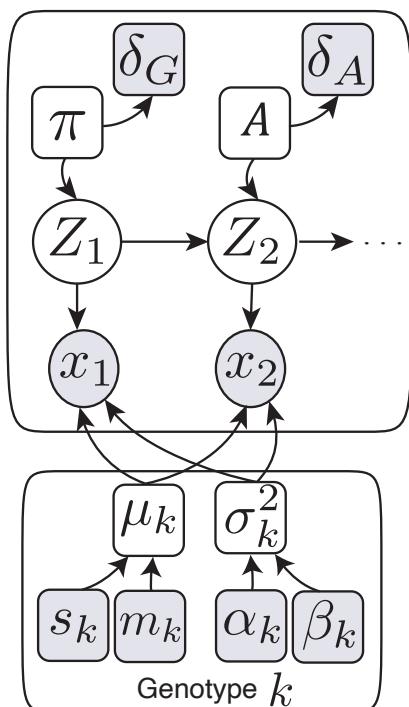
Iterate between E-Step and M-Step: stop when $\log \mathbb{P}$ changes less than ϵ compared to previous EM iteration.

Algorithm 1 HMM Parameter Learning using EM

- 1: **Inputs:**
 Data: $x_{1:T}$
 Initial parameters: $\pi^{(0)}, \mu_{1:K}^{(0)}, (\sigma_{1:K}^2)^{(0)}, A^{(0)}$
 Hyperparameters: $\delta^\pi, m_{1:K}, s_{1:K}, \alpha_{1:K}, \beta_{1:K}, \delta^A$
- 2: **Initialize:**
 $\pi \leftarrow \pi^{(0)}, \mu_{1:K} \leftarrow \mu_{1:K}^{(0)}, \sigma_{1:K}^2 \leftarrow (\sigma_{1:K}^2)^{(0)}, A \leftarrow A^{(0)}$
- 3: Compute observed likelihood using initial parameters:
4: `obs.lik` \leftarrow `compute.gauss.lik()`
- 5: **while** converged = false **do**
- 6: **E-Step:** Compute responsibilities using current parameters:
7: $(\gamma(Z_{1:T}), \text{loglik}) \leftarrow .\text{Call}(\text{"forward_backward"})$
- 8: **M-Step:** Update parameters:
9: $\hat{\pi} \leftarrow \text{update.pi}()$
10: $\hat{\mu}_{1:K} \leftarrow \text{update.mu}()$
11: $\hat{\sigma}_{1:K}^2 \leftarrow \text{update.var}()$
12: $\hat{A} \leftarrow \text{update.A}()$
- 13: Assign updated parameters:
14: $\pi \leftarrow \hat{\pi}, \mu_{1:K} \leftarrow \hat{\mu}_{1:K}, \sigma_{1:K}^2 \leftarrow \hat{\sigma}_{1:K}^2, A \leftarrow \hat{A}$
- 15: Re-compute observed likelihood using updated parameters:
16: `obs.lik` \leftarrow `compute.gauss.lik()`
- 17: Compute log Posterior:
18: `logP[curr.iter]` \leftarrow `compute.log.posterior(loglik, ...)`
- 19: **if** (`logP[curr.iter]` - `logP[prev.iter]` < ϵ) **then**
- 20: converged = true
- 21: **end if**
- 22: `logP[prev.iter]` \leftarrow `logP[curr.iter]`
- 23: **end while**
- 24: **return** Converged parameters $\hat{\pi}, \hat{\mu}_{1:K}, \hat{\sigma}_{1:K}^2, \hat{A}$

3. Copy Number Profiling using a HMM

- Defining the HMM for copy number analysis
- Copy number segmentation using Viterbi
- References:
 - **HMMcopy** - Ha et al. *Genome Research* **22**:1995-2007 (2012).
 - **ichorCNA** - Adalsteinsson*, Ha* Freeman* et al. *Nature Communications* **8**:1324 (2017).
 - **TitanCNA** - Ha et al. TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequencing data. *Genome Research* **24**:1881-1893 (2014).
 - Murphy, K. (2012). Machine Learning: A Probabilistic Perspective. MIT Press. ISBN: 9780262018029
 - Bishop, C. M. (2006). Pattern Recognition and Machine Learning (Information Science and Statistics). Springer. ISBN: 0387310738



Probabilistic Model for Copy Number Analysis

Input Data: log ratios

There are T different genomic bins with log ratio data $x = \{x_1, \dots, x_T\}$.

Latent State Model: copy number states

There are 5 different possible copy number states (genotypes), $K = \{1, 2, 3, 4, 5\}$

1. A specific genotype $k \in K$ can be assigned to each of the **latent states** $Z = \{Z_1, \dots, Z_T\}$
2. The **initial state distribution** $\pi = \{\pi_1, \dots, \pi_5\}$ is used for the first latent state Z_1

Transition Model

3. The probabilities for transitioning to copy number state j in bin t from state i in bin $t - 1$ are contained in matrix $A \in \mathbb{R}^{K \times K}$

$$p(Z_t = j | Z_{t-1} = i) = A_{ij}$$

Emission Model: likelihood for log ratio data

For each copy number state, the log ratio means are $\mu = \{\mu_1, \dots, \mu_5\}$ and variance $\sigma^2 = \{\sigma_1^2, \dots, \sigma_5^2\}$

4. The **emission model** is a mixture of Gaussians with *unknown* parameters, μ and σ^2 ,

$$p(x_i | Z_i = k, \mu, \sigma^2) = \mathcal{N}(x_i | \mu_k, \sigma_k^2)$$

Prior Model

5. The **priors** in the model have hyper-parameters δ^π , $m_{1:K}$, $s_{1:K}$, $\alpha_{1:K}$, $\beta_{1:K}$, $\delta_{1:K}^A$

$$p(\pi | \delta^\pi) = \text{Dirichlet}(\pi | \delta^\pi)$$

$$p(\mu_k | m_k, s_k) = \mathcal{N}(\mu_k | m_k, s_k)$$

$$p(\sigma_k^2 | \alpha_k, \beta_k) = \text{InvGamma}(\sigma_k^2 | \alpha_k, \beta_k)$$

$$p(A_{k,1:K} | \delta^A) = \text{Dirichlet}(A_{k,1:K} | \delta_k^A)$$

	j				
i	0	...	5		
0					
...					
5					

$\sum_{j=1}^K A_{ij} = 1$

Probabilistic Model for Copy Number Analysis

Input Data: log ratios

There are T different genomic bins with log ratio data $x = \{x_1, \dots, x_T\}$.

Latent State Model: copy number states

There are 5 different possible copy number states (genotypes), $K = \{1, 2, 3, 4, 5\}$

1. A specific genotype $k \in K$ can be assigned to each of the latent states $Z = \{Z_1, \dots, Z_T\}$
2. The initial state distribution $\pi = \{\pi_0, \dots, \pi_5\}$ is used for the first latent state Z_1

Transition Model

3. The probabilities for transitioning to copy number state j in bin t from state i in bin $t - 1$ are contained in matrix $A \in \mathbb{R}^{K \times K}$
- $$p(Z_t = j | Z_{t-1} = i) = A_{ij}$$

Emission Model: likelihood for log ratio data

For each copy number state, the log ratio means are $\mu = \{\mu_0, \dots, \mu_5\}$ and variance $\sigma^2 = \{\sigma_0^2, \dots, \sigma_5^2\}$

4. The emission model is a mixture of Gaussians with unknown parameters, μ and σ^2 ,

$$p(x_i | Z_i = k, \mu, \sigma^2) = \mathcal{N}(x_i | \mu_k, \sigma_k^2)$$

Prior Model

5. The priors in the model have hyper-parameters δ^π , $m_{1:K}$, $s_{1:K}$, $\alpha_{1:K}$, $\beta_{1:K}$, $\delta_{1:K}^A$

$$p(\pi | \delta^\pi) = \text{Dirichlet}(\pi | \delta^\pi)$$

$$p(\mu_k | m_k, s_k) = \mathcal{N}(\mu_k | m_k, s_k)$$

$$p(\sigma_k^2 | \alpha_k, \beta_k) = \text{InvGamma}(\sigma_k^2 | \alpha_k, \beta_k)$$

$$p(A_{k,1:K} | \delta^A) = \text{Dirichlet}(A_{k,1:K} | \delta_k^A)$$



	j				
i	A	0	...	5	
0					
...					
5					

$\sum_{j=1}^K A_{ij} = 1$

Copy number segmentation using Viterbi

Viterbi algorithm (Max-Sum)

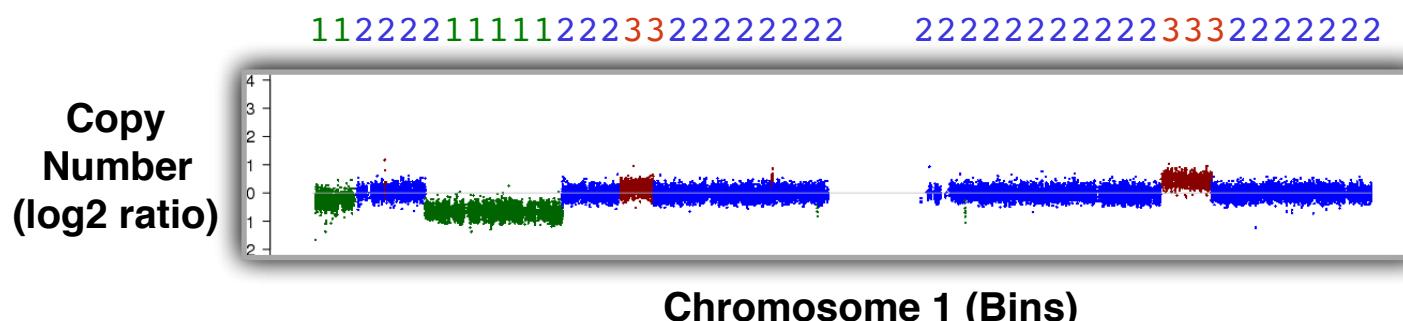
- Find the most probable sequence of copy number states

$$\hat{Z}_{1:T} = \max_{Z_{1:T}} \log p(Z_{1:T} | x_{1:T})$$

- Perform max-sum of probabilities in trellis

$$\omega(Z_{t+1} = k) = \log \mathcal{N}(x_{t+1} | \mu_k, \sigma_k^2) + \max_{Z_t} \left\{ \log A_{Z_t, k} + \log \omega(Z_t) \right\}$$

- Back trace from $\omega(Z_T)$ to find overall most probable path



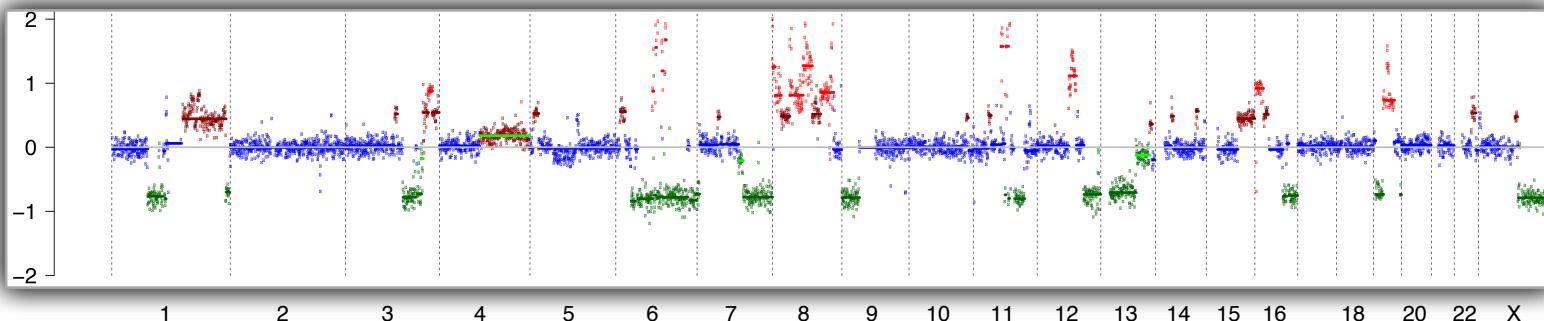
Rationale for Estimating Likelihood Parameters

Why should we estimate the mixture distribution parameters?

- Can account for technical and biological “noise” by estimating model parameters
 $\mu = \{\mu_0, \dots, \mu_5\}$ and $\sigma^2 = \{\sigma_0^2, \dots, \sigma_5^2\}$?

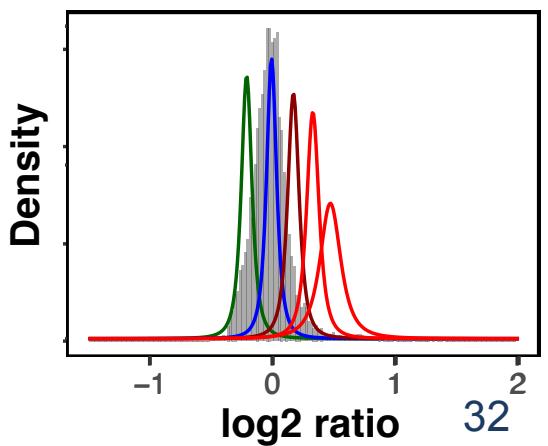
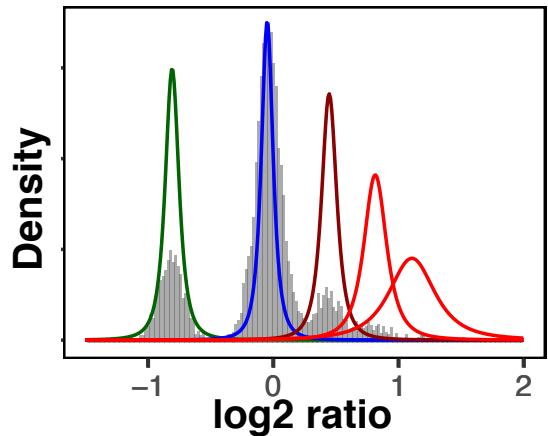
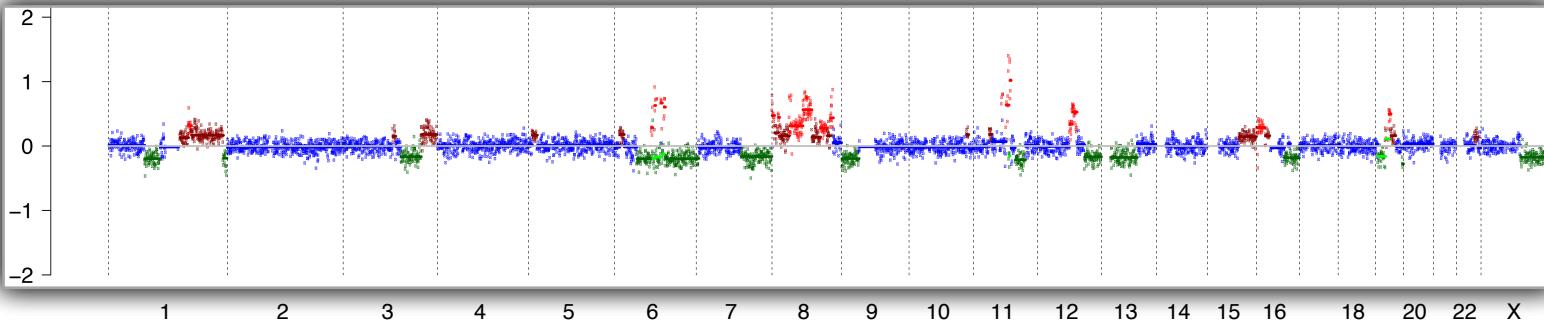
Patient 288 - Time 1

Copy Number (log2 ratio)



Patient 288 - Time 2

Copy Number (log2 ratio)



Homework #6: Profiling copy number alterations

A. Implement a copy number alteration (CNA) caller described in Lecture 3

- Implement components of a continuous HMM in a Bayesian framework
- Learn the parameters and infer the genotypes using EM
- Predict the copy number alteration segments for a chromosome.
- Expected outputs for each question will be provided so that you can check your code.

B. Power calculations for mutation detection described in Lecture 4

Due: May 15th

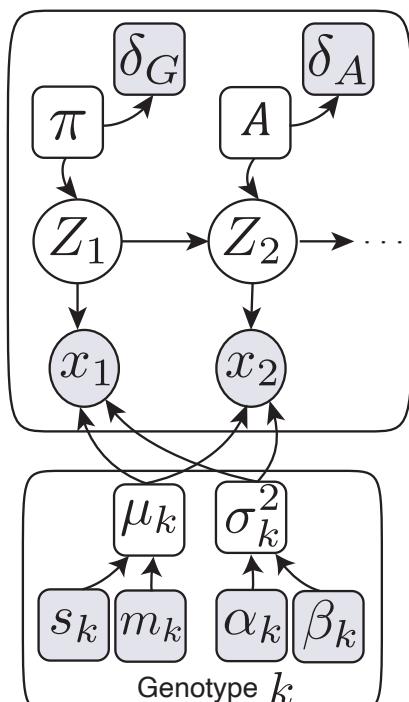
Office Hours with Anna-Lisa Doebley (adoebley@uw.edu)

Zoom Meeting ID: 446 356 7725 Password: GS541

- Wednesday, May 7, 2-3pm (Homework 5 questions)
- Monday, May 11, 2-3pm
- Wednesday, May 13, 2-3pm

Extra Slides

- Continuous hidden Markov models (HMMs)
- Parameter inference using EM and copy number segmentation
- References:



- **ichorCNA** - Adalsteinsson*, Ha* Freeman* et al. *Nature Communications* **8**:1324 (2017).
- **HMMcopy** - Ha et al. *Genome Research* **22**:1995-2007 (2012).
- **TitanCNA** - Ha et al. TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequencing data. *Genome Research* **24**:1881-1893 (2014).
- Murphy, K. (2012). Machine Learning: A Probabilistic Perspective. MIT Press. ISBN: 9780262018029
- Bishop, C. M. (2006). Pattern Recognition and Machine Learning (Information Science and Statistics). Springer. ISBN: 0387310738

ichorCNA: Model inference using EM (extra slide 1)

Complete data likelihood: joint distribution of latent and observed variables

$$\begin{aligned} p(x_{1:T}, Z_{1:T} | \boldsymbol{\theta}) &= p(Z_1 | \pi_{1:K}) \left[\prod_{t=2}^T p(Z_t | Z_{t-1}, A) \right] \prod_{t=1}^T p(x_t | Z_t, \mu, \sigma^2) \\ &= \prod_{k=1}^K \pi_k^{\mathbb{I}(Z_i=k)} \left[\prod_{t=2}^T \prod_{k=1}^K \prod_{j=1}^K A_{jk}^{\mathbb{I}(Z_{t-1}=j)\mathbb{I}(Z_t=k)} \right] \prod_{t=1}^T \prod_{k=1}^K \mathcal{N}(x_t | \mu_k, \sigma_k^2)^{\mathbb{I}(Z_t=k)} \end{aligned}$$

where $\boldsymbol{\theta} = \{\pi_{1:K}, \mu_{1:K}, \sigma_{1:K}^2, A\}$

Complete data log likelihood

$$\log p(x_{1:T}, Z_{1:T} | \boldsymbol{\theta}) = \sum_{k=1}^K \mathbb{I}(Z_i=k) \log \pi_k + \sum_{t=2}^T \sum_{j=1}^K \sum_{k=1}^K \mathbb{I}(Z_{t-1}=j, Z_t=k) \log A_{jk} + \sum_{t=1}^T \sum_{k=1}^K \mathbb{I}(Z_i=k) \log \mathcal{N}(x_t | \mu_k, \sigma_k^2)$$

Expected complete data log likelihood

$$Q = \sum_{k=1}^K \gamma(Z_1 = k) \log \pi_k + \sum_{t=2}^T \sum_{j=1}^K \sum_{k=1}^K \xi(Z_{t-1} = j, Z_t = k) \log A_{jk} + \sum_{t=1}^T \sum_{k=1}^K \gamma(Z_t = k) \log \mathcal{N}(x_t | \mu_k, \sigma_k^2)$$

ichorCNA: Model inference using EM (extra slide 2)

E-Step: compute responsibilities using the forwards-backwards algorithm (Baum-Welch)

$$\gamma(\mathbf{Z}_t) = p(\mathbf{Z}_t | \mathbf{x}, \theta^{old}) = \frac{p(\mathbf{x} | \mathbf{Z}_t | \theta^{old}) p(\mathbf{Z}_t | \theta^{old})}{p(\mathbf{x} | \theta^{old})}$$

$$\gamma(\mathbf{Z}_t) = \frac{p(x_1, \dots, x_t, \mathbf{Z}_t) p(x_{t+1}, \dots, x_T | \mathbf{Z}_t)}{p(\mathbf{x})}$$

$$\gamma(\mathbf{Z}_t) = \frac{\alpha(\mathbf{Z}_t)\beta(\mathbf{Z}_t)}{p(\mathbf{x})} \quad \begin{matrix} \text{Responsibilities} \\ \text{Matrix } K \times T \end{matrix}$$

Where $\alpha(Z_t = k) = \mathcal{N}(x_t | Z_t = k) \sum_{j=1}^K \left\{ A_{jk} \alpha(Z_t = j) \right\}$ is the forward recursion probability

Where $\beta(Z_t = k) = \sum_{j=1}^K \left\{ \mathcal{N}(x_{t+1} | Z_{t+1} = j) A_{kj} \alpha(Z_{t+1} = j) \right\}$ is the backward recursion probability

Forward Probabilities
Matrix $K \times T$

Backward Probabilities
Matrix $K \times T$

$$\xi(\mathbf{Z}_{t-1}, \mathbf{Z}_t) = p(\mathbf{x} | \mathbf{Z}_{t-1}, \mathbf{Z}_t) P(\mathbf{Z}_{t-1}, \mathbf{Z}_t)$$
$$\xi(\mathbf{Z}_{t-1}, \mathbf{Z}_t) = \frac{\alpha(\mathbf{Z}_{t-1}) p(x_t | \mathbf{Z}_t) p(\mathbf{Z}_t | \mathbf{Z}_{t-1}) \beta(\mathbf{Z}_t)}{p(\mathbf{x})}$$

Likelihood function $\ell = \log p(\mathbf{x}) = \sum_{t=1}^T \log \left(\sum_{k=1}^K \alpha(Z_t = k) \right)$

2 Slice Marginals
Matrix $K \times K \times T$

Chapter 13 in Bishop (2006).
Pattern Recognition and Machine Learning. Springer

ichorCNA: Model inference using EM (extra slide 3)

M-Step: Update the parameters given the responsibilities

$$\text{Prior}(\pi_{1:K}, \mu_{1:K}, \sigma_{1:K}^2, A) = \prod_{k=1}^K \text{Dir}(\pi_k | \delta_k) \text{Dir}(A_k | \delta_A) \mathcal{N}(\mu_k | \alpha, \beta) \text{InvGamma}(\sigma_k^2 | \alpha_k, \beta_k) \quad \text{Priors}$$
$$\mathcal{O} = Q + \log \mathbb{P}(\pi_{1:K}, \mu_{1:K}, \sigma_{1:K}^2, A) \quad \text{Complete data log likelihood} \\ + \log \text{priors}$$

- The object function \mathcal{O} is used to obtain the update equations for $\pi_{1:K}$ and $\mu_{1:K}$

$$\frac{\partial \mathcal{O}}{\partial \pi_k} = 0, \text{ find } \hat{\pi}_k \quad \text{MAP for initial state distribution}$$

$$\frac{\partial \mathcal{O}}{\partial \mu_k} = 0, \text{ find } \hat{\mu}_k \quad \text{MAP for Gaussian means}$$

$$\frac{\partial \mathcal{O}}{\partial \sigma_k^2} = 0, \text{ find } \hat{\sigma}_k^2 \quad \text{MAP for Gaussian variance}$$

$$\frac{\partial \mathcal{O}}{\partial A_{jk}} = 0, \text{ find } \hat{A}_{jk} \quad \text{MAP for transition probabilities}$$

EM Convergence: after each iteration, monitor the log posterior

$$\ell = \log p(x) = \sum_{t=1}^T \log \left(\sum_{k=1}^K \alpha(Z_t = k) \right) \quad \text{Incomplete Data Log likelihood}$$

$$\log \mathbb{P} = \ell + \log \text{Prior}(\pi_{1:K}, \mu_{1:K}, \sigma_{1:K}^2, A) \quad \text{Log posterior}$$