# A Semiparametric Bayesian Model for Comparing DNA Copy Numbers

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(joint with Y Ji & V.Baladandayuthapani)

# Contents

- Introduction
- Model
- Inference
- Results

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    - Detecting differences across disease subtypes

# Example

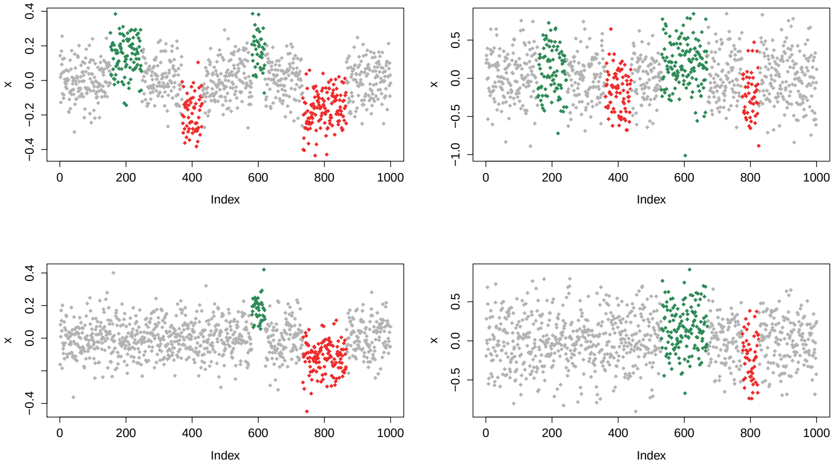

Figure : Simulated genome profile.

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- Yau et al. (2011): mixture model that combines a hidden Markov model for the locations (states), with a Dirichlet process prior for the scales

# Definitions

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- Let $g_j$ indicate the disease subtype for sample $j$. Say $g_j \in \{1, 2\}$.

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- That is, $Y_{ij}$ arises from the sum of a population mean $\mu_{k,g_j}$, a sample-specific mean $m_{lj}$, plus a measurement error $\epsilon_{ij}$.

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$$\boldsymbol{\mu}_k \mid G \overset{\text{ind}}{\sim} G, \quad \text{for } k = 1, \ldots, K$$

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- Introducing a latent indicator $z_k = I(\mu_{k1} \neq \mu_{k2})$

$$\boldsymbol{\mu}_k \mid z_k, G_0, G_1 \overset{\text{ind}}{\sim} G_{z_k}, \;\; z_k \overset{\text{ind}}{\sim} \text{Ber}(\pi), \;\; G_r \overset{\text{ind}}{\sim} \mathcal{DP}(a_r, F_r) \quad (2)$$

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- For the precision parameter of the Dirichlet processes:

$$a_r \overset{\text{iid}}{\sim} \mathrm{Ga}(a_\alpha, b_\alpha),$$

for $r = 0, 1$.

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- Sample specific: segment-specific mean copy number is

$$(\mu_{k,g_j} + m_{l,j})$$

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- We added random errors $\mathrm{N}(0, \sigma^2)$ to the mean profiles, with $\sigma^2 \in \{0.1, 0.3\}$ to show low and high levels of noise in the log2 ratios

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- Therefore, we had a total of 6 different scenarios: (3 prevalence levels × 2 noise levels).

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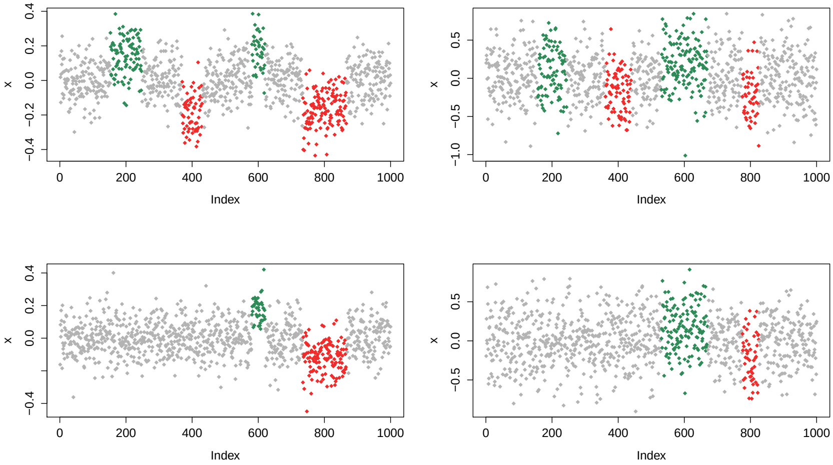

Figure : Simulated genome profile.

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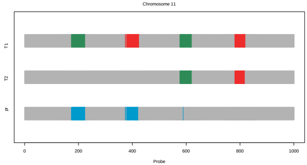

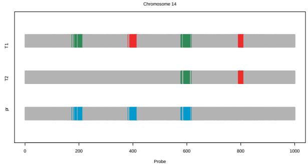

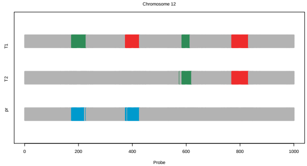

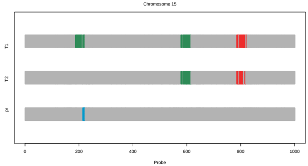

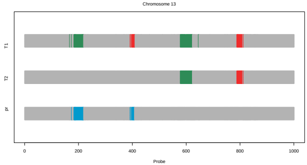

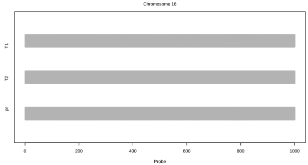

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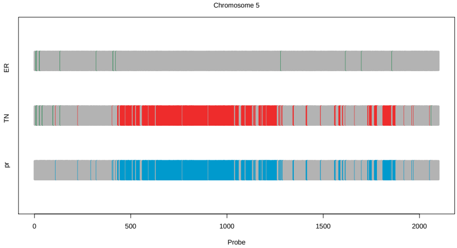
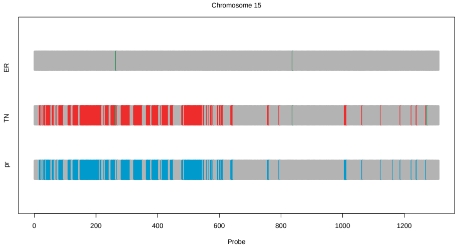
- Chromosome 15 is a new finding

# Breast Cancer Data





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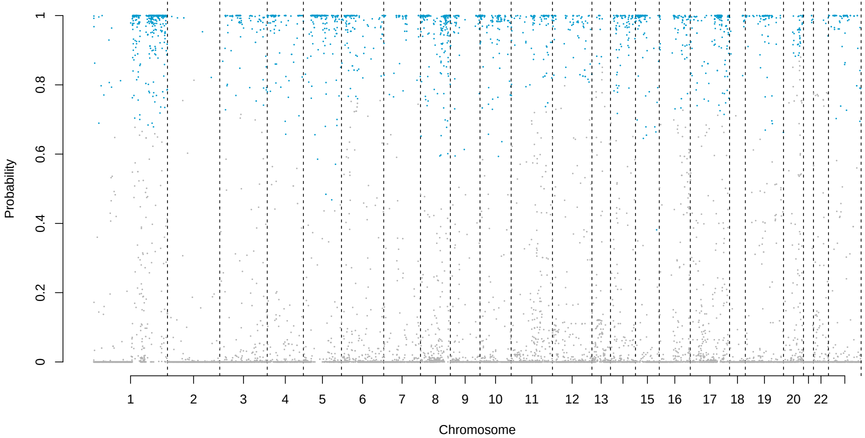

Figure : Differential CNA probabilities for all chromosomes.

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