Multi-regime models for DNA copy number and gene expression association

Gwénaël Leday

Joint work with:

Mark van de Wiel
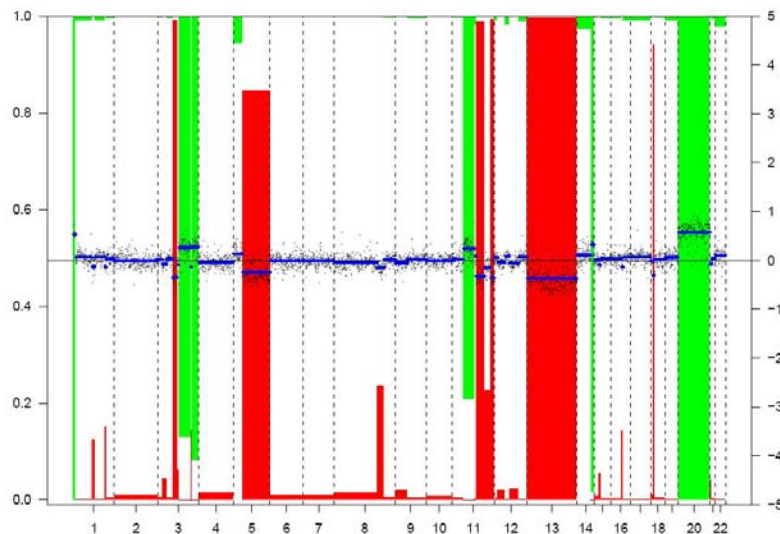
Aad van der Vaart

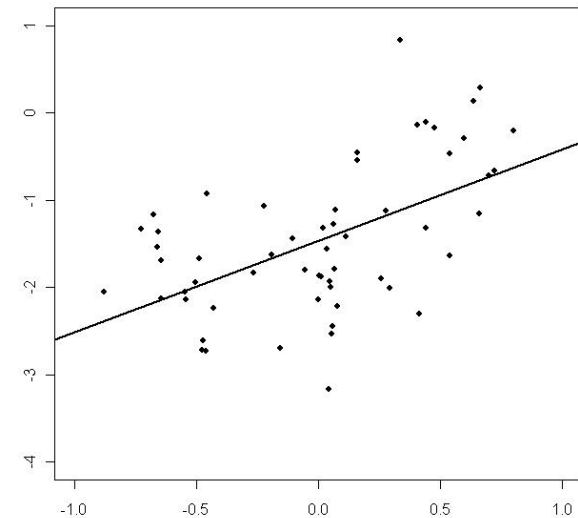Department of Mathematics, Vrije Universiteit, Amsterdam

Department of Epidemiology and Biostatistics, VUMC, Amsterdam

❑ Preprocessing of DNA copy number data is complex

– *normalization, segmentation, calling*
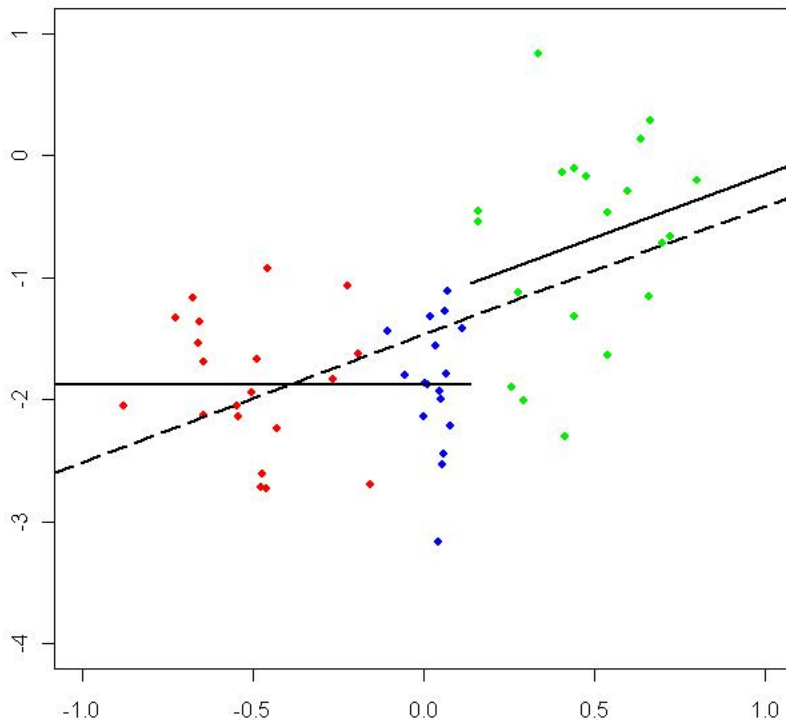
❑ Linear (or step-wise) assumption for DNA-mRNA

❑ General framework:

– Goal: identifying the relationship

– Use piecewise linear regression splines
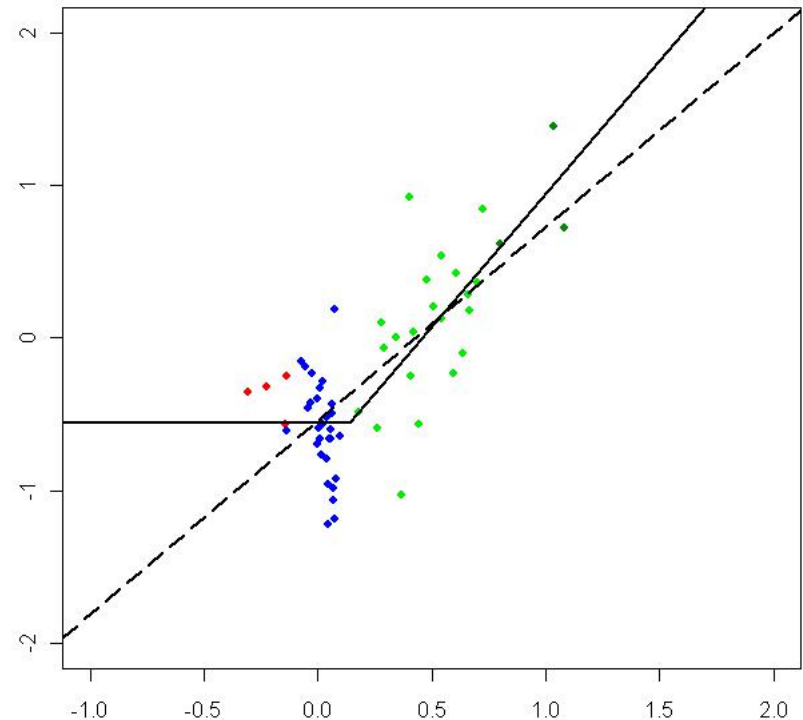
– Include biologically motivated constraints

❏ Application to colorectal cancer data (Carvalho et al, 2009)

Type of model	Number
Intercept	12868
Linear	3853
Piecewise	8225

» TCFL5

» TH1L