Cancer research

R package to analyze genomic alterations and tumor pathways based on array data from single nucleotide polymorphism (SNP) and comparative genomic hybridization (CGH) experiments

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Our research focus

Cancer development / progression
(e.g. Breast, Ewing's Sarcoma, Osteosarcoma)

- Prognostic / therapeutic factors
- Analysis of the regulatory system on the level of DNA, RNA and proteins

based on

- Comprehensive sample archive
- Lab techniques like: TMA, Affymetrix 4C, TaqMan, Cell culture

Development of analysis solutions on this research background

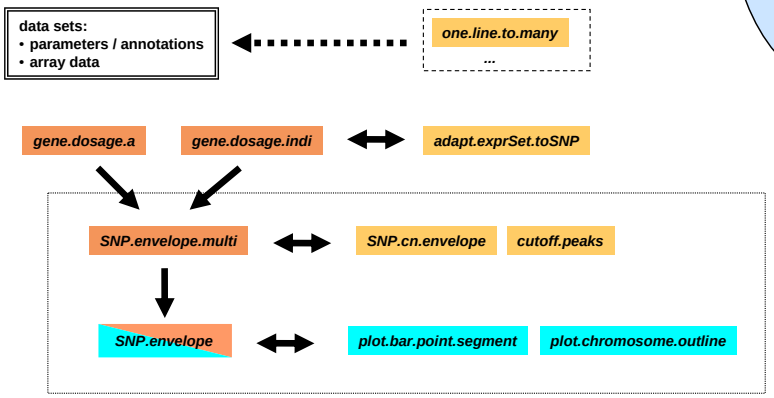
Core platform : S-Plus – Fortran, now establishing R – Fortran

Design

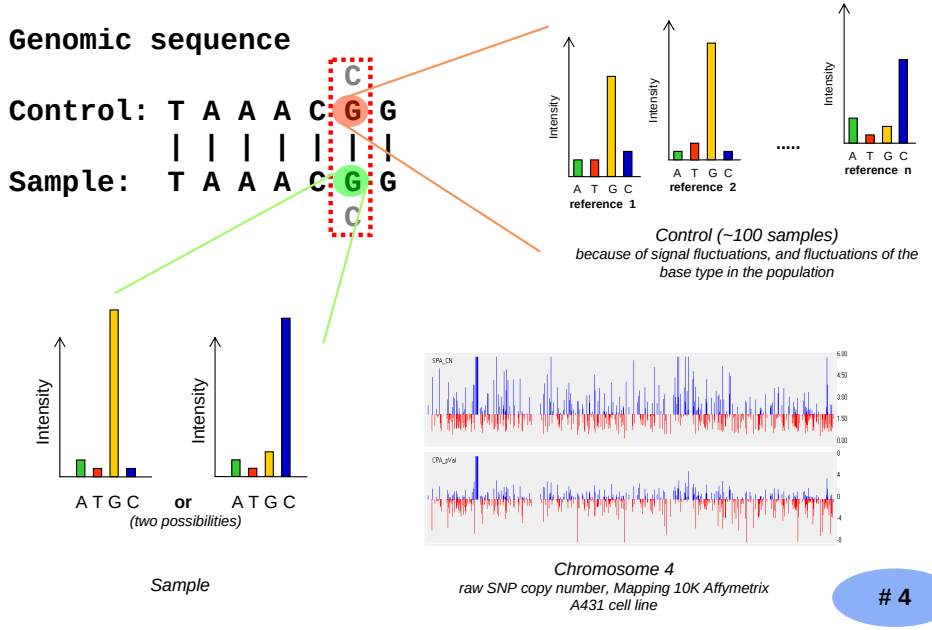
From S-Plus to R – Reasons:
- Community
- Technical shortcomings – e.g. S-Plus has memory leaks

Task – migrating from S-Plus to R:
Primarily the graphics routines have to be adapted

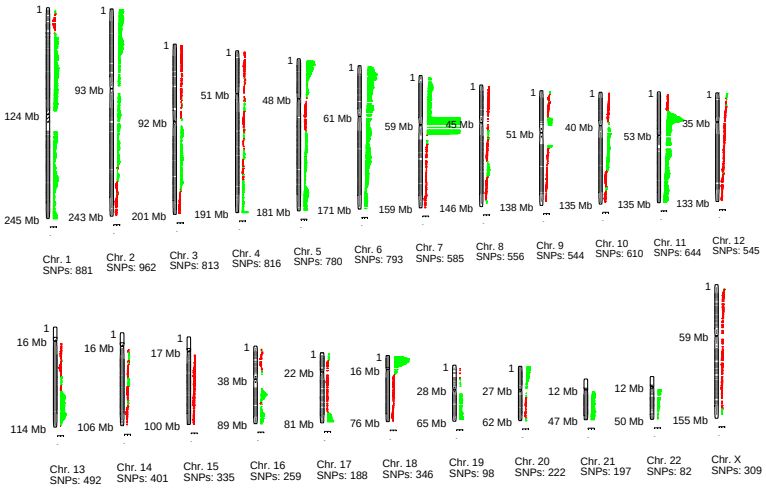
nice to have:
- a data browser like in S-Plus for the workspace content
- more concern on big data sets > 600 MB
- R to Fortran translator for time critical calculations - or similar



Biology – SNP Copy Number Analysis



Visualization



SNP copy number across genome
MDA-MB-468 cell line, Mapping 10K Affymetrix, smoothing window: 40
The colored area indicates genetic alterations - Gains: green, losses: red

Take home message

- S-Plus to R is an easy task

- SNPs are capable to replace the CGH technique
- Old CGH data can be integrated

Improvements in the Analysis Strategy Make Single Nucleotide Polymorphism Analysis a Powerful Tool in the Detection and Characterization of Amplified Chromosomal Regions in Human Tumors

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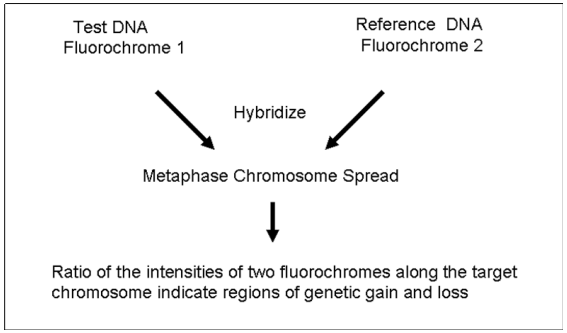
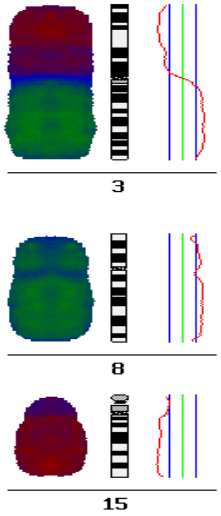
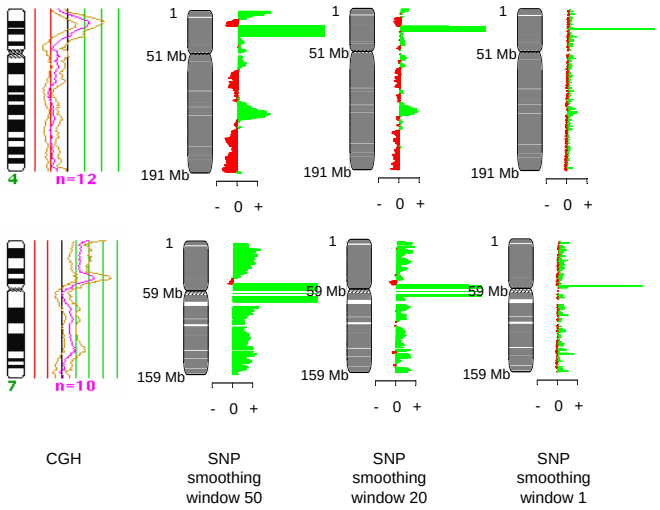
Biology – CGH vs. SNP Analysis

Comperative Genomic Hybridisation



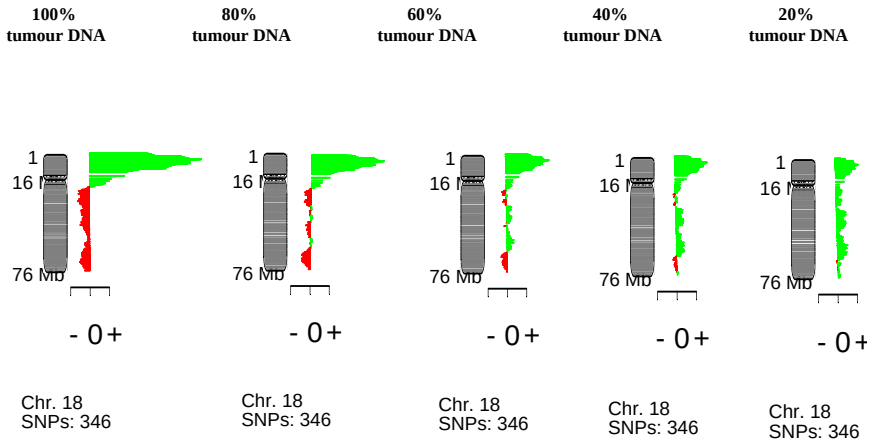


Results I



CGH | SNP smoothing window 50 | SNP smoothing window 20 | SNP smoothing window 1

Results II



Chr. 18
SNPs: 346