

An Introduction to R and Bioconductor

Robert Gentleman
Program in Computational Biology
Fred Hutchinson Cancer Research Center

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Overview

- **biology is a computational science**
- **problems of data analysis, data generation, reproducibility require computational support and computational solutions**
- **we value code reuse**
 - many of the tasks have already been solved
 - if we use those solutions we can put effort into new research
- **well designed, self-describing data structures help us deal with complex data**

Goals

- Provide access to powerful statistical and graphical methods for the analysis of genomic data.
- Facilitate the integration of biological metadata (**GenBank, GO, Entrez Gene, PubMed**) in the analysis of experimental data.
- Allow the rapid development of extensible, interoperable, and scalable software.
- Promote high-quality documentation and reproducible research.
- Provide training in computational and statistical methods.

Bioconductor

- Bioconductor is an **open source** and **open development** software project for the analysis of biomedical and genomic data.
- The project was started in the Fall of 2001 and includes core developers in the US, Europe, and Australia.
- **R** and the **R package system** are used to design and distribute software.
- A goal of the project is to develop software modules that are integrated and which make use of available web services to provide comprehensive software solutions to relevant problems.
- **ArrayAnalyzer**: Commercial port of Bioconductor packages in S-Plus.

Why are we Open Source

- **so that you can find out what algorithm is being used, and how it is being used**
- **so that you can modify these algorithms to try out new ideas or to accommodate local conditions or needs**
- **so that they can be used as components (potentially modified)**

Bioconductor packages

Release 2.3, 294 Software Packages!

- **General infrastructure:**
Biobase, Biostrings, biocViews
- **Annotation:**
annotate, annaffy, biomaRt, AnnotationDbi → data packages.
- **Graphics/GUIs:**
geneflotter, hexbin, limmaGUI, exploRase
- **Pre-processing:**
affy, affycomp, oligo, makecdfenv, vsn, gcrn, limma
- **Differential gene expression:**
genefilter, limma, ROC, siggenes, EBArrays, factDesign
- **GSEA/Hypergeometric Testing**
GSEABase, Category, GOstats, topGO
- **Graphs and networks:**
graph, RBGL, Rgraphviz
- **Flow Cytometry:**
prada, flowCore, flowViz, flowUtils
- **Protein Interactions:**
ppiData, ppiStats, ScISI, Rintact
- **Sequence Data:**
Biostrings, ShortRead, chipseq, rtracklayer, HilbertVis
- **Other data:**
xcms, DNACopy, PROcess, aCGH, rsbml, SBMLR, Rdisop

Component software

- **most interesting problems will require the coordinated application of many different techniques**
- **thus we need integrated interoperable software**
- **web services are one tool**
- **well designed software modules are another**
- **you should design your piece to be a cog in a big machine**

Data complexity

- Dimensionality.
- Dynamic/evolving data: e.g., gene annotation, sequence, literature.
- Multiple data sources and locations: in-house, WWW.
- Multiple data types: numeric, textual, graphical.

No longer $X_{n \times p}$!

We distinguish between biological metadata and experimental metadata.

Experimental metadata

- **Gene expression measures**
 - scanned images, i.e., raw data;
 - image quantitation data, i.e., output from image analysis;
 - normalized expression measures,
 - Reliability/quality information for the expression measures.
- **Information on the probe sequences printed on the arrays (array layout).**
- **Information on the target samples hybridized to the arrays.**
- **See Minimum Information About a Microarray Experiment (MIAME) standards and the `MAGEML` package.**

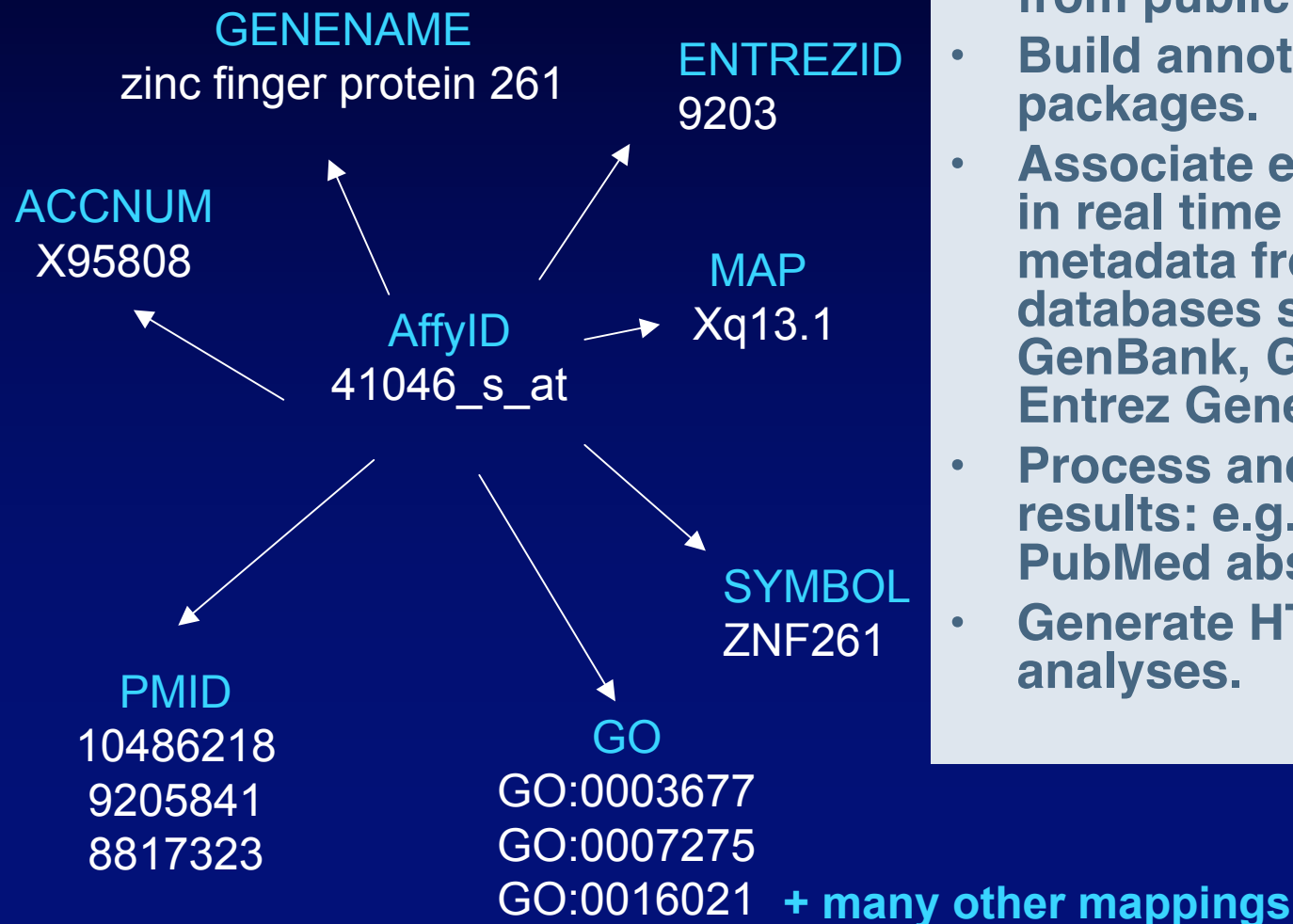
Biological metadata

- **Biological attributes that can be applied to the experimental data.**
- **E.g. for genes**
 - chromosomal location;
 - gene annotation (Entrez Gene, GO);
 - relevant literature (PubMed).
- **Biological metadata sets are large, evolving rapidly, and typically distributed via the WWW.**
- **Tools:** `annotate`, `annaffy`, `biomaRt`, and `AnnotationDbi` **packages, and annotation data packages.**
- **Please use the db versions of all meta-data packages.**

Annotation packages

annotate, annafy, biomaRt, and AnnotationDbi

Metadata package `hgu95av2` mappings between different gene IDs for this chip.



- Assemble and process genomic annotation data from public repositories.
- Build annotation data packages.
- Associate experimental data in real time to biological metadata from web databases such as GenBank, GO, KEGG, Entrez Gene, and PubMed.
- Process and store query results: e.g., search PubMed abstracts.
- Generate HTML reports of analyses.

Vignettes

- Bioconductor developed a new documentation paradigm, the vignette.
- A **vignette** is an **executable document** consisting of a collection of documentation text and code chunks.
- Vignettes form **dynamic, integrated, and reproducible statistical documents** that can be automatically updated if either data or analyses are changed.
- Vignettes can be generated using the `Sweave` function from the R `tools` package.

Short Courses/Conferences

- we have given many short courses
 - see bioconductor.org for more details on upcoming courses
- **BioC2009 - Seattle, July 27-29**

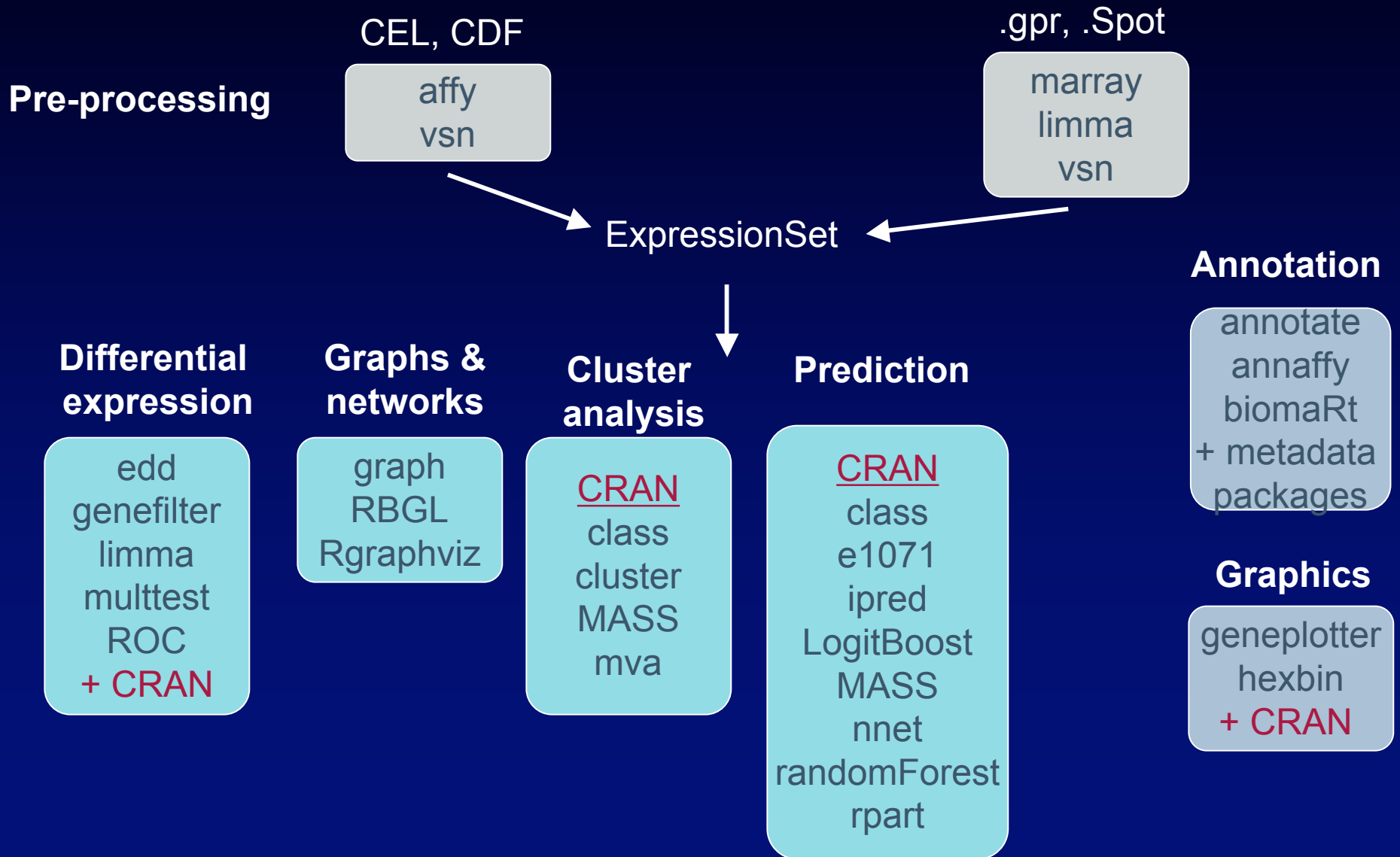
Bioconductor Software

- we concentrate our development on a few important aspects
- **Biobase**: core classes and definitions that allow for succinct description and handling of the data
- **annotate**: generic functions for annotation that can be specialized
- **genefilter**: fast filtering via virtually every mechanism
- **graph/Rgraphviz/RBGL**: code for handling graphs and networks
- **Biostrings/ShortRead** (and soon friends): string manipulations, sequence analysis

Biobase:ExpressionSet

- software should help organize and manipulate your data
- this was the intention of the original exprSet class
- the data need to be assembled correctly once, and then they can be processed, subset etc without worrying about them
- exprSet was too limited (and too oriented to single channel arrays)
- we developed the new ExpressionSet class

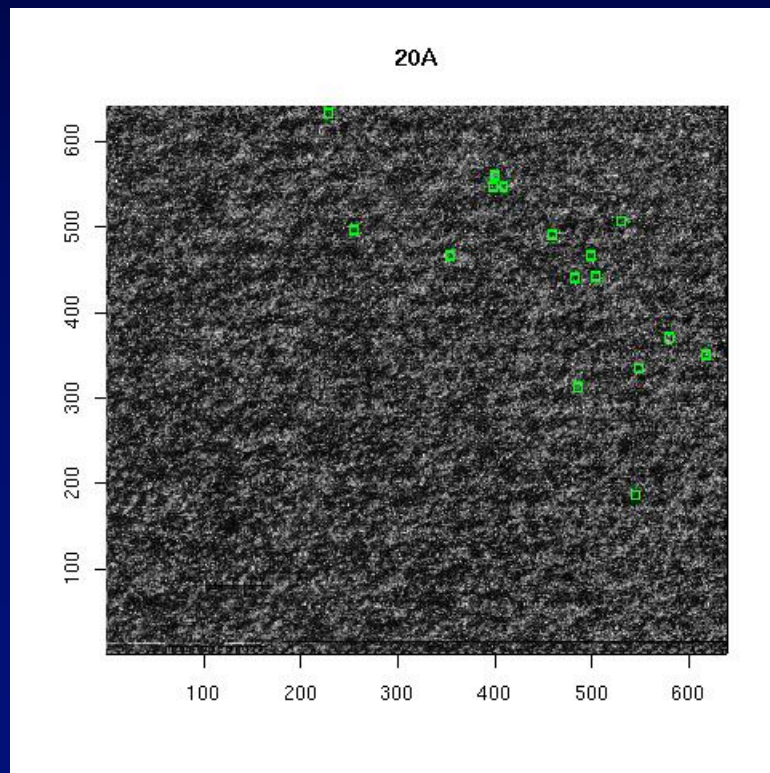
Microarray data analysis



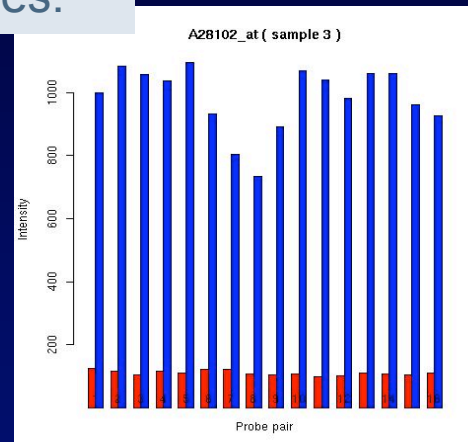
affy/oligo package

Pre-processing oligonucleotide chip data:

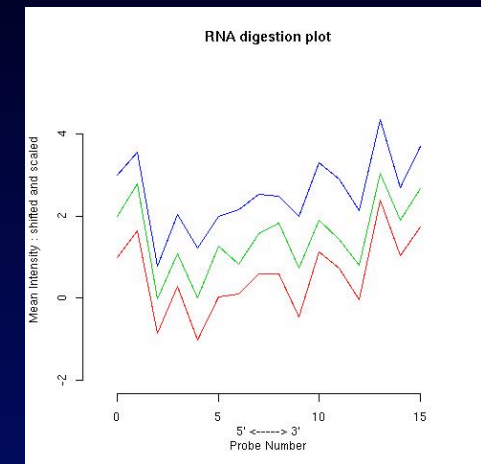
- diagnostic plots,
- background correction,
- probe-level normalization,
- computation of expression measures.



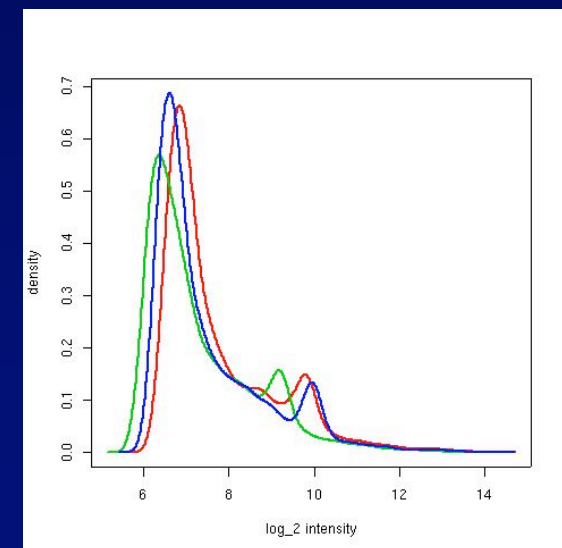
image



barplot.ProbeSet

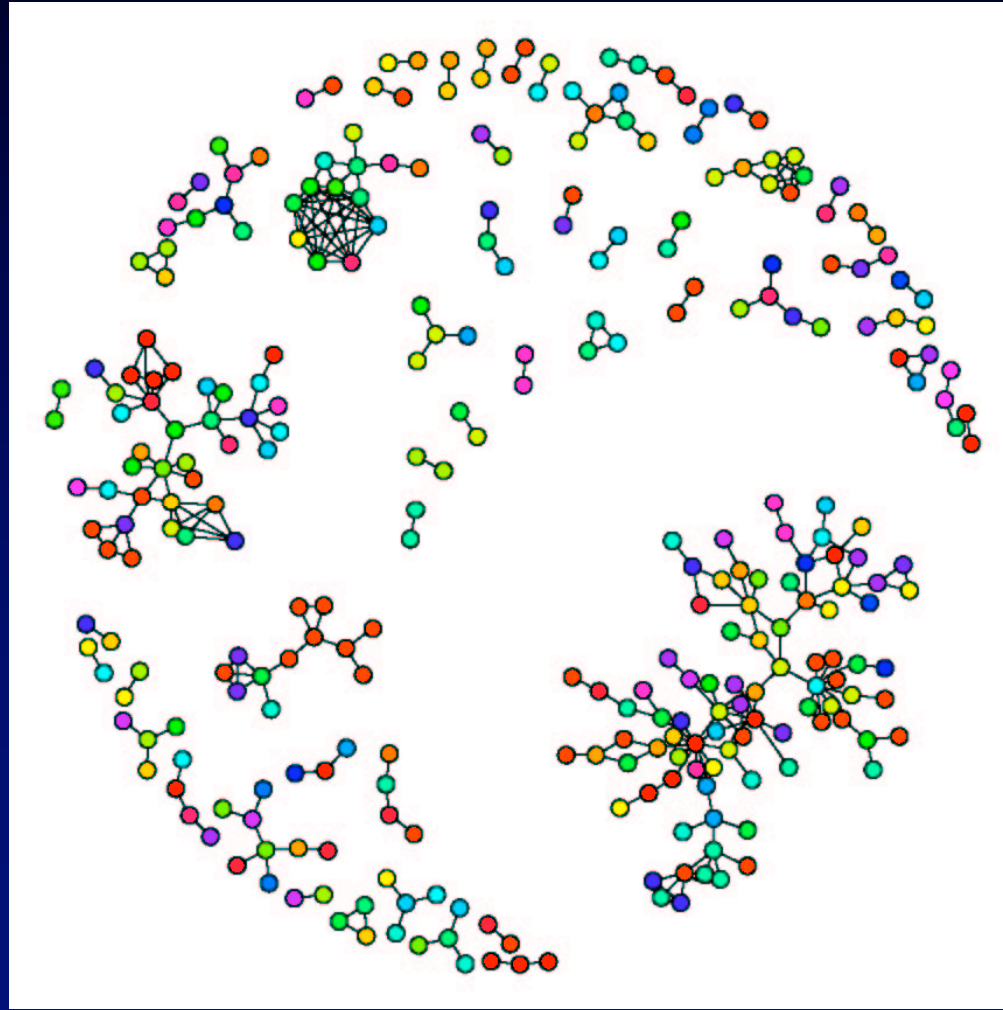


plotAffyRNAdeg



plotDensity

graph and Rgraphviz



apComplex

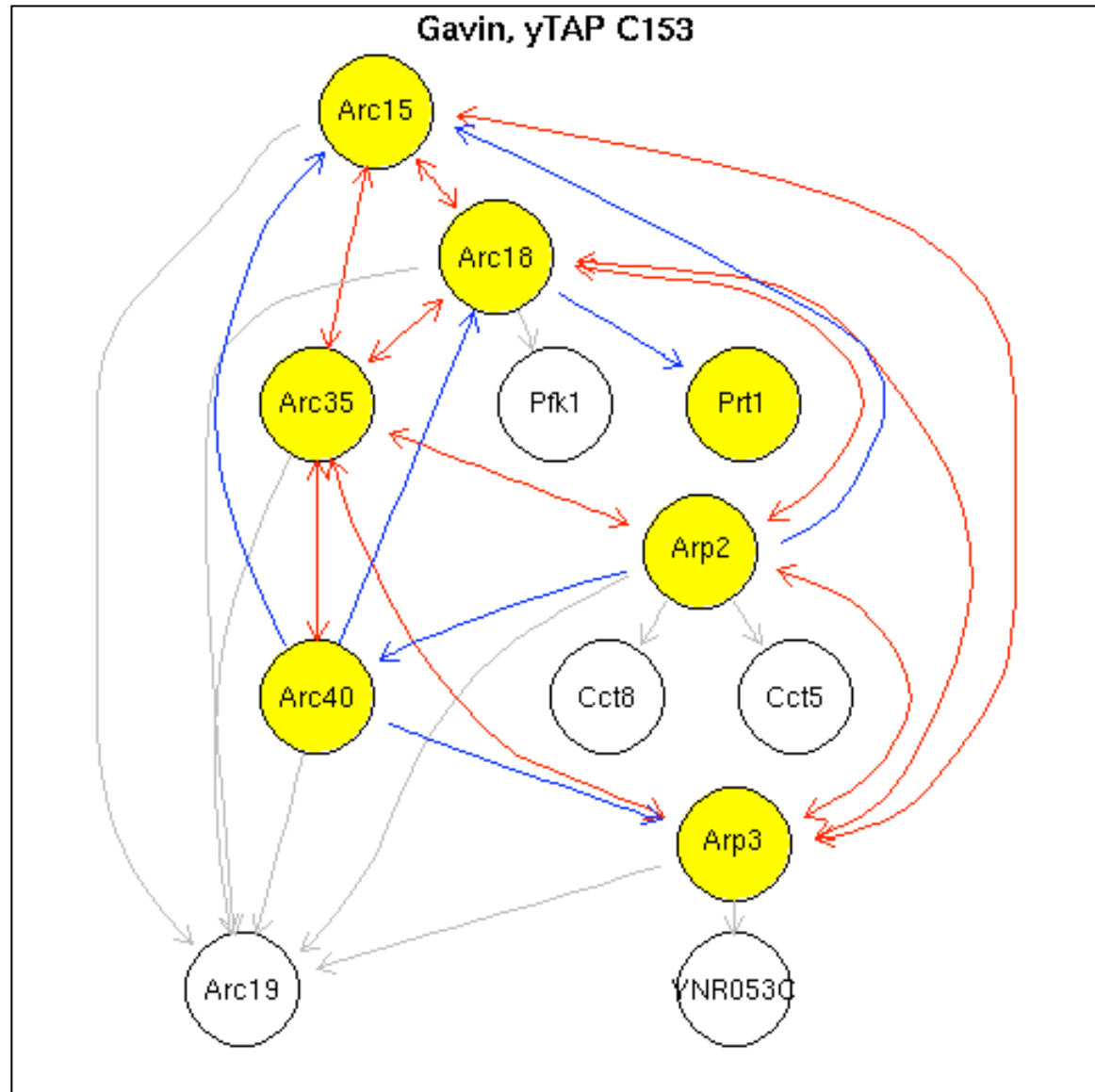
Arp2/3

Arp2/3 complex:

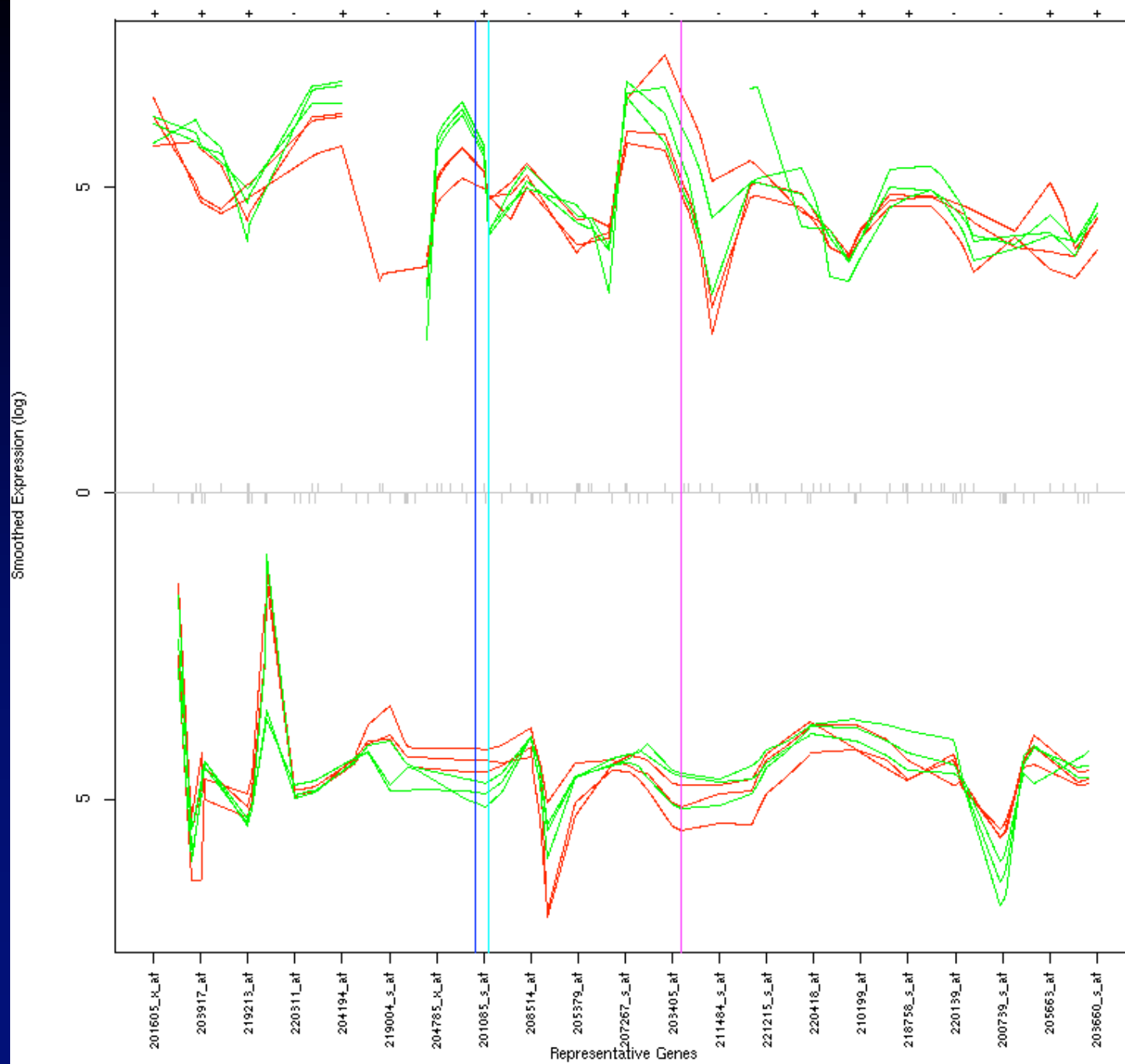
- Arp2
- Arp3
- Arc15
- Arc18
- Arc19
- Arc35
- Arc40

'The Arp2/3 complex is a stable multiprotein assembly required for the nucleation of actin filaments in all eukaryotic cells and consists of seven proteins in human and yeast.'

Winter, et al (1997). *Curr Biol.*
Higgs and Pollard (2001). *Annu Rev Biochem.*



Chromosome 21



Quality Assessment using arrayQualityMetrics

- **comprehensive QA assessment of microarrays (one color or two color)**
- **easy to browse HTML**

Machine Learning

- A new machine learning package
MLInterfaces
- goal is to provide uniform calling sequences and return values for all machine learning algorithms
- we have postpended a B (e.g. knnB)
- return values are of class **classifOutput**
- see the **MLInterfaces** vignette for more details

Publications

- **Bioconductor: Open software development for computational biology and bioinformatics, *Genome Biology* 2004, 5:R80, <http://genomebiology.com/2004/5/10/R80>**
- **Bioinformatics and Computational Biology Solutions using R and Bioconductor, Springer, 2005, R. Gentleman, V. Carey, W. Huber, R. Irizarry, S. Dudoit eds.**
- **Bioconductor Case Studies, Springer**
- **R Programming for Bioinformatics, Chapman Hall**

References

- **R** www.r-project.org, cran.r-project.org
 - software (CRAN);
 - documentation;
 - newsletter: R News;
 - mailing list.
- **Bioconductor** www.bioconductor.org
 - software, data, and documentation (vignettes);
 - training materials from short courses;
 - mailing list (please read the posting guide)