

Data Analysis Guidelines for New Microarray Platforms

::: aCGH practise with waviCGH

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Daniel Rico
drico@cniio.es



Bioinformatics Unit
CNIO

Wilting aCGH dataset

Custom aCGH arrays of cell lines from cervix squamous cell carcinomas (SSC) and adenocarcinomas (AdCAs).

The Log-Ratios were obtained from Bioconductor CGHcall package.

Journal of Pathology

J Pathol 2006; **209**: 220–230

Published online 14 March 2006 in Wiley InterScience (www.interscience.wiley.com). DOI: 10.1002/path.1966

Original Paper

Increased gene copy numbers at chromosome 20q are frequent in both squamous cell carcinomas and adenocarcinomas of the cervix

SM Wilting,¹ PJF Snijders,¹ GA Meijer,¹ B Ylstra,¹ PRLA van den IJssel,¹ AM Snijders,² DG Albertson,² J Coffa,³ JP Schouten,³ MA van de Wiel,¹ CJLM Meijer¹ and RDM Steenbergen^{1*}

¹Department of Pathology, VU University Medical Center, Amsterdam, The Netherlands

²Cancer Research Institute, University of California San Francisco, CA, USA

³MRC Holland, Amsterdam, The Netherlands

<http://wavi.bioinfo.cnio.es/>

1. Select file LogRatiosWilting.txt containing the log-ratios from the cell lines subset.
2. Enter your email and you will receive a project link (active for 5 days only!!).
3. Paper is from 2006, what genomic coordinates they used? Convert them.
4. Normalize, preprocess, and segment with any method.
5. Do the segmentation-based calling. What is behind that name?
6. Redo the calling using probability-based method (hint: Run Step Again button).
7. Calculate MCRs using Permutations.
8. Explore your results in Cytogenetic Browser, click on Ensembl links...
9. Start over with Copy Number Protocol using CallsWilting.txt file.
10. Homework: Select some MCRs and extract their genes with Biomart.

1. Select Log-Ratios protocol

5. Finally, press "Run"

2. Write you email

3. Select file

4. Genomic Coordinates: YES

The screenshot shows the waviCGH web application interface. At the top, there are three buttons: "Log Ratios", "Copy Numbers", and "Raw Data". A yellow banner says "Press Run to start". Below this is a "Run" button with a play icon. The main content area features the waviCGH logo and a "Welcome to waviCGH!" message. A sidebar on the left contains a "Help" section with instructions on data format, an "Input Data" section with fields for "eMail", "File", and "Genomic Coordinates" (set to "No"), and a list of analysis steps: "Normalization", "Pre processing", "Segmentation", "Calling", "MCR", and "Cytogenetic Browser". The main content area includes a "select your input file and then simply click:" section with buttons for "Raw Data", "Log Ratios", "Copy Numbers", and "Run". Below this is a list of capabilities after loading input data, such as "Convert genomic coordinates", "Pre-processing", "Segmentation", "Calling of Gains and Losses", "Search for Minimal Common Regions (MCRs)", "Visualize and explore", and "Karyotypes". At the bottom, there are buttons for "Run Next Step" and "Run All", along with a warning: "Please be aware that some of the methods can take a significant amount of time. Please be patient".