Introduction to the use of
Simulated bivariate flow karyogram

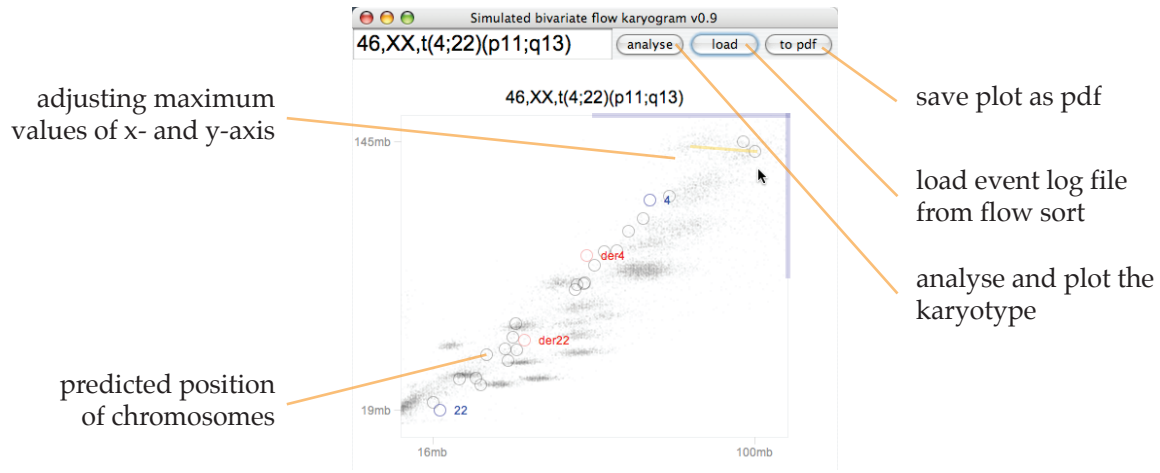
This is the one page short introduction to the once in a while average user with the need to predict the positions of derivative chromosomes from a balanced translocation in a bivariate karyogram.

Background

Mapping of translocation breakpoints is usually done by FISH using numerous probes until a split signal is detected. Using arrayCGH it is possible to detect unbalanced rearrangements, but to detect translocations it is necessary to separate the individual chromosomes. Flow sorting using DNA binding fluorescent dyes allows separation of chromosomes according to sequence characteristics i.e. chromomycin A3 binds primarily to `G-C` and Hoechst 33258 to `A-T` base pairs. By construction virtual derivative chromosomes from a karyotype it is possible to predict the fluorescence values of chromosomes, and thereby predict the location of the derivative translocation chromosomes and select the gate values for flow sorting.

Interface

The program is distributed as a Java Web start application available at http://www.wjc.ku.dk/bioinformatics and should run on most modern operating systems. Start by entering a karyotype in the syntax provided by ISCN 1995. Press analyse to plot normal and derivative chromosomes in a `GC` vs. `AT` plot. If an event log of a flow sorting is available it can be loaded in form of a tabulator separated text file. The resulting plot can be exported to a pdf file.



The event log values will most likely not fit the predicted values perfectly, therefore it is possible to adjust the axis by dragging the data. By dragging from different areas of the plot you can adjust minimum and maximum of each axis. When dragging the ends of the axis being adjusted will be highlighted.

Contact

If you have question, comments or suggestions for improvement you are welcome to contact Mads Hjorth at madsh@medgen.ku.dk

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