An Introduction to *ggbio*

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1   Introdunction

ggbio is a package for visualizing genomic data, the imporant concept underlying this package is the extension of Leland Wilkinson's grammar of graphics, this separate components into differnt part including statistical tranformatoin, geometric object, coordinate system, layout, scale and data.

R is a perfect platform for prototyping a object oriented graphic design, because Bioconductor really have nice designed data structure and powerful analytical tools. *ggbio* is built on *ggplot2* package, so almost all utils which works for *ggplot2* could directly works for *ggbio* object.

We extending the grammar, and have more interesting experimental graphics, like circular view, kayrogram view, and some specialized graphics like splicing summary and mismatch summary. We always keep fexibility to lower level API such as stat_*, geom_*, layout_* functions, and always provide a generic function `autoplot` for all-in-one usage.

2   On-line documentation

From this version of *ggbio*, I am going to move documentation and demofrom pdf to on-line version, new website is here

http://tengfei.github.com/ggbio

On that website, it contains all documentation and case studies, I will use knitr + jekyll + github pages to create this website, and still keep the reproducibility, all markdown examples parse example from the same names, and build by github into pages, markdown files are under /inst/md_example, and all examples R code are under /inst/example.

On-line documentation is google search-able and multi-media friendly, more flexible for visualization package demonstration.