

An Introduction to *ggbio*

Tengfei Yin

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1 Introduction

ggbio is a package for visualizing genomic data, the important concept underlying this package is the extension of Leland Wilkinson's grammar of graphics, this separates components into different parts including statistical transformation, geometric object, coordinate system, layout, scale and data.

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

We extend 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 flexibility 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 demo from 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.