

Introduction to VisNAB: An Interactive Toolkit for Visualizing and Exploring Genomic Data

Tengfei Yin

March 21, 2011

Contents

1	Introduction	3
2	Individule View	3
2.1	Circular View	3
2.2	Interval View	3
2.3	Alignment View	3
2.4	Stacked View	3
3	Linking for Multiple Views	3
4	Case Study	3

1 Introduction

VisNAB(VisNAB is Not A Browser) is a package developed in R, which is designed for visualization of genomic data, especially for next generation sequencing data. Besides traditional track-based views, VisNAB also aims to offer alternative views, including Bird-Eye overview, circular view, etc. At the same time, it also provides statistical cues and analytical tools for guiding scientists to find the information of interests. With support of QT library and related API in R, it's possible to make interactive graphics for visualizing and exploring huge amount of data with high performance. This toolkit with other packages in Bioconductor could form a powerful analytical pipeline for exploring the genomic data.

2 Infrastructure

We have two types of graphic parameters, one is individual graphic attributes, A *GraphicPars* class is defined to keep those attributes, such as background color, foreground color, fill color, stroke color, etc. So far, the *GraphicPars* is an environment with a set of accessors.

The other type of attributes is designed to specify observation oriented behaviour. Each observation has some extra attributes that indicate some specific status, such as selected or not, brushed or not, highlighted or not. To achieve this goal, mutable data structure is preferred, so any signal could be attached to it conveniently. For genomic data, we use *MutableRanges* package to handle this basic structure, which is a *MutableGRanges* object, this object has common accessors for *GRanges* object, and what's more, it's mutable. So signal could be attached to this data structure. For common data structure, we use *mutalist* and *mutaframe* in *plumbr* package. For more details about these mutable data structure and signal handling method, please refer to the documentation of package *MutableRanges* and *plumbr*.

visnab is a package which provides sets of views for visualization of genomic data, especially the next generation data. For fast and interactive graphics in R, we use QT API, please refer to documentation of package *qtbases* and *qtpaint* for more details.

VisnabView is a virtual class which define a top level view object in *visnab*, it contains basic information like graphic parameters, show status, etc. *QtVisnabView* is a virtual class which contains *VisnabView* and has extra information about Qt device, this object will store scene, view and rootLayer object. This feature may have potential use for integration of multiple views later.

Then for other individual views, we define specific view class, such as *IntervalView*, *CircularView*, *StackedView*, etc, which will be described in details in following sections.

3 Individule View

3.1 Circular View

3.2 Interval View

3.3 Alignment View

3.4 Stacked View

4 Linking for Multiple Views

5 Case Study

Appendix

```
> sessionInfo()
```

```
R version 2.13.0 Under development (unstable) (2011-03-07 r54691)
```

```
Platform: x86_64-unknown-linux-gnu (64-bit)
```

```
locale:
```

```
[1] en_US.utf8
```

```
attached base packages:
```

```
[1] tools      stats      graphics  grDevices  utils      datasets  methods
```

```
[8] base
```

```
other attached packages:
```

```
[1] rtracklayer_1.11.12  RCurl_1.5-0          bitops_1.0-4.1  
[4] visnab_0.0.1         MutableRanges_0.1.1  GenomicRanges_1.3.28  
[7] IRanges_1.9.27       scales_0.0.0         plumbr_0.6.2  
[10] qtpaint_0.7.18       qtbase_0.8-12
```

```
loaded via a namespace (and not attached):
```

```
[1] Biobase_2.11.10      Biostrings_2.19.17   BSgenome_1.19.5     colorspace_1.0-1  
[5] dichromat_1.2-3      munsell_0.2          plyr_1.4             RColorBrewer_1.0-2  
[9] Rsamtools_1.3.23     stringr_0.4          XML_3.2-0
```