Interactive Visualization of Genomic Data

Interfacing Qt and R

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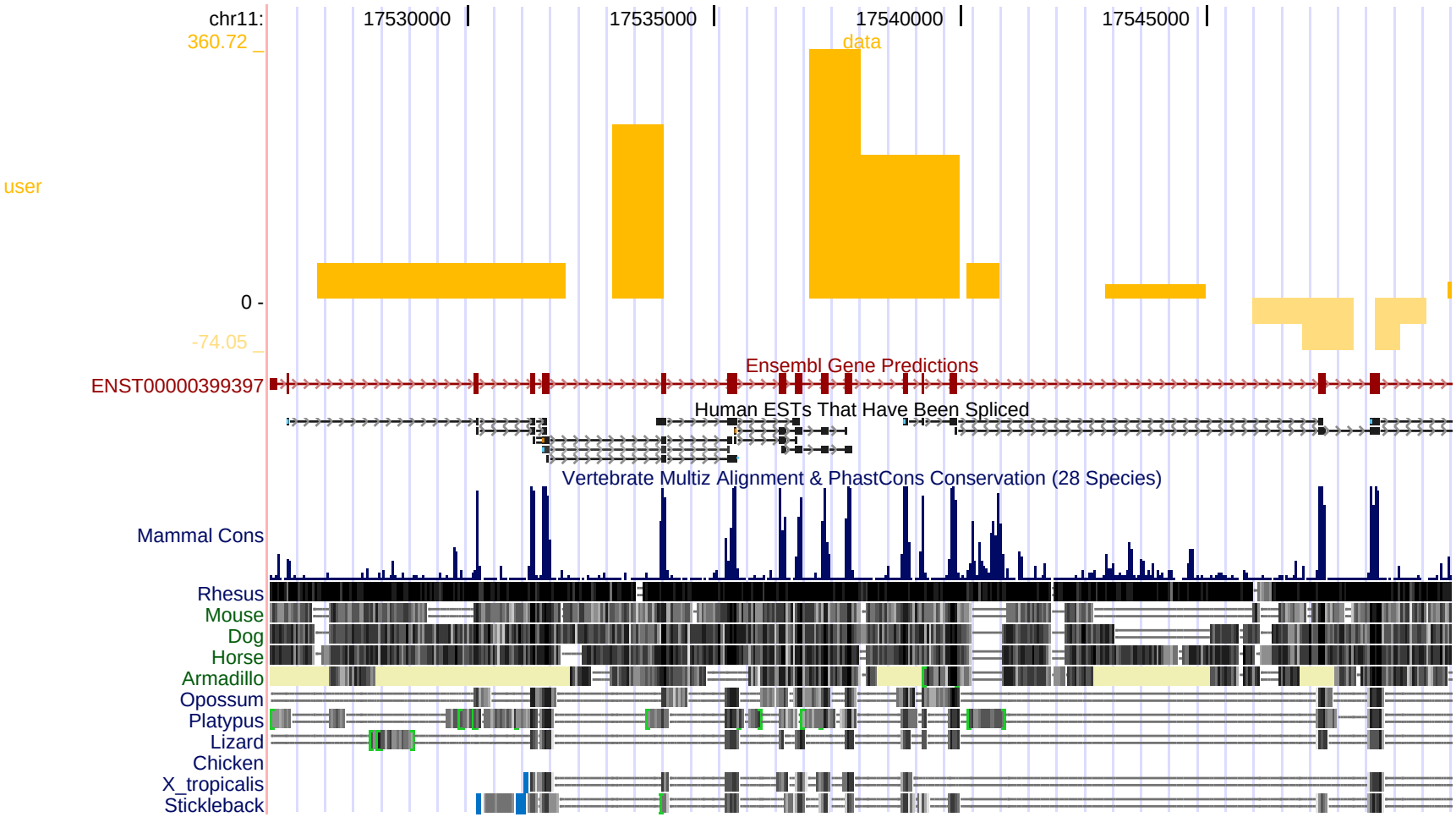
November 17, 2010

Typical Genome Browser Plot



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- Useful picture (if a bit ugly)

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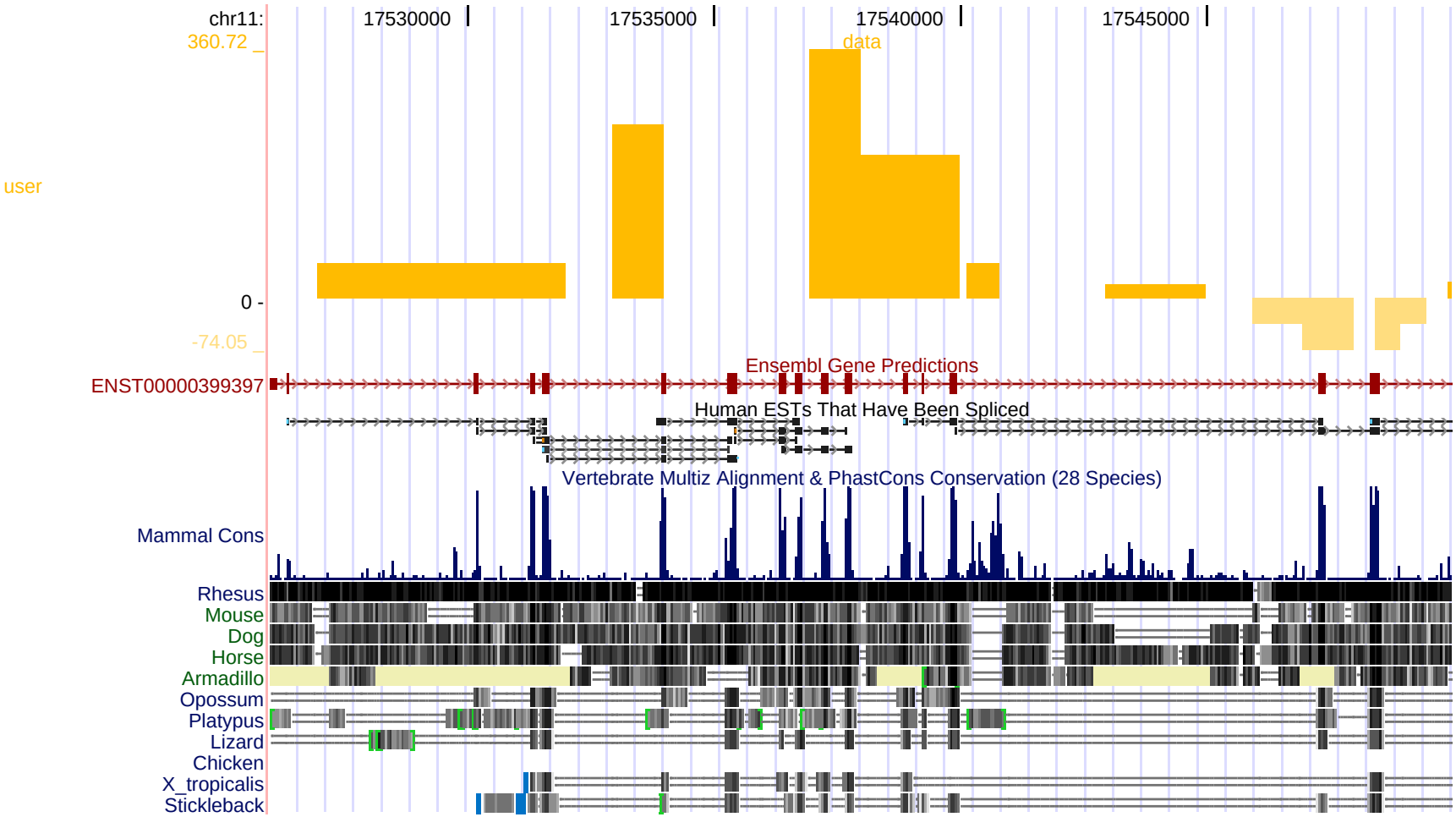

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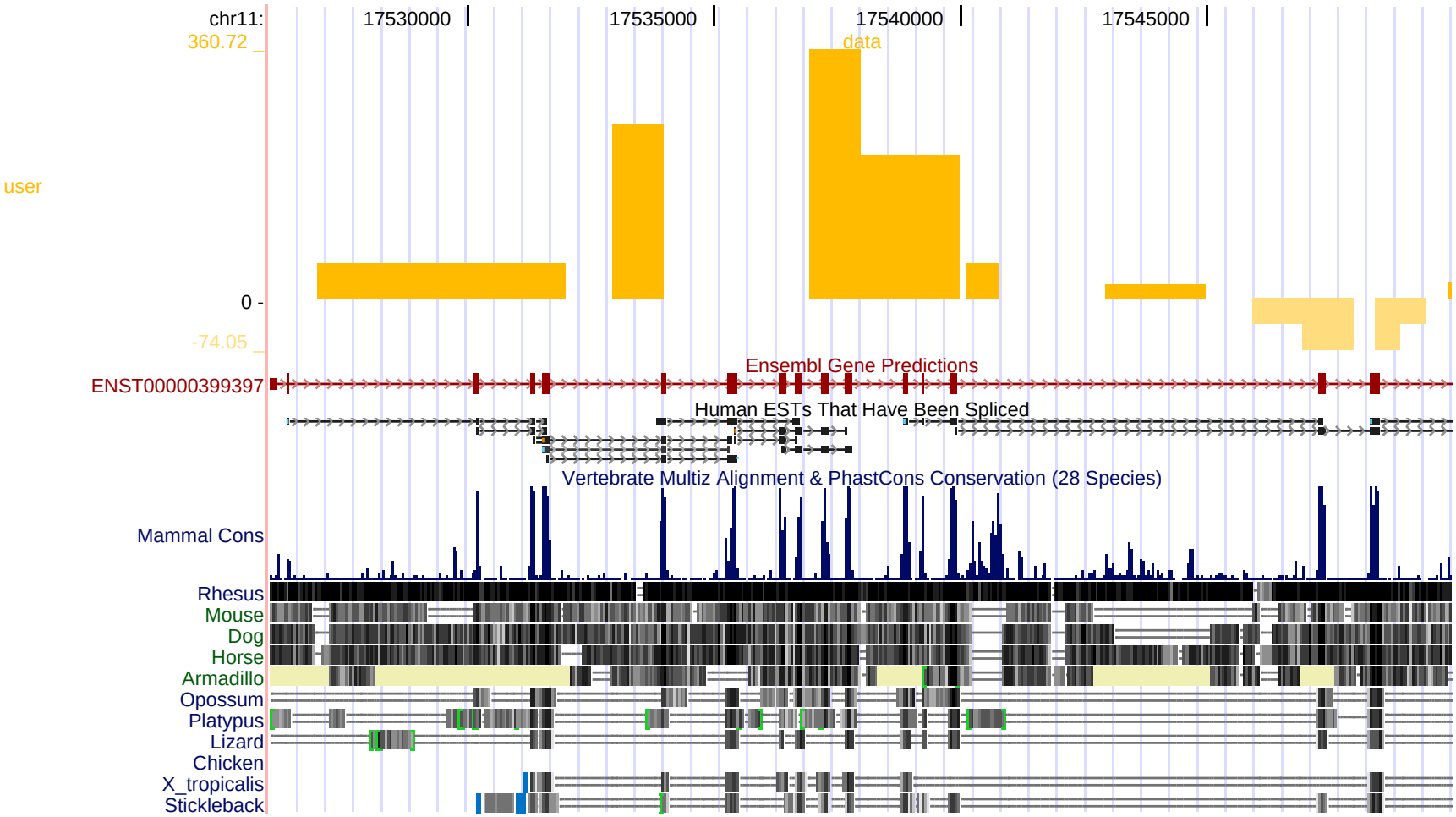

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R and Genome Browsers: *rtracklayer*

- Original goal of *rtracklayer*: abstraction around genome browsers, internal or external
- First (and still only) implementation was the UCSC Genome Browser

```
> session <- browserSession("UCSC")
> session\$user <- userTrack
> browserView(session, full = "user")
```

Thinking Outside the Browser

Genome Browser

- Look at the data in multiple, coordinated views
- Jump to the most interesting parts of the data
- Move beyond the genome axis

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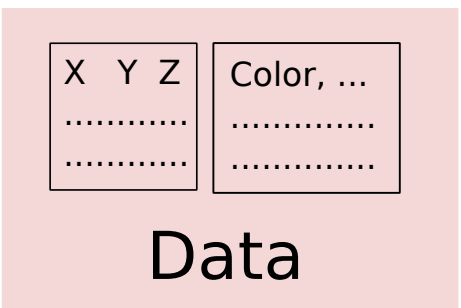
Interactive Graphics

- Many types of data
- Many types of plots, interactions
- Many preprocessing approaches, statistics, transformations, ...



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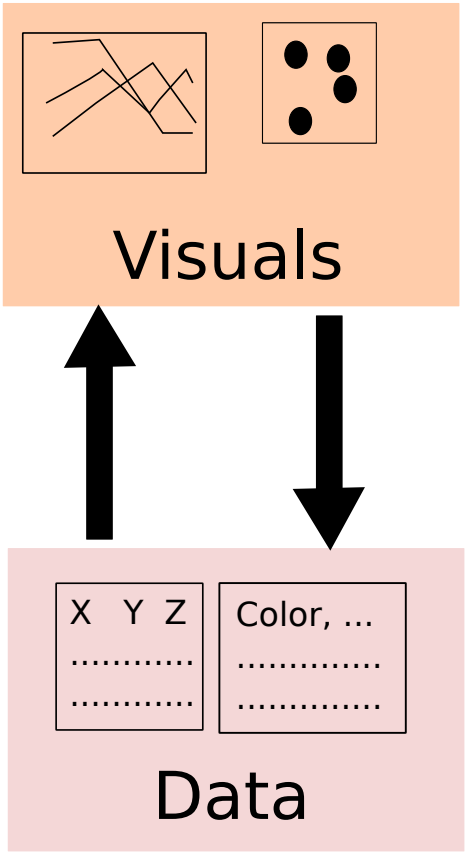

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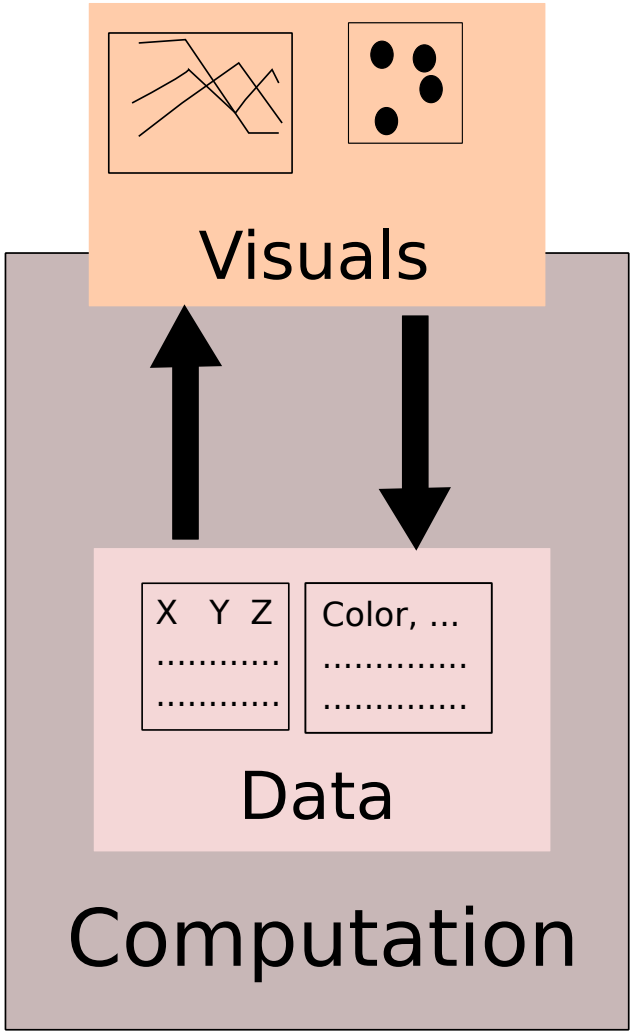

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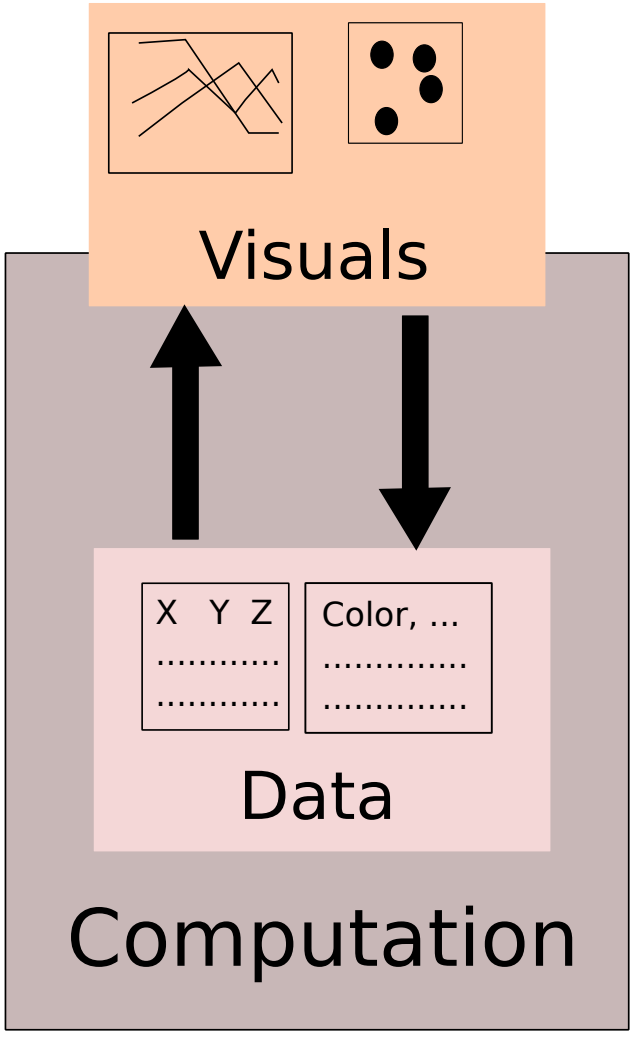
Exploring this space requires lots of rapid experimentation



Outline

Overview

- Support constructing interactive graphics "from scratch" in R
  - R draws every graphical primitive
  - R handles every user event
- Maximize performance
  - Static graphics: Be lazy, little work as possible
  - Dynamic graphics: Only redraw what needs to be redrawn
  - Interactive graphics: Quickly map actions in the plot to actions on the data
- Leave high-level graphics to other packages (e.g. mosaiq)

Optimized Rendering Layer

- Draw each unique glyph only once, blit to buffer
- Use hardware (OpenGL) whenever possible
  - Rarely-used GL_POINT_SPRITE mode draws glyphs (small textures) at roughly same rate as GL_POINTS (fastest primitive)
  - Drawing cached as texture through FBO

Layered Buffering Strategy

- Plot updates tend to be incremental, only a part of the plot changes
- Divide the plot elements into layers, such that elements within the same layer tend to change together
- Cache each layer in a buffer, only redraw when necessary
- Compose plot by compositing/stacking the layers

Spatial Indexing

- Spatial indices (e.g. quad tree) provide fast ($O(log(n))$) lookup of data elements from coordinates
- Lazily update spatial index whenever element positions have changed and R requests a lookup
- Populate spatial index by passing a special renderer to the R drawing callback, thus indexing is transparent to R user
- Sometimes additional or separate logic is required (e.g. area plots, smooth scatter)

Outline

Qt

- C++ application library for GUIs, graphics and lots more
- Professionally developed, open-source, maintained by Nokia
- Basis of *KDE* desktop on Linux, *MeeGo*
- Official installer for all major platforms

Qt Modules

Core	Basic utilties, collections, threads, I/O, ...
Gui	Widgets, models, canvas etc for graphical user interfaces
OpenGL	Convenience layer (e.g., 2D drawing API) over OpenGL
Webkit	Embeddable HTML renderer (shared with Safari, Chrome)
Others	DBus, Designer, Help, Multimedia, Network, Xml, Script (Javascript), Sql, Svg, Declarative (UI language)

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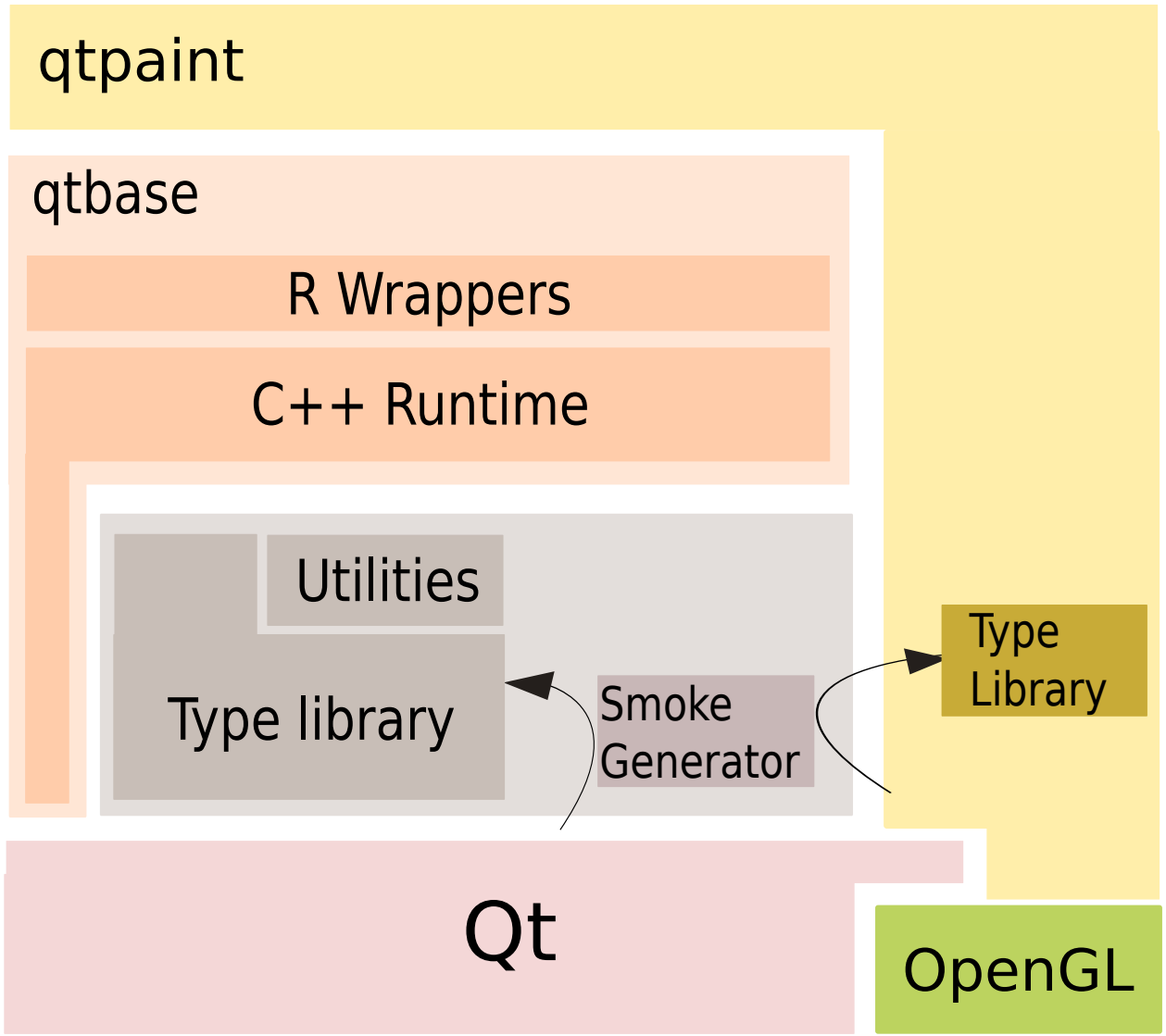
The *qtpaint* Package



The *qtpaint* Package

- **qtpaint** implements our approach using QGraphicsView
- Each layer of the plot corresponds to a canvas item, which is cached and composited by *Qt*
- In a callback, R draws canvas items through optimized renderer based on QPainter
- All user events handled in R, using *Qt*'s spatial index for fast mapping of event coordinates to data elements

Impressionistic Example: Interactive Scatterplot

Code

```
circle <- qglyphCircle()
scatterplot <- function(item, painter) {
  qdrawGlyph(painter, circle, df[,1], df[,2],
             fill = fill)
}
scene <- qscene()
root <- qlayer(scene)
points <- qlayer(root, scatterplot,
                 hoverMove = pointIdentifier)
labels <- qlayer(root, labeler, cache = FALSE)
view <- qplotView(scene = scene, opengl = TRUE)
print(view)
```

VisNAB: VisNAB is Not A Browser

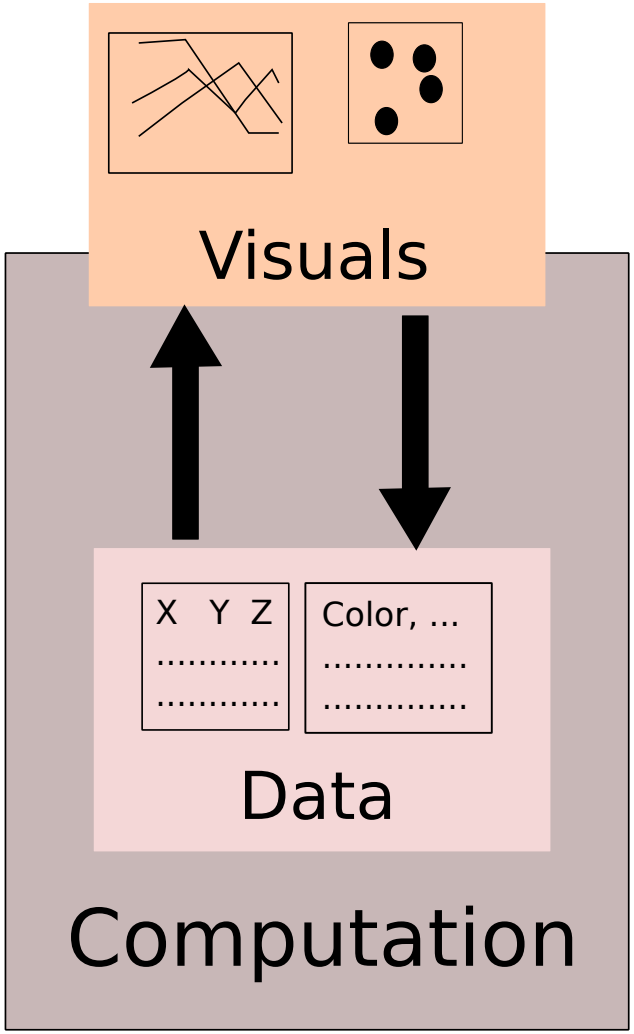
- Toolbox for interactive visualization of genomic data in R
- Joint work with Teng Fei Yin (intern), Nicholas Lewin-Koh
- Leverages Bioconductor infrastructure

  Preprocessing *ShortRead*, *Biostrings*
  Data Manipulation *IRanges*
- Relies on *plumbr* package from GGobi foundation for its reference-based data model
- Demonstration on ChIP-seq data

Outline

Data and Computation: The Pipeline Pattern

- Every interactive graphics software needs to compute on the data
- During drawing, and in response to user input
- Data must be mutable, not copy-on-write, so that graphic implicitly updates upon user changes
- *plumbr* package provides a mutable data frame and list



Interval Data into Pipeline

- Need mutable data structures specific for interval data
- *MutableRanges* extends data structures in *IRanges* and *GenomicRanges* using "R5" reference classes
- Defines *Signal* class for registering R functions as callbacks that are invoked upon data changes

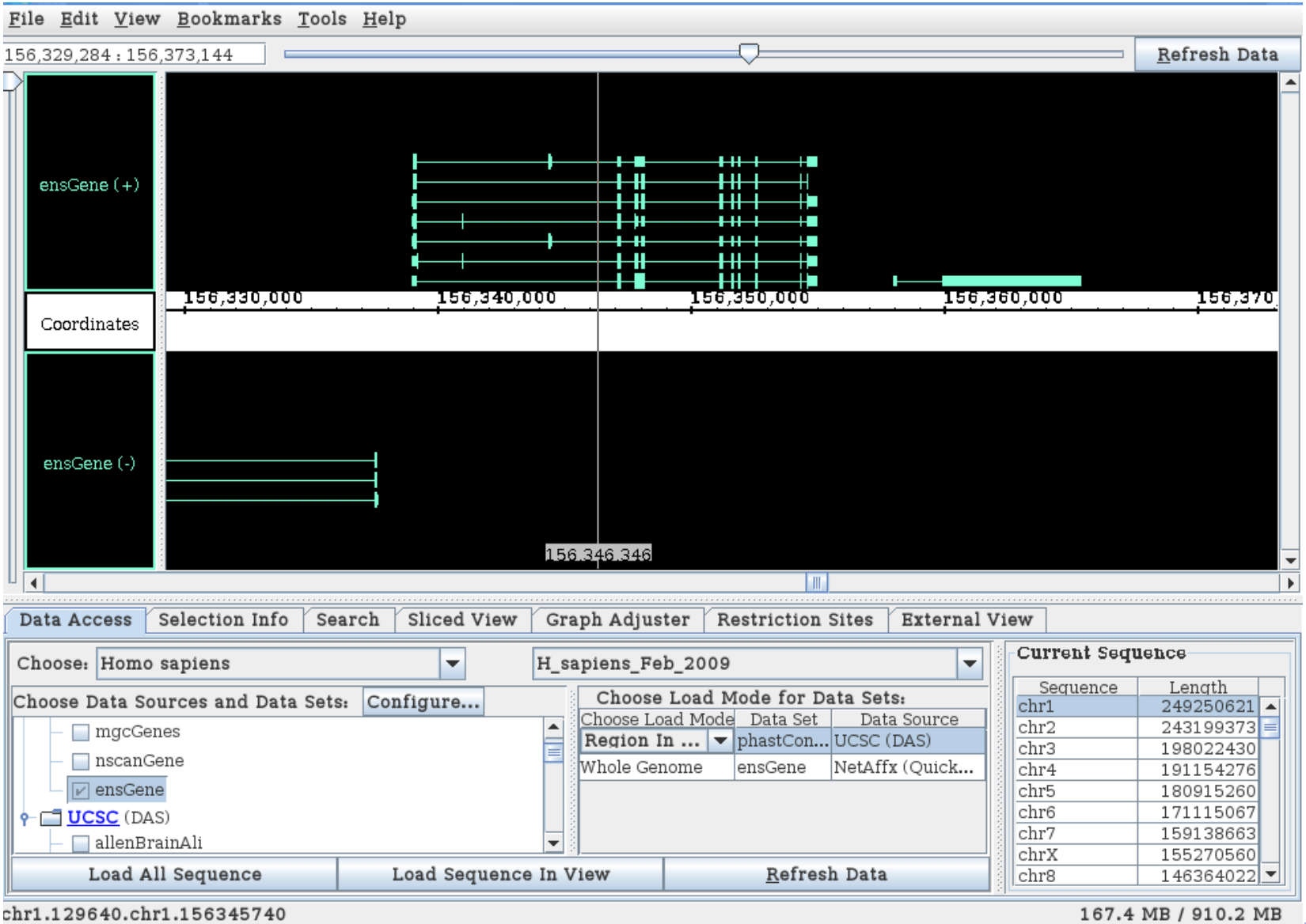
```
connect(mutableRanges, "rangesChanged",
        function(i) { ... })
```

Outline

Examples of Existing Browsers

- Web-based
  - *UCSC* (restrictive license)
  - *Ensembl* (open)
- Desktop (Java, open-source)
  - *IGB* (Integrated Genome Browser, Affy)
  - *IGV* (Integrative Genomics Viewer, Broad)

IGB: Integrated Genome Browser



Key *IGB* Features

Data All standard track formats, including SAM/BAM, also DAS and QuickLoad

Visualization Many plot types, combining plots, smooth zoom, some limited linked views (slice, external)

Computation Coverage, thresholding, track arithmetic

Future *IGB* Features

Adaptability Plugins, more configurable GUI

Visualization Multiple views

Computation More operations on tracks

IGB + R Integration: Requirements

Data Set genome, load URL, synchronize through shared data models (mutable ranges)

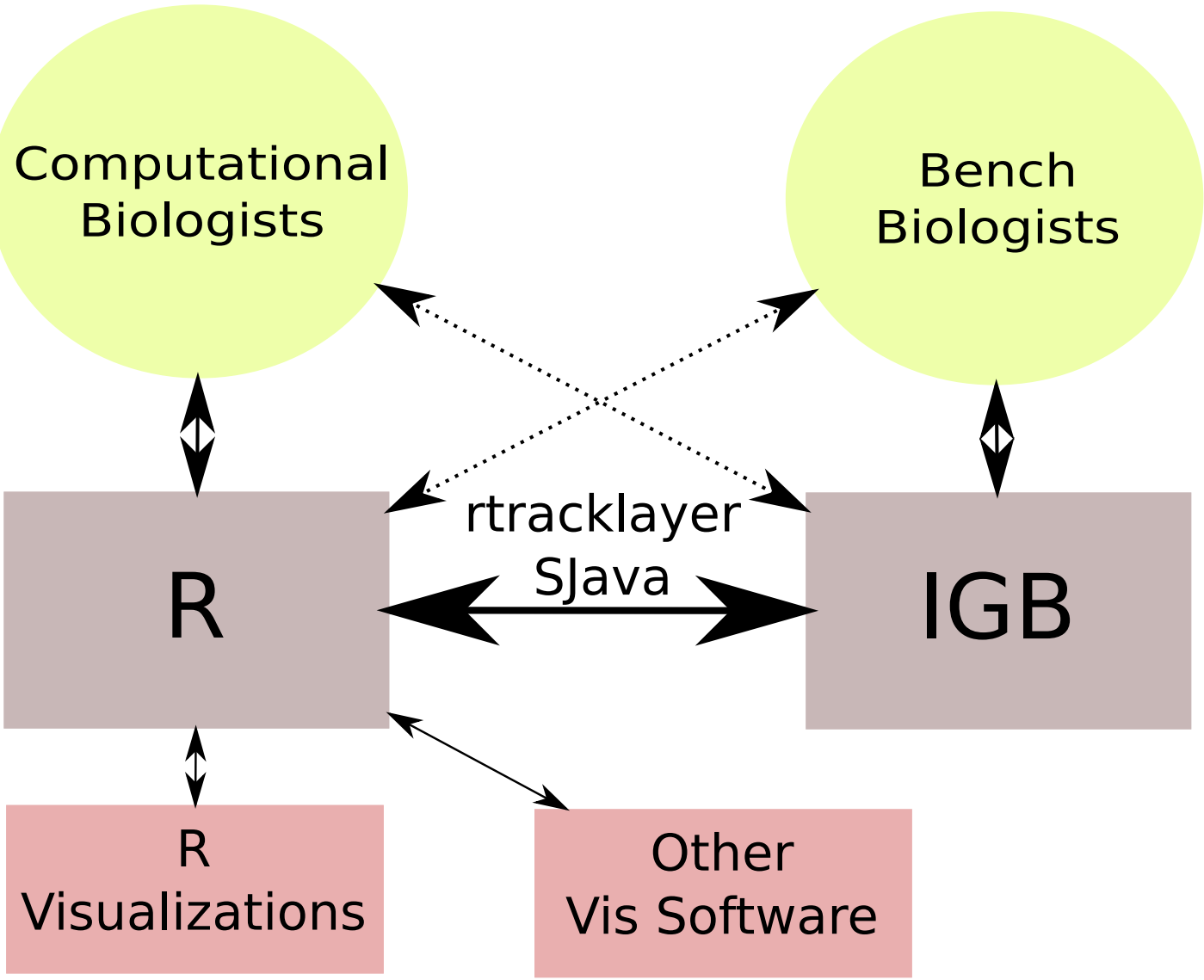
Visualization Set view range, select features, control tier visibility, respond to changes in range and selection, customize

GUI Add R-driven actions, customize

IGB + R Integration: Design

- Direct embedding through R and Java bridge (*SJava*).
- Embedding should be bi-directional
- Implement *rtracklayer* API for basic operations

Big Picture Design



Availability

qtinterfaces http://github.com/ggobi

visnab http://github.com/tengfei/visnab

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Robert Gentleman

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