The Pviz User Guide

Renan Sauteraud*

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Contents

*rsautera@fhcrc.org

1 Example of plot

```
> library(HIV.db)
> library(Pviz)
> ################### Get reference scale from alignment
> alignObj<-readAlign()
> refScale<-alignObj[[1]]
> refSeq<-alignObj[[2]]
> ################### Load database
> HIV_db<-loadFeatures(ref="env")
> envBase<-getFeature(HIV_db)
> envStart=getHXB2Coordinates(envBase)[1,][1]
> envEnd=getHXB2Coordinates(envBase)[1,][2]
> ################### Getting Features from database for annotation
> proteins<-getFeature(HIV_db,category="protein",start=envStart,end=envEnd,frame=getF
> antis<-getEpitope(envBase,name=c("VRC01"))
> helix<-getChildren(envBase,category=c("helix"))

> ## ProteinAxisTrack using the extended coordinates system
> rpext<-ProteinAxisTrack(littleTicks=TRUE)
> ## ProteinAxisTrack with coordinates relative to the reference
> rpref<-ProteinAxisTrack(refScale=refScale, adNC=TRUE)

> sTrack<-SequenceTrack(refSeq)

> data(pepMicroarrayEx)
> p1Track<-ProbeTrack(pepMicroarrayEx$probeSeq, pepMicroarrayEx$probeFreq, pepMicroar
+                 , protein="gp120", name="sequence(B)")

> a2Track<-ATrack(id=proteins@values@unlistData@listData[["name"]],start=start(protei
> a3Track<-ATrack(id=helix@values@unlistData@listData[["name"]],start=start(helix),en
> a6Track<-ATrack(id=antis@values@unlistData@listData[["name"]],start=start(antis),en

> data(pepExprEx)
> library(IRanges)
> d6Track<-DTrack(range=IRanges(start=pepExprEx$dPos,width=1),groups=rownames(pepExpr

> plotTracks(trackList=c(rpext,rpref,sTrack,a2Track,a3Track,a6Track,p1Track,d6Track),
```

2 Using the extended coordinates system

The extended coordinate system is based on a multiple alignment. It is a scale from 0 to the length of the alignmenat (i.e: reference sequence + gaps).

The refScale is a scale used to translate coordinates between the extended system and the normal system (which is based uniquely on the reference sequence length).

2.1 Data formating

In the following examples, hxb2 is the reference sequence and is aligned with different subtypes.

First, get the refScale:

```
> alignObj<-readAlign(filename=system.file("extdata/alignment.fasta", package="Pviz")
> refScale<-alignObj[[1]]
> refSeq<-alignObj[[2]]
```

Now, the refScale can be used to translate coordiantes into the extended system.

Example of loading HIV_db using extended coordinates.

```
> library(HIV.db)
> HIV_db<-loadFeatures(ref="env", refScale=refScale)
> envBase<-getFeature(HIV_db)
```

The positions in envBase are the ones observed in the alignment.

To translate all the positions in pep_hxb2, use convertPep().

```
> data(pep_hxb2)
> nrd<-convertPep(rd=pep_hxb2)
```

nrd is pep_hxb2 with updated ranges, aligned and trimmed columns.

To convert coordinates into the extended system, use coord2ext() with the refScale defined earlier:

```
> start<-coord2ext(c(200,450), ref=refScale)
> start

[1] 223 474
```

2.2 Plotting with both coordinates system

All objects used to create tracks should be in extended coordinate system.

```
> sTrack<-SequenceTrack(refSeq)
> pax1<-ProteinAxisTrack()
> pax2<-ProteinAxisTrack(refScale=refScale, col.gap="blue")
> proteins<-getFeature(HIV_db,category="protein",start=envStart,end=envEnd,frame=getF
> aTrack<-ATrack(id=proteins@values@unlistData@listData$name,start=start(proteins),en
> aTrack<-ATrack(id=helix@values@unlistData@listData$name,start=start(helix),end=end(
> plotTracks(c(pax1,pax2,sTrack,aTrack), from=1, to=160)
```

The first axis track displays the extended scale, while the second displays the reference coordinates, it also shows the gaps in the reference sequence with respect of the alignment.