Visualising ChIP-seq data – tracktables

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Abstract

tracktables provides a set of tools to organise visualise your ChIP-seq data.

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1 Standard workflow

1.1 Quick start

Simple guide to the two main sets of functions in tracktables. The first set of functions are for summarising and visualising coverage of genomic regions across samples and gene/genomic-interval sets. The regionPlot function calculates normalised coverage across or over user specified regions to produce *ChIPprofile* object.

```
print("Coming Soon!")
```