

# DNAPlotR package example (version 0.1)

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## Abstract

This is a collection of examples of usage for the **DNAPlotR** package.

*Keywords:* visualization, alignment, display, genome, DNA, sequence, multiple sequence alignment, reference sequence.

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## 1. General description

This is an example of using the **DNAPlotR** package in R.

```
> set.seed(1234)
> fakeSeqs<-createFakeDNA(5000,500)
> refSeq<-fakeSeqs[1]
> fakeSeqs<-fakeSeqs[-1]
> species<-sprintf('Species %s',sub('[0-9]','$',' ',names(fakeSeqs)))
> par(mar=c(3.5,4.4,.5,7),mgp=c(2.5,1,0))
> dummy<-plotDNA(fakeSeqs,groups=species)
```

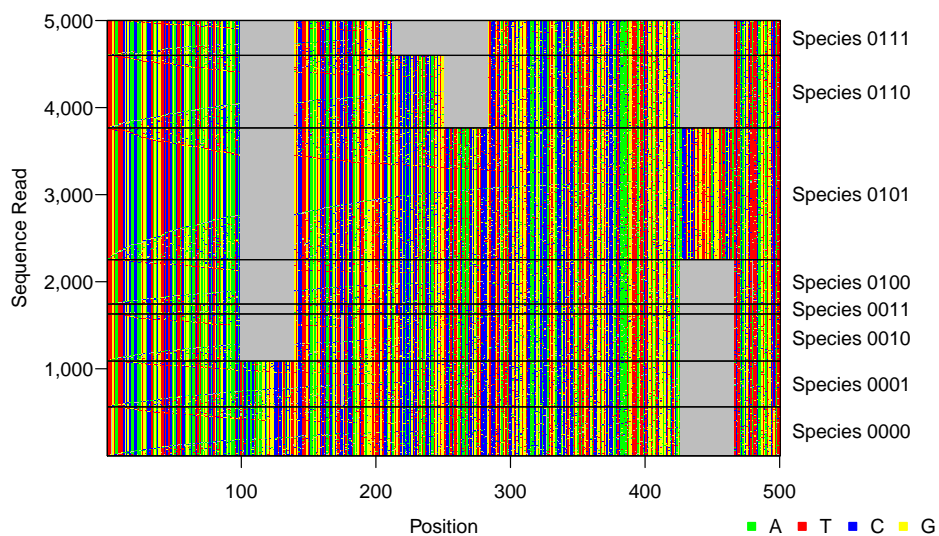


Figure 1: An example of a DNA plot

**Affiliation:**

Github: <http://github.com/sherrillmix/dnaplotr>