Submitting your organism to *GenomeInfoDb*

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This document is meant for package developers wanting to submit an organism which does not already exist in *Genome-InfoDb*, to be a part of *GenomeInfoDb*.

1 Background

GenomeInfoDb provides a multitude of functions to subset and access seqName mappings and styles associated with an organism. One can use the supplementary manual "GenomeInfoDb.pdf" to see such functions. Alternately if there is no support for an organism for one's choice, one can submit a tab delimited file (as detailed by the sections below) to request their favorite organism to become a part of GenomeInfoDb package.

2 Support for existing organisms

GenomeInfoDb already provides support for a multitude of organisms, to see a detailed list of organism and the supported seqname styles associated with those organism, one can simply run :

```
library(GenomeInfoDb)
names(genomeStyles())

##  [1] "Arabidopsis_thaliana"    "Caenorhabditis_elegans"   "Canis_familiaris"
##  [4] "Cyanidioschyzon_merolae" "Drosophila_melanogaster"  "Homo_sapiens"
##  [7] "Mus_musculus"            "Oryza_sativa"             "Populus_trichocarpa"
## [10] "Rattus_norvegicus"       "Saccharomyces_cerevisiae" "Zea_mays"
```

3 File format for new organism

If your favorite organism does not exist in the above list, one can submit a tab-delimited file in the following format and request for your organism to be added to *GenomeInfoDb*

1. The file name should be in the following format: 'genus_species.txt'
2. The columns should be tab-delimited in the following order
   - circular
   - auto
   - sex
   - 1 column per seqname style and 1 row per chromosome name (not all chromosomes of a given organism necessarily belong to the mapping) where circular denotes all the circular chromosomes, auto denotes all the autosomes and sex denotes all the allosomes or sex chromosomes.
3. The entries should be in T/F format for columns circular, auto and sex.

4 Example File

One can look at existing organism files under GenomeInfoDb/extdata/dataFiles in their R/library to get a further idea about the format of files.

5 Contacting us with your new file

Once your file is ready, Please send your file to:

```
packageDescription("GenomeInfoDb")$Maintainer
```

```
## [1] "Bioconductor Package Maintainer <maintainer@bioconductor.org>"
```