GenomeInfoDbData

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`GenomeInfoDb-package` *Species and taxonomy ID look up tables*

Description

This package contains one mapping object:

- specData: A data frame with columns 'tax_id', 'genus', and 'species'. Used to retrieve taxonomy ID by species and returns list of available species.

Usage

```
data(specData)
```

Details

Scripts to generate these files are in GenomeInfoDbData/inst/scripts. All originate from the taxdummp download at ftp://ftp.ncbi.nih.gov/pub/taxonomy/taxdump.tar.gz.

Author(s)

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Examples

```
data(specData)
sapply(specData, class)   #      tax_id       genus     species
     #   "integer"    "factor" "character"

subset(specData, c(genus=="Homo" &  species=="sapiens"))$tax_id # [1] 9606
```

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