GenomeInfoDbData

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

Description

This package contains three mapping objects:

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

- validTaxIds: An integer vector of valid taxonomy IDs created from `speciesMap`. Used internally for quick taxonomy ID look ups.

- specData: A data frame with columns 'taxon' and 'species'. Used internally to retrieve species by taxonomy ID.

Usage

```
data(speciesMap)
data(validTaxIds)
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(speciesMap)
sapply(speciesMap, class)   #       taxon     species
                            #    "integer" "character"
subset(speciesMap, species=="Homo sapiens")$taxon # [1] 9606
```

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