# Package: neuroimaGene (via r-universe)

May 30, 2026

**Type** Package

**Title** Transcriptomic Atlas of Neuroimaging Derived Phenotypes

**Version** 0.1.4

**Maintainer** Xavier Bledsoe <`xbledsoe22@gmail.com`>

**Description** Contains functions to query and visualize the Neuroimaging features associated with genetically regulated gene expression (GReX). The primary utility, neuroimaGene(), relies on a list of user-defined genes and returns a table of neuroimaging features (NIDPs) associated with each gene. This resource is designed to assist in the interpretation of genome-wide and transcriptome-wide association studies that evaluate brain related traits. Bledsoe (2024) <doi:10.1016/j.ajhg.2024.06.002>. In addition there are several visualization functions that generate summary plots and 2-dimensional visualizations of regional brain measures. Mowinckel (2020).

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**Imports** data.table, ggplot2, DBI, stringr, ggseg, sf, RSQLite

**Depends** R (>= 3.5.0)

**RoxygenNote** 7.3.3

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Config/pak/sysreqs** libabsl-dev cmake libgdal-dev gdal-bin libgeos-dev libicu-dev libssl-dev libproj-dev libsqlite3-dev libudunits2-dev

**Repository** https://xbledsoe.r-universe.dev

**Date/Publication** 2026-04-29 18:53:12 UTC

**RemoteUrl** https://github.com/cran/neuroimaGene

**RemoteRef** HEAD

**RemoteSha** 97229eb655b487a3f005a4c4bbe6e865d40bc94d

# Contents

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## anno *NIDP annotation data*

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### Description

annotation data for all NIDPs taken from the UKbiobank

### Format

A data.table with 10 columns and 3935 rows:

**gwas_phenotype** character: UKB-derived neuroimaging derived phenotype (NIDP)

**modality** character: MRI neuroimaging modality

**atlas** character: neuroimaging cortical atlas

**side** character: right or left hemisphere or midline/whole brain

**primary** character: primary cortical region

**secondary** character: secondary cortical region

**region** character: named region of the brain

**measurement** character: morphology measurement

**fMRI_node_1** character: fMRI node 1

**fMRI_node_2** character: fMRI node 2

**NIDP** character: user-friendly name for each NIDP

### Value

This script has no return. This is a documentation file for the annotation dataset for all neuroimaging derived phenotypes.

### Source

Bledsoe, X. (2024) A transcriptomic atlas of the human brain reveals genetically determined aspects of neuropsychiatric health

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## `check_db` *Check neuroimaGene database downloaded*

### Description

Check if the NeuroimaGene database exists in the proper location prior to running the query and prompt user to download if not.

### Usage

```
check_db(timeout = 900, localdb = NA)
```

### Arguments

| | |
|---|---|
| `timeout` | time to spend downloading the NeuroimaGene database in seconds (default = 900) |
| `localdb` | path to local copy of NeuroimaGenefast.db file (default = NA) |

### Value

no return value, called to give information on status of neuroimaGene database and prompt user the user to download if resource file is missing.

### Examples

```
check_db(timeout = 600)
```

---

## `fs_anno` *NIDP freesurfer annotation data*

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### Description

Freesurfer names for select cortical and subcortical NIDPs

### Usage

```
data(fs_anno)
```

### Format

A data.table with 7 columns and 890 rows:

**gwas_phenotype** character: UKB-derived neuroimaging derived phenotype

**atl** character: neuroimaging cortical atlas

**hemisphere** character: right or left hemisphere or midline/whole brain

**secondary** character: secondary cortical region

**fs_name** character: freesurfer name

**label** character: label name for the region

**atlas** character: freesurfer name for neuroimaging cortical atlas

### Value

This script has no return. This is a documentation file for the annotation dataset for all neuroimaging derived phenotypes in the fsbrain package.

### Source

Bledsoe, X. (2024) A transcriptomic atlas of the human brain reveals genetically determined aspects of neuropsychiatric health

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## `listNIDPs` *List NIDPs*

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### Description

Supplies a list of all NIDPs by name for any given modality or atlas

### Usage

```
listNIDPs(modality = NA, atlas = NA, filename = NA, verbose = FALSE)
```

### Arguments

| | |
|---|---|
| `modality` | Neuroimaging modality. Defaults to NA; see README for additional options |
| `atlas` | Neuroimaging parcellation atlas for NIDP query. Defaults to NA; see README for additional options |
| `filename` | optional filename for writing data to a table |
| `verbose` | print runtime messages to R console. Default to FALSE |

### Value

a list of NIDP names satisfying the required criteria

### Examples

```
dk_names <- listNIDPs(modality = 'T1', atlas = 'Desikan')
```

---

## `neuro_vis` *2D visualization plot of a neuroimaGene object*

### Description

Generates a 2D visualization plot of the neuroimaGene object. Neuroimaging regions are defined by the atlas parameter and colored according to the magnitude and direction of the aggregate effect from each gene in the NeuroimaGene object. Colors can be defined by the user.

### Usage

```
neuro_vis(
  ng_obj,
  atlas = "Desikan",
  lowcol = "red2",
  midcol = "white",
  highcol = "royalblue2",
  title = NA
)
```

### Arguments

| | |
|---|---|
| `ng_obj` | NeuroimaGene object produced by neuroimaGene() function |
| `atlas` | desired atlas for visualization. Desikan (default), Subcortex, DKT, Destrieux. |
| `lowcol` | color for low end of Zscore spectrum. Default is red |
| `midcol` | color for middle of Zscore spectrum. Default is white |
| `highcol` | color for top end of Zscore spectrum. Default is blue |
| `title` | optional title tag for the plot |

### Value

class: ggplot object depicting 2D visualization of the NIDPs from the neuroimaGene object portrayed on the brain and shaded by mean effect size.

### Examples

```
gene_list <- c('TRIM35', 'PROSER3', 'EXOSC6', 'PICK1', 'UPK1A', 'ESPNL', 'ZIC4')
ng <- neuroimaGene(gene_list, atlas = NA, mtc = 'BH', vignette = TRUE)
neuro_vis(ng, atlas = 'DKT')
```

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## `neuroimaGene` *Main neuroimaGene query*

### Description

Using a user supplied vector of genes (Ensembl ID's or HUGO names), this function queries the NeuroimaGene resource for all statistically significant GReX-NIDP associations and returns all findings as a data.table.

### Usage

```
neuroimaGene(
  gene_list,
  modality = "T1",
  atlas = "Desikan",
  mtc = "BH",
  nidps = NA,
  filename = NA,
  verbose = FALSE,
  vignette = FALSE
)
```

### Arguments

| | |
|---|---|
| `gene_list` | List of genes to work as inputs. There are no defaults. |
| `modality` | Neuroimaging modality for NIDP query. Defaults to T1 structural NIDPs. Other common options include 'dMRI' for diffusion MRI imaging and 'fMRI' for fucntional MRI image results. |
| `atlas` | Neuroimaging parcellation atlas for NIDP query. Defaults to Desikan structural atlas. Common T1 atlases include the 'DKT', and 'Destrieux' cortical atlases and 'Subcortex' for freesurfer parcellation of subrotical regions. See package documentation or vignette for full list. |

| | |
|---|---|
| `mtc` | Statistical multiple testing correction for NIDP query. This defaults to 'BH' for the Benjamini Hochberg False Discovery Rate. Other options include 'BF' for the bonferroni family wise error rate and 'nom' for nominal findings at pvalue <= 0.05. |
| `nidps` | optional user defined vector of target NIDPs to query. Specific NIDP names can be obtained from the listNIDPnames() function. Use of this parameter overrides the multiple testing correction, returning all nominally significant findings. |
| `filename` | optional user defined path/filename to which the script will write the nueroimaGene output data table. |
| `verbose` | print runtime messages to R console. Default to FALSE |
| `vignette` | use for building vignette on installation. Default to FALSE |

### Value

a neuroimaGene object: data table with all significant associations between the user provided genes and the UKB NIDPs satisfying the multiple testing correction and atlas/modality/name filters.

### Examples

```
gene_list <- c('TRIM35', 'PROSER3', 'EXOSC6', 'PICK1', 'UPK1A', 'ESPNL', 'ZIC4')
ng <- neuroimaGene(gene_list, atlas = NA, mtc = 'BH', vignette = TRUE)
```

---

## `ng_vignette` *NeuroimaGene object for vignette illustration*

### Description

NeuroimaGene data table containing select associations used in the package vignette.

### Usage

```
data(ng_vignette)
```

### Format

A data.table with 6 columns and 3824 rows:

**gene** character: ENSEMBL Gene ID

**gene_name** character: HUGO gene name

**gwas_phenotype** character: neuroimaging derived phenotype

**training_model** character: JTI derived tissue gene expression model

**zscore** numeric: normalized effect size of GReX on NIDP morphology

**mod_BHpval** character: Benjamini Hochberg corrected pvalue corrected by modality

### Value

This script has no return. This is a documentation file for the neuroimaGene data subset required to build the vignette.

### Source

Bledsoe, X. (2024) A transcriptomic atlas of the human brain reveals genetically determined aspects of neuropsychiatric health

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## `plot_gnNIDP` *Gene by NIDP summary plot of neuroimaGene object*

### Description

Generate overview plot of the neuroimagene object according to gene/NIDP pair

### Usage

```
plot_gnNIDP(
  ng_obj,
  maxNidps = 20,
  maxGns = 15,
  title = NA,
  shortnames = TRUE,
  verbose = FALSE
)
```

### Arguments

| | |
|---|---|
| `ng_obj` | NeuroimaGene object |
| `maxNidps` | maximum number of NIDPs to visualize. default=20 |
| `maxGns` | maximum number of genes to visualize. default=15 |
| `title` | optional title tag for the plot |
| `shortnames` | optional boolean tag for simplified names. Default to TRUE |
| `verbose` | print runtime messages to R console. Default to FALSE |

### Value

a ggplot class heatmap showing tissue models per NIDP/Gene pair

### Examples

```
gene_list <- c('TRIM35', 'PROSER3', 'EXOSC6', 'PICK1', 'UPK1A', 'ESPNL', 'ZIC4')
ng <- neuroimaGene(gene_list, atlas = NA, mtc = 'BH', vignette = TRUE)
plot_gnNIDP(ng)
```

## `plot_gns` *Gene summary plot of neuroimaGene object*

### Description

Generates an overview plot of the neuroimaGene object according to each gene input.

### Usage

```
plot_gns(ng_obj, maxGns = 15, title = NA, verbose = FALSE)
```

### Arguments

| | |
|---|---|
| `ng_obj` | NeuroimaGene Object |
| `maxGns` | maximum number of genes to visualize. default=15 |
| `title` | optional title tag for the plot |
| `verbose` | print runtime messages to R console. Default to FALSE |

### Value

a ggplot class plot detailing NIDPs per gene, colored by brain measure type

### Examples

```
gene_list <- c('TRIM35', 'PROSER3', 'EXOSC6', 'PICK1', 'UPK1A', 'ESPNL', 'ZIC4')
ng <- neuroimaGene(gene_list, atlas = NA, mtc = 'BH', vignette = TRUE)
plot_gns(ng)
```

## `plot_nidps` *NIDP summary plot of NeuroimaGene object*

### Description

Generate overview plot of the neuroimagene object according to nidps

### Usage

```
plot_nidps(
  ng_obj,
  maxNidps = 30,
  title = NA,
  shortnames = TRUE,
  mag = TRUE,
  verbose = FALSE
)
```

## Arguments

| | |
|---|---|
| `ng_obj` | NeuroimaGene Object |
| `maxNidps` | maximum number of NIDPs to visualize. default=30 |
| `title` | optional title tag for the plot |
| `shortnames` | optional boolean tag for simplified names. Default to TRUE |
| `mag` | boolean to present effect sizes by magnitude rather than as a vector. Default to TRUE |
| `verbose` | print runtime messages to R console. Default to FALSE |

## Value

a ggplot class object detailing mean effect size magnitude per NIDP, colored by brain region

## Examples

```
gene_list <- c('TRIM35', 'PROSER3', 'EXOSC6', 'PICK1', 'UPK1A', 'ESPNL', 'ZIC4')
ng <- neuroimaGene(gene_list, atlas = NA, mtc = 'BH', vignette = TRUE)
plot_nidps(ng)
```

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