# Package ‘GANPAdata’

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**Type** Package

**Title** The GANPA Datasets Package

**Version** 1.0

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**Suggests** GANPA

**Description** This is a dataset package for GANPA, which implements a network-based gene weighting approach to pathway analysis. This package includes data useful for GANPA, such as a functional association network, pathways, an expression dataset and multi-subunit proteins.

**License** GPL-2

**LazyLoad** yes

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**NeedsCompilation** no

## Contents

GANPAdata-package . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 2
gExprs.p53 . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 2
gNET . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 3
gsets.msigdb.pnas . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 4
msp.groups . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 4

**Index** **6**

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## `GANPAdata-package` *The GANPA Datasets Package*

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### Description

This is a dataset package for GANPA, which implements a network-based gene weighting approach to pathway analysis. This package includes data useful for GANPA, such as a functional association network, pathways, an expression dataset and multi-subunit proteins.

### Details

| | |
|---|---|
| Package: | GANPAdata |
| Type: | Package |
| Version: | 1.0 |
| Date: | 2011-05-26 |
| License: | GPL-2 |
| LazyLoad: | yes |

### Author(s)

Zhaoyuan Fang, Weidong Tian and Hongbin Ji

Maintainer: Zhaoyuan Fang <`fangzhaoyuan@sibs.ac.cn`>

### References

Zhaoyuan Fang, Weidong Tian and Hongbin Ji. A Network-Based Gene Weighting Approach for Pathway Analysis. *Submitted*.

Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov. Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles. *PNAS* 2005 102(43): 15545-15550.

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## `gExprs.p53` *Gene expression data for the P53 dataset*

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### Description

The P53 dataset is consisted of gene expression profiling of 17 P53-wildtype (WT) and 33 P53-mutated (MUT) cancer cell lines.

## Usage

```
data(gExprs.p53)
```

## Format

A List of 2 matrices.

$ gExprs : num [1:10100, 1:50]

$ sampleinfo: chr [1:50, 1:2]

## Source

http://www.broadinstitute.org/gsea/index.jsp

## References

Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov. Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles. *PNAS* 2005 102(43): 15545-15550.

Zhaoyuan Fang, Weidong Tian and Hongbin Ji. A Network-Based Gene Weighting Approach for Pathway Analysis. *Submitted.*

## Examples

```
data(gExprs.p53)
```

---

# `gNET` *gNET: A comprehensive gene functional association network*

## Description

gNET was constructed from protein-protein interactions (PPI), co-annotation in GO Biological Process (BP), and co-expression in large scale gene expression microarray data. Several limits have been applied to these data sources to achieve specificity.

## Usage

```
data(gNET)
```

## Format

A List of 16979 character vectors.

## References

Zhaoyuan Fang, Weidong Tian and Hongbin Ji. A Network-Based Gene Weighting Approach for Pathway Analysis. *Submitted.*

### Examples

```
data(gNET)
```

---

## `gsets.msigdb.pnas` *Functional Gene Sets Used in GSEA PNAS Publication*

### Description

A list of 522 C2 functional gene sets, see reference for details.

### Usage

```
data(gsets.msigdb.pnas)
```

### Format

A List of 522 character vectors.

### Source

http://www.broadinstitute.org/gsea/index.jsp

### References

Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov. Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles. *PNAS* 2005 102(43): 15545-15550.

### Examples

```
data(gsets.msigdb.pnas)
```

---

## `msp.groups` *A List of Human Multi-subunit Proteins*

### Description

A list of genes encoding 82 multi-subunit proteins were extracted from human genes.

### Usage

```
data(msp.groups)
```

### Format

A List of 82 character vectors.

## Details

A multi-subunit protein is named in the format of Multi.XXX where XXX is a member gene picked arbitrarily from the subunit gene group. Note this naming rule is just for convenience.

## References

Zhaoyuan Fang, Weidong Tian and Hongbin Ji. A Network-Based Gene Weighting Approach for Pathway Analysis. *Submitted*.

## Examples

```
data(msp.groups)
```

# Index

∗ **datasets**
    gExprs.p53, 2
    gNET, 3
    gsets.msigdb.pnas, 4
    msp.groups, 4
∗ **package**
    GANPAdata-package, 2

GANPAdata *(*GANPAdata-package*)*, 2
GANPAdata-package, 2
gExprs.p53, 2
gNET, 3
gsets.msigdb.pnas, 4

msp.groups, 4