

# signatureMaker

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**Type** Package

**Title** Build Signature Files for the httrpathway package

**Version** 0.1.0

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**Description** Formats the input signature files into 3 main outputs

catalog

list of gene lists

list of pipe-delimited gene lists.

The main functions are signatureBuilder.v2() and signatureBuilderRandom().

The first function reads in files for each of the sources and combines them

to build the signature RData files with gene lists, and the catalog. The second

builds the random signatures and adds these to the catalog. Each signature

source has its own function to put data into the proper format. To add a new

source, copy one of these and format your new data in the proper way. The

function signatureDBupdate() saves the current signature files into the

folder saved\_versions. This is just a safety measure.

**Imports** stats,

stringr,

grDevices,

graphics,

utils,

methods,

data.table,

future.apply,

future,

GSVA,

moments,

numDeriv,

openxlsx,

parallel,

RColorBrewer,

reshape2,

data.table,

openxlsx,

e1071,

tidyverse

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**Encoding** UTF-8  
**LazyData** true  
**RoxygenNote** 7.3.1  
**Suggests** knitr,  
rmarkdown  
**VignetteBuilder** knitr

**R topics documented:**

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printCurrentFunction	<i>Print the name of the current function</i>
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**Description**

Print the name of the current function

**Usage**

```
printCurrentFunction(comment.string = NA)
```

**Arguments**

comment.string An optinal string to be printed

---

`signatureBuildBioplanet`*Build the standard input file for the Bioplanet signatures*

---

**Description**

Build the standard input file for the Bioplanet signatures

**Usage**`signatureBuildBioplanet()`**Value**

No output.

---

`signatureBuildCho`*Build the standard input file for the stress signatures from Bryan Chambers*

---

**Description**

Build the standard input file for the stress signatures from Bryan Chambers

**Usage**`signatureBuildCho()`**Value**

No output.

---

`signatureBuildCMAP`*Build the standard input file for the CMAP signatures*

---

**Description**

Build the standard input file for the CMAP signatures

**Usage**`signatureBuildCMAP()`**Value**

No output.

---

signatureBuildCorton	<i>Build the standard input file for the Corton signatures</i>
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---

**Description**

Build the standard input file for the Corton signatures

**Usage**

```
signatureBuildCorton()
```

**Value**

No output.

---

signatureBuildDisGeNET	<i>Build the standard input file for the Ryan signatures</i>
------------------------	--

---

**Description**

Build the standard input file for the Ryan signatures

**Usage**

```
signatureBuildDisGeNET()
```

**Value**

No output.

---

signatureBuildDorothea	<i>Build the standard input file for the Dorothea signatures</i>
------------------------	--

---

**Description**

Build the standard input file for the Dorothea signatures

**Usage**

```
signatureBuildDorothea()
```

**Value**

No output.

---

signatureBuilder.v2	Create the files needed for the signature calculations before adding random genes
---------------------	---

---

**Description**

Create the files needed for the signature calculations before adding random genes

**Usage**

```
signatureBuilder.v2(min.ngene = 10, max.ngene = 1e+05)
```

**Arguments**

min.ngene	Signatures will only be saved if the number of genes is $\geq$ this value
max.ngene	Signatures will only be saved if the number of genes is $\leq$ this value

**Value**

No output.

---

signatureBuilderRandom	Add the random gene sets to the signature files
------------------------	---

---

**Description**

Add the random gene sets to the signature files

**Usage**

```
signatureBuilderRandom(nrandom = 1000, mc.cores = 1)
```

**Arguments**

nrandom	Number of random gene sets
mc.cores	The number of cores to use in parallel

**Value**

No output.

---

signatureBuildMsigDB	<i>Build the standard input file for the MSigDB signatures</i>
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---

**Description**

Build the standard input file for the MSigDB signatures

**Usage**

```
signatureBuildMsigDB()
```

**Value**

No output.

---

signatureBuildRyan	<i>Build the standard input file for the Ryan signatures</i>
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---

**Description**

Build the standard input file for the Ryan signatures

**Usage**

```
signatureBuildRyan()
```

**Value**

No output.

---

signatureBuildStress	<i>Build the standard input file for the stress signatures from Bryan Chambers</i>
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---

**Description**

Build the standard input file for the stress signatures from Bryan Chambers

**Usage**

```
signatureBuildStress()
```

**Value**

No output.

---

signatureDBupdate	<i>Save the current set of signatures before rebuilding</i>
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---

**Description**

Save the current set of signatures before rebuilding

**Usage**

```
signatureDBupdate(do.save = T)
```

**Value**

No output.

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