# Package 'flowWorkspaceData'

April 24, 2025

**Type** Package

**Title** A data package containing two flowJo, one diva xml workspace and the associated fcs files as well as three GatingSets for testing the flowWorkspace, openCyto and CytoML packages.

**Version** 3.20.0

**Date** 2011-03-31

**Author** Greg Finak

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**Description** The necessary external data to run the flowWorkspace and openCyto vignette is found in this package.

**biocViews** ExperimentData, FlowCytometryData

**License** GPL-2

**LazyLoad** yes

**git_url** https://git.bioconductor.org/packages/flowWorkspaceData

**git_branch** RELEASE_3_21

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`flowWorkspaceData-package` *A flowJo XML Workspace and Associated Data for testing the flowWorkspace package.*

## Description

This package contains fcs data files and xml workspaces for testing the flowWorkspace and openCyto packages and building the their vignettes. These can be located in the inst/extdata directory of the flowWorkspaceData package. The sample files and workspaces contain data from whole blood. The primary purpose of this data set is to test the import code and export code in the flowWorkspace package and running automated gating pipeline in the openCyto package.

## Details

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|---|---|
| Package: | flowWorkspaceData |
| Type: | Package |
| Version: | 1.1.0 |
| Date: | 2011-03-31 |
| License: | GPL 2.0 |
| LazyLoad: | yes |

flowWorkspaceDataInfo() provides information about the package.

## Author(s)

Greg Finak

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## See Also

`flowWorkspace` `openCyto`

## Examples

```
flowWorkspaceDataInfo()
```

flowWorkspaceDataInfo *Print some information about this package and the data.*

## Description

Contains the data necessary to build the flowWorkspace and openCyto vignettes.

## Usage

```
flowWorkspaceDataInfo()
```

## Author(s)

Greg Finak

## See Also

flowWorkspace-package openCyto

## Examples

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flowWorkspaceDataInfo();
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