Issue809 Editing

msg 9029 created issue 809 messages edited ok

clear this message



Created on 2013-11-14.17:35:48 by cdurden, last changed 2013-11-30.21:48:32 by cdurden.

Files

File name	Uploaded	Туре	
dotpipeR_0.99.0.tar.gz	cdurden, 2013-11-14.17:35:48	application/x-gzip	
<pre>dotpipeR_0.99.0.tar.gz</pre>	cdurden, 2013-11-15.14:12:31	application/x-gzip	

Messages

msg9029 (view) Author: cdurden Date: 2013-11-30.21:48:31

Hi Martin,

Thank you for your timely preview of this package. I have decided that I will follow your suggestion to augment the vignette with a relevant bioinformatics work flow, because this project was originally intended to support collaborations between biologists and bioinformaticians through the formulation of pipelines as graphs.

I have designed this R package to be used with a companion web-application that can be used to present these pipelines to users and support the visualization, post-processing (e.g. querying), and hyperlinking of pipeline node data.

Chris

msg8989 (view) Author: mtmorgan Date: 2013-11-25.10:34:10

Hi Christopher

This looks like a really cool project, but I'm not sure that it is suitable for Bioconductor. CRAN might provide better exposure for this general purpose tool. I realize that there is a level of hypocrisy here, e.g., the Bioconductor Streamer package, but the motivation in this case was specifically to develop solutions for bioinformatic work flows. If you feel strongly that your package is appropriate for Bioconductor, then I think it would be very helpful to augment the very clearly written vignette with an example or illustration of a relevant work flow, particularly if possible illustrating the benefits that formulation of pipelines as graphs brings to day-to-day analysis.

Martin

msg8895 (view) Author: pkgbuild Date: 2013-11-15.14:13:45

Dear Package contributor,

This is the automated single package builder at bioconductor.org.

Your package has been built on Linux, Mac, and Windows.

On one or more platforms, the build results were: "skipped, ERROR". This may mean there is a problem with the package that you need to fix. Or it may mean that there is a problem with the build system itself.

Please see the following build report for more details:

http://bioconductor.org/spb_reports/dotpipeR_0.99.0_buildreport_20131115141343.html

msg8894 (view) Author: cdurden Date: 2013-11-15.14:12:31

This submission fixes a broken link in the vignette file DOTpipeR.Rnw.

msg8886 (view) Author: mcarlson Date: 2013-11-15.11:12:02

Paul has agreed to review this package.

Thanks Paul,

Marc

msg8879 (view) Author: pkgbuild Date: 2013-11-14.17:37:01

Dear Package contributor,

This is the automated single package builder at bioconductor.org.

Your package has been built on Linux, Mac, and Windows.

On one or more platforms, the build results were: "skipped, ERROR". This may mean there is a problem with the package that you need to fix. Or it may mean that there is a problem with the build system itself.

Please see the following build report for more details:

http://bioconductor.org/spb_reports/dotpipeR_0.99.0_buildreport_20131114173659.html

msg8878 (view) Author: cdurden Date: 2013-11-14.17:35:48

dotpipeR is an interpreter for computational pipelines written using the DOT grammar. The flow of information is constrained by the topology of the pipeline's graph structure, which can be used to assist analysis and design of complicated computational pipelines.

History

Date	User	Action	Args
2013-11-30 21:48:32	cdurden	set	messages: + msg9029
2013-11-25 10:34:10	mtmorgan	set	nosy: + mtmorgan messages: + msg8989
2013-11-15 14:13:45	pkgbuild	set	messages: + msg8895
2013-11-15 14:12:31	cdurden	set	files: + dotpipeR_0.99.0.tar.gz messages: + msg8894
2013-11-15 11:12:02	mcarlson	set	status: new-package -> preview-in-progress assignedto: pshannon messages: + msg8886 nosy: + pshannon
2013-11-14 17:37:01 2013-11-14 17:35:48	pkgbuild cdurden	set create	messages: + msg8879