

Introduction to R Markdown

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Section 1

Publishing with R Markdown

Bioconductor Workflows

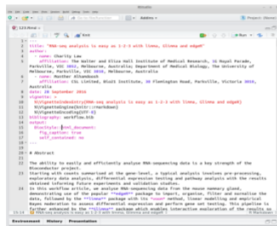
- Educational documents detailing how to use multiple packages
- Regularly checked on Bioconductor servers
 - Ensures changes in component tools are identified quickly
 - Allows rapid updates by author
 - Provides users a platform to easily access the complete suite of tools
- Difficult to get credit

F1000Research

- F1000Research provides a citable, peer-reviewed publication platform
- Intention is for the same document to be submitted to both platforms - updates are

F1000Research
PDF

Source
R Markdown



```
1 ---
2 title: "RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR"
3 author:
4   - name: Charity Lee
5     affiliation: The Walter and Eliza Hall Institute of Medical Research, 36 Royal Parade,
6     Melbourne, VIC 3000, Melbourne, Australia
7     name: Matthew Alhamoud
8     affiliation: The University of Melbourne, 478 Flemington Road, Melbourne, Victoria 3000,
9     Australia
10 date: 20 September 2016
11 keywords:
12   - limma
13   - Glimma
14   - edgeR
15   - RNA-seq
16   - differential expression
17   - bioinformatics
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```

BiocWorkflowTools

```
source("https://bioconductor.org/biocLite.R")  
biocLite("BiocWorkflowTools")
```

Conclusions

- R Markdown is great for:
 - Lab book / journal recording
 - Reports
 - Supplementary materials
- As a principle document for journal articles - we're not there yet!

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Andrzej Oles
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