

# liftr & sbgr kickstart

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# Two R/Bioconductor Packages

- liftr: Dockerize R Markdown Documents
- sbgr: R Client for SBG and CGC Platform API

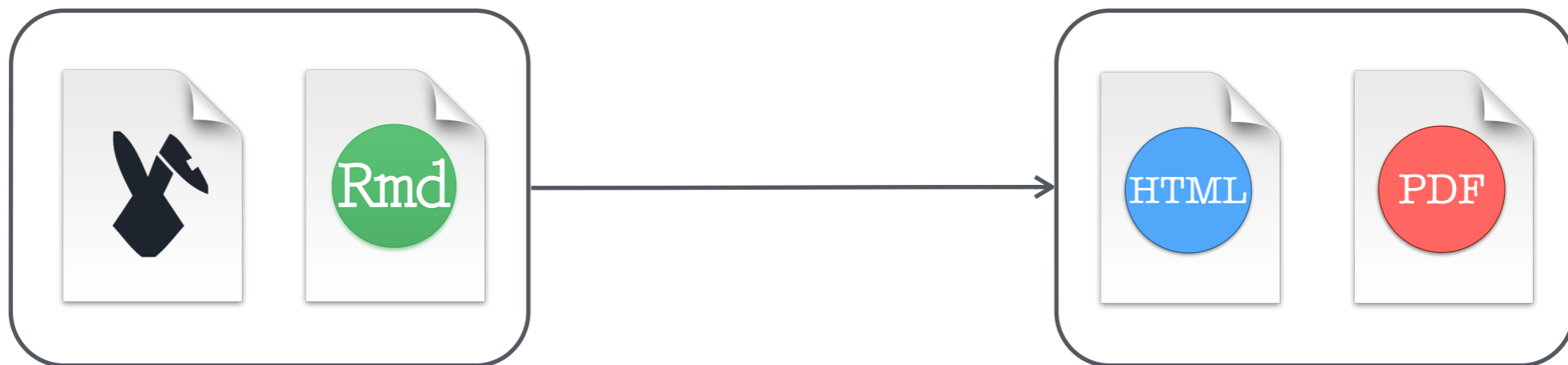


**liftr.me**

# Idea

A Framework and Tool for  
Dockerizing R Markdown Documents,  
with Rabix Support.

# Alternative Approach



R Markdown Documents  
as Rabix Input

Rendered HTML/  
PDF/Docx Reports

Knitr as a report generation tool embedded in Rabix.  
`rabix --input foo.vcf foo.Rmd --output foo.html`

# Alternative Approach

- **Pros**

- Default report binding with specific tools

- **Cons**

- Hard to modify the report template
- Hard to write report for particular workflows

# The Road We Took

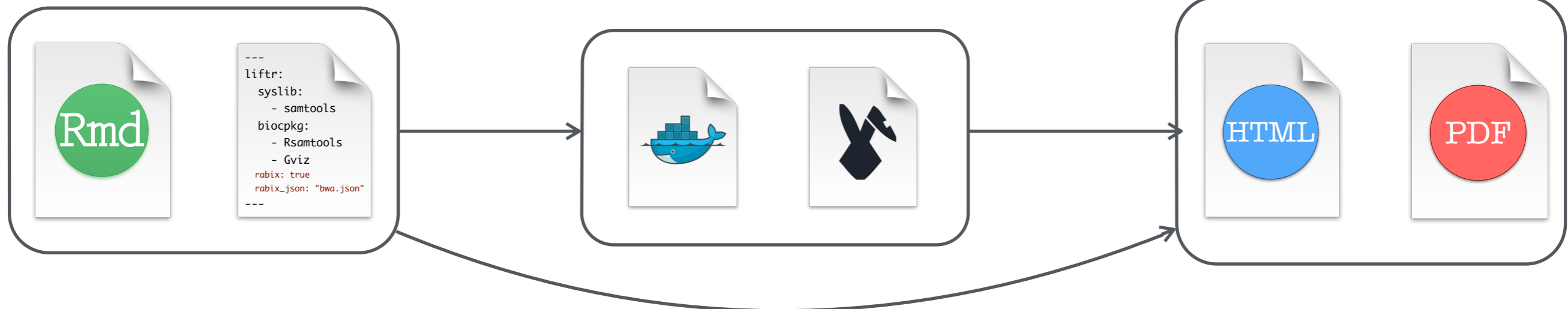
`lift("foo.Rmd")`



`drender("foo.Rmd")`



Read and share!



Rmd Documents  
with ``liftr``  
options in metadata

Generated Dockerfile  
(Rabixfile)

Rendered HTML/  
PDF/Docx Reports

Separate containers for Rabix and dockerized Rmd.

# The Road We Took

- Pros

- Run with/without Rabix
- Easy to share and modify reports

- Cons?

- Separate containers needed for rendering reports and running Rabix tools



# The Road We Took

- Make bioinformatics tools/workflows with Rabix.
- Make statistical data analysis reports with R Markdown.
- Make the best use of each tool.

# Demo

```
vignette("liftr-intro")
```



[github.com/road2stat/sbgr](https://github.com/road2stat/sbgr)

# R API Client

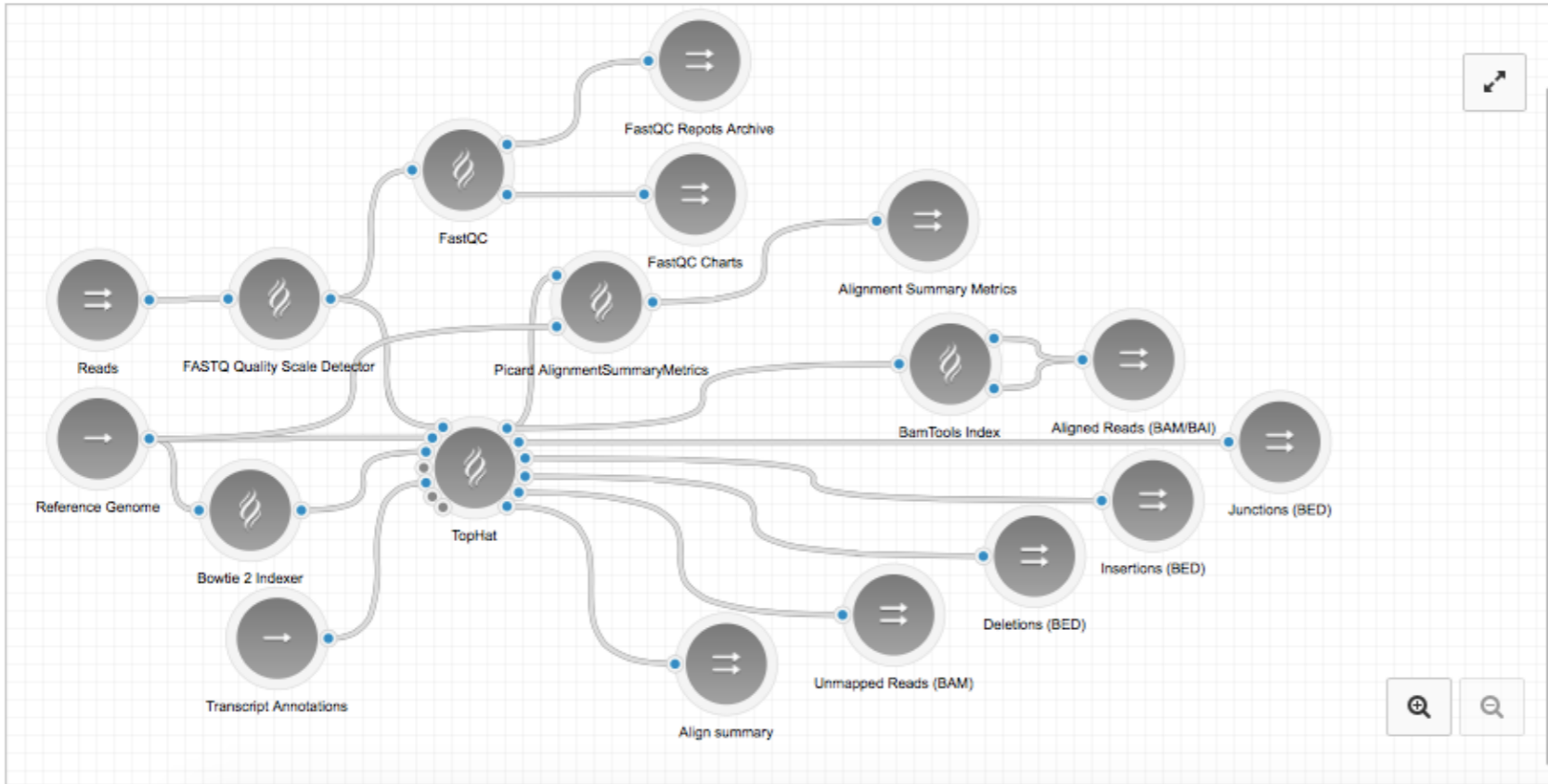
- SBG IGOR platform
- NCI Cancer Genomics Cloud (CGC) platform

Back to public pipelines

## RNA-Seq Alignment - TopHat

Version 1.4 published by [sanja.mijalkovic](#) on June 25, 2015.

Align sequence reads to a reference from RNA-Seq experiments using the split-read aligner, TopHat.



### Apps

### Change Log

Show All

Collapse

#### FASTQ Quality Scale Detector (1.0.14)

Override True

#### BamTools Index (2.3.0)

#### Picard AlignmentSummaryMetrics (1.111)

Maximum insert size 100000

Adapter sequence No value

Metric accumulation level ALL\_READS

Validation stringency SILENT

Is bisulfite sequenced False

Assume sorted True

Compression level 5

Create Index True

#### TopHat (2.0.12)

SBG IGOR Platform  
[igor.sbgenomics.com](http://igor.sbgenomics.com)

HOME

SNEAK PEEK



PRE-REGISTER

FUNDING

There is more cancer genomics data than print material in all US academic libraries.

Learn from it.

NCI Cancer Genomics Cloud Platform  
[genomicscloud.org](http://genomicscloud.org)

# Demo

```
vignette("sbgr")
```

# Our Goal

- Making bioinformatics / data analysis pipelines much **more reproducible** with Docker, Rabix, and knitr.
- Sharing portable bioinformatics pipelines, and reproducible data analysis reports, as a **community**.



Welcome to the poster  
session @ 5:15

**liftr: <http://liftr.me>**

**sbgr: <https://github.com/road2stat/sbgr>**