

liftr & sbgr kickstart

Nan Xiao @road2stat

BioC 2015

Two R/Bioconductor Packages

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

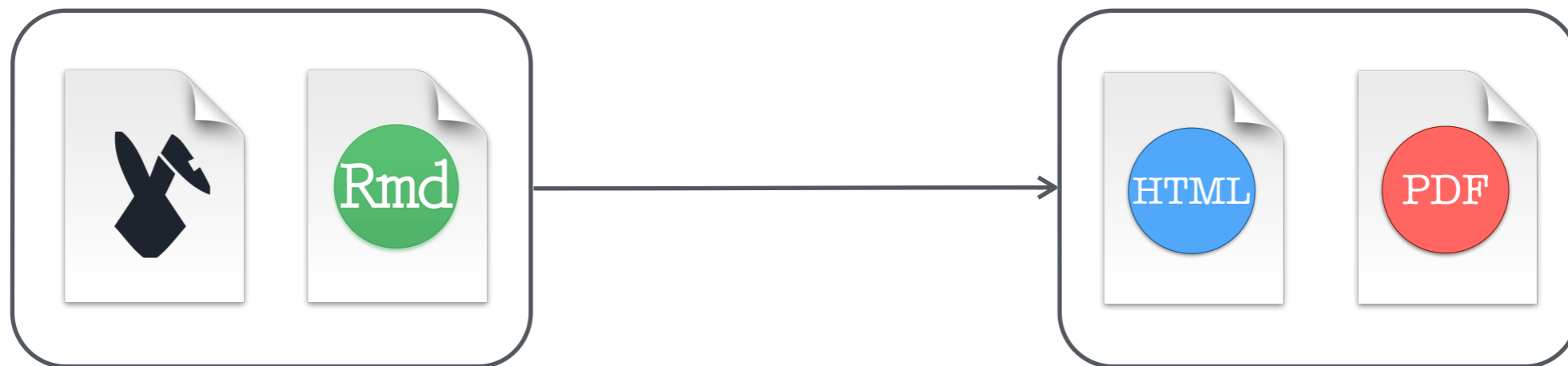


liftr.me

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

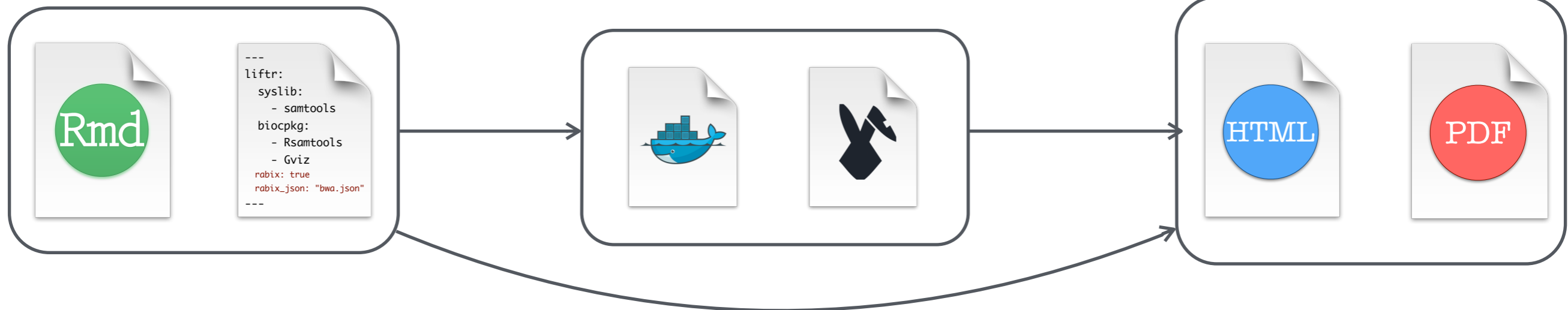
`lift("foo.Rmd")`



`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

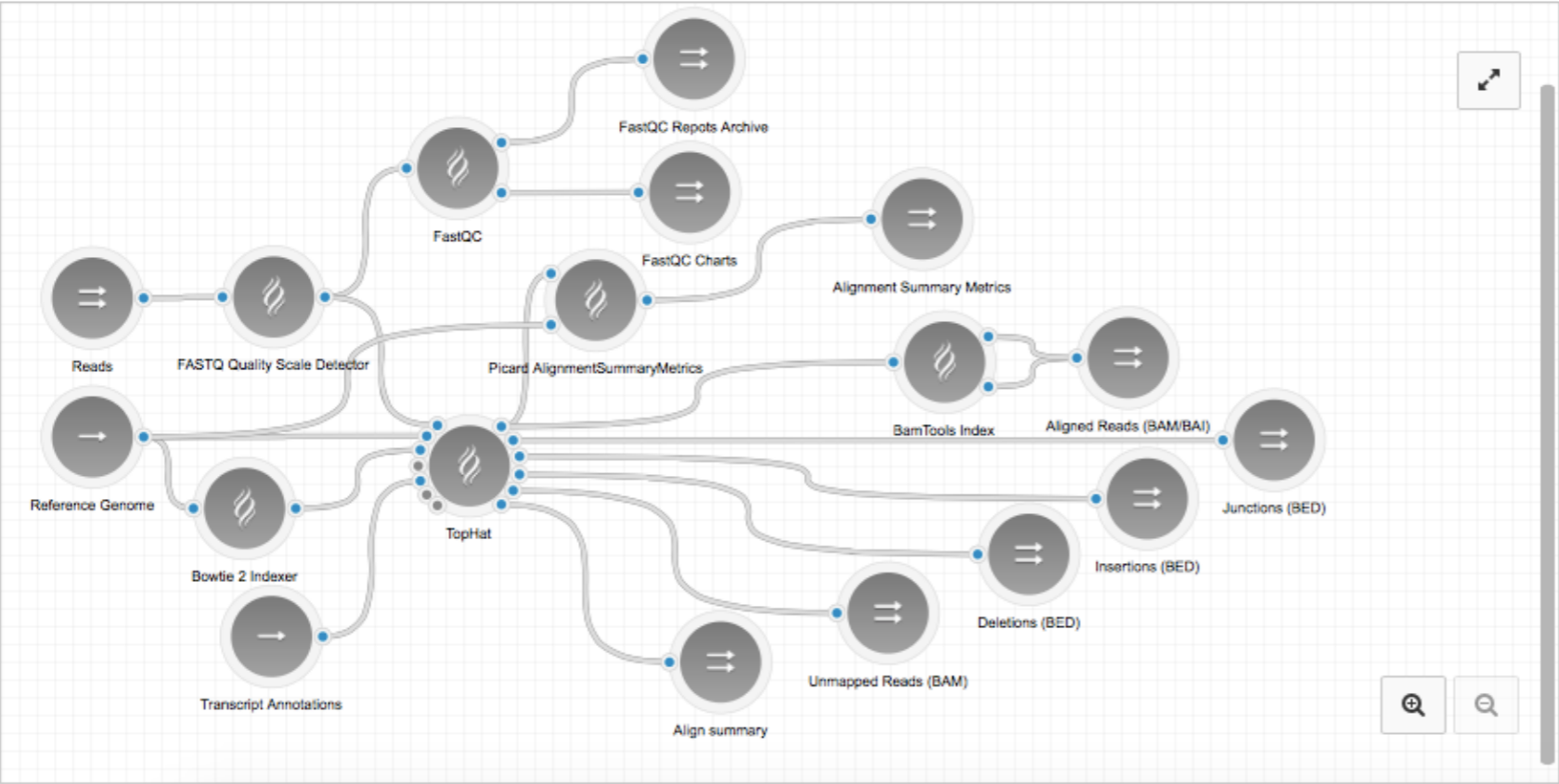
R API Client

- 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

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

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>