

Conda and Bioconda

The best thing since sliced bread

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The curse of software installation

- At least 2 help queries per week
- Manually compile dependencies?!?
- Multiple package versions?!?
- Dependencies conflict between packages?!?



Sam Nicholls @samstudio8

15h

manually compiling cmake on an ancient VM so i can run cmake to build a tool that is probably not going to even work on this ancient VM is the sort of hopeless hollow computing that bioinformatics is all about

We all have better things to do!

Have you heard the good news?

The word "CONDA" is displayed in a bold, green, sans-serif font. The letter 'C' is stylized with a white, interlocking geometric pattern on its left side, resembling a woven mesh or a stylized 'X' pattern. The remaining letters 'O', 'N', 'D', and 'A' are solid green.

Conda is easy

- Trivial to install conda
- No root needed
 - For anything
 - Ever
 - No joke
- No more compiling
- Dependencies handled for you
- Many many many versions
 - Update frequently

Conda has what you need - Channels



7100+ recipes:

python, R, numpy
scipy, CRAN packages, etc.



6300+ recipes:

samtools, STAR, salmon,
deepTools, cutadapt, blast, etc.

Add your own channel, it's free!

The cool kids use it

Snakemake



CGAT-core / Ruffus

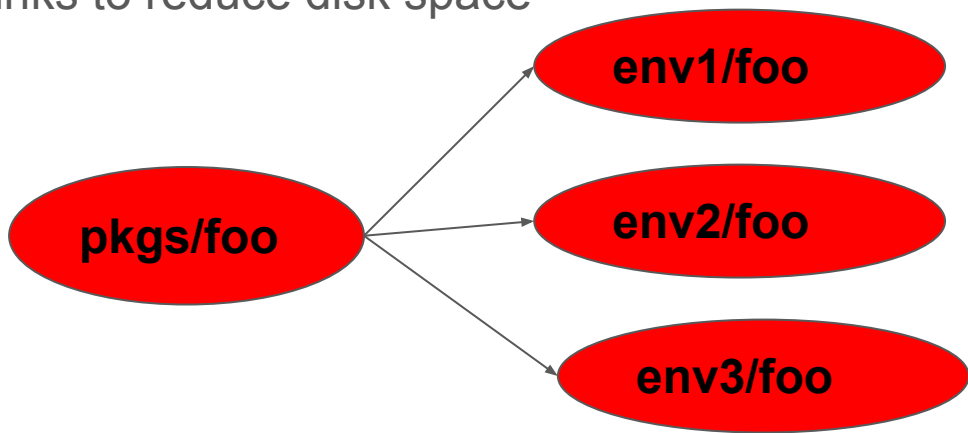
nextflow

 Galaxy
EUROPE

Many clusters (mine included)

Per-project/version environments

- A (mostly) self-contained directory with a set of compatible packages
- Often use links to reduce disk space



```
$ ls -i envs/*/bin/salmon pkgs/*/bin/salmon
20844181 envs/foo/bin/salmon
20844181 envs/salmon/bin/salmon
20844181 pkgs/salmon-0.14.1-h86b0361_1/bin/salmon
```

Biocon*

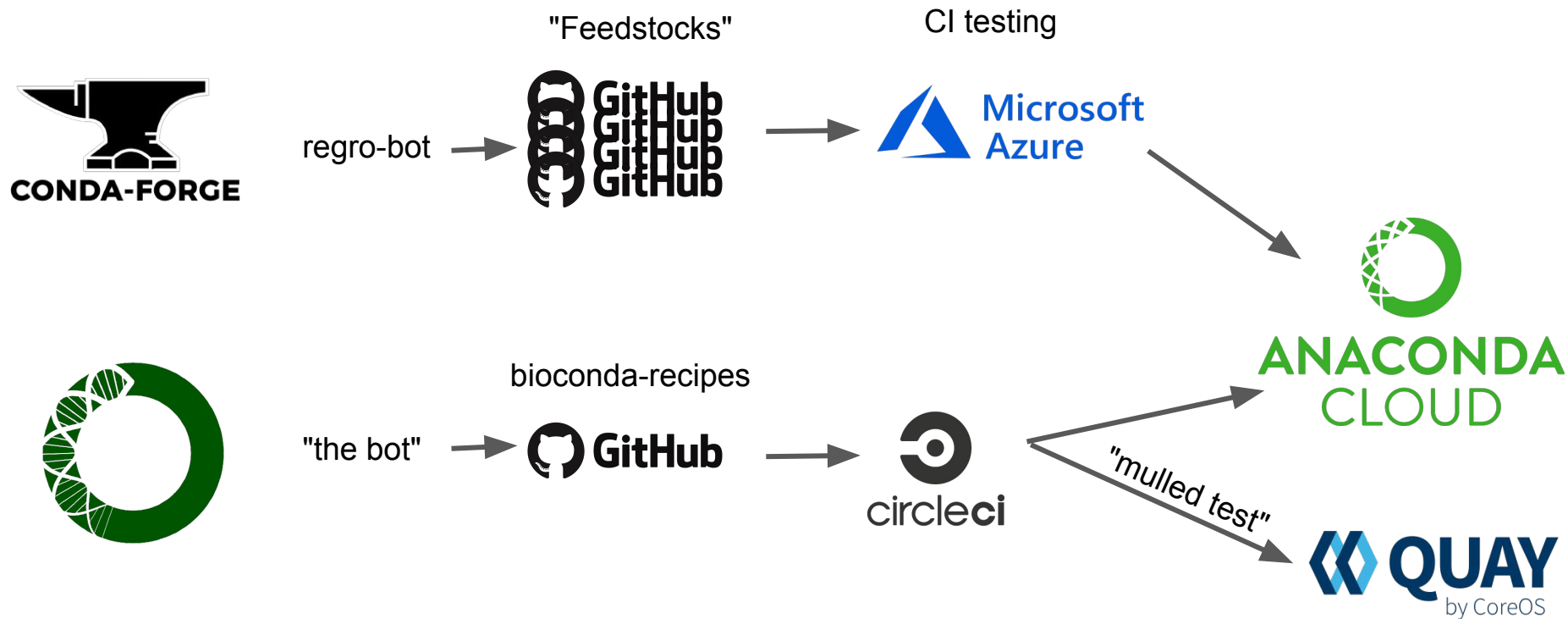


Bioconda ships all bioconductor packages



All packages have containers for
docker/singularity

Build infrastructure and automation



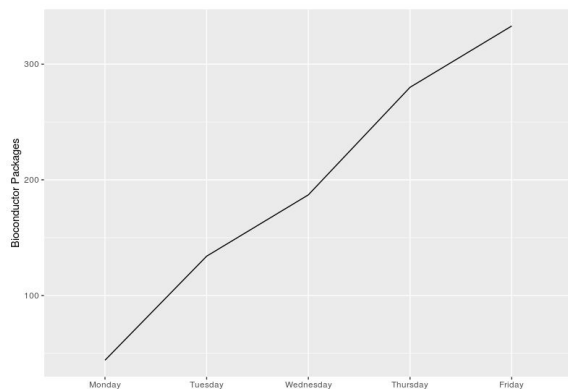
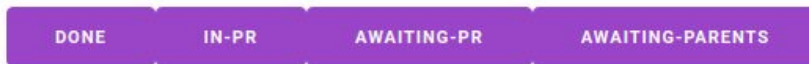
Automation is great



3 days
R 3.6
750 CRAN packages

r-base-3.6.1 Migration Status

done (740)	in-pr (63)	awaiting-pr (763)	awaiting-parents (164)
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~350 Bioconductor package updates
R 3.6

You are Bioconda

- Anyone can contribute
 - 700+ Bioconda contributors
- Release your tools here!
- Fewer reviewer complaints
- Fewer user complaints

Thanks



Dr BioinfoGoogling

@GooglingBioinfo

why is conda so slow right now

11:43am · 18 Jul 2019 · Twitter for iPhone

4 Replies 1 Like



- Channel order (conda-forge then bioconda then defaults)
- Specify R/python version
- Use envs! Always!
- Try mamba

