

Nextflow on the go

Alessia Visconti

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 @_alessia

Rewinding...

Nextflow Hackathon 2017

Nextflow Retweeted

Evan Floden @EvanFloden · 14 Sep 2017

Nextflow Hackathon 17 @nextflowio

#NFHACK17

@NEXTFLOWIO

YAMP

“ A workflow that enables the analysis of whole shotgun metagenomic data while using containerization to ensure computational reproducibility and facilitate collaborative research.

”

[Visconti et al, GigaScience, 2018](#)

Reproducibility 😍

retweeted by Nextflow Retweeted



alessia @_alessia · Apr 5

Agree: [@nextflowio](#) has been a game changer, and has dramatically improved our daily work and the way we do (#reproducible) #science. Glad to have joined the community as well!

Francesco Strozzi @fstrozzi

Nextflow turns five. Since it's adoption, it dramatically improved the way we think, build and run high quality production workflows. Glad to have joined this amazing community and contributed (a little) to the growth of this project. [twitter.com/nextflowio/sta...](https://twitter.com/nextflowio/status/111111111111111111)

YAMP

“ Being based on Nextflow, YAMP can be executed on any UNIX-like system and offers seamless support for multiple job schedulers as well as for the Amazon AWS cloud.

”

[Visconti et al, GigaScience, 2018](#)

Portability 😍

 **Francesco Strozzi**
@fstrozzi

Following ▾

Replying to [@larsgt](#) [@ljdursi](#) and 3 others

For our case [@nextflowio](#) was the most mature system supporting both local, HPC clusters and cloud computing execution. In particular we used PBS/Torque locally and then moved on to AWS cloud. Nextflow allowed us to transition without issues and port all our pipelines

3:25 PM - 10 Jul 2018

Anywhere else?

NEXTFLOW

REPRODUCIBLE COMPUTATIONAL WORKFLOWS
ACROSS CLOUDS AND CLUSTERS

NF Hackathon 2018

Evan Floden

22 November 2018

nextflow





Time for testing 😰

Natalia Jiménez
@njlozano

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High Precision Computing for Precision Medicine #BioDataHack

A photograph of a man standing on a stage, giving a presentation. He is wearing a plaid shirt and dark pants. Behind him is a large screen displaying a slide titled "HACKATHON CHALLENGE!" with the question "How can we use mobile technology to transform biological data processing?". The slide also features logos for arm, Atos, CAVIUM, and Wellcome Genome Campus Advanced Research and Scientific Computing. The date and time at the bottom of the slide are "10:41 AM - 2 Jul 2018".

ARM Cavium® ThunderX2

Test passed 😊

 WellcomeGenomeCampus
@wellcomegenome

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GO GUT takes the first prize for the @Atos
@Cavium @Arm challenge at #BioDataHack

👍😊



3:54 PM - 3 Jul 2018

How?

Nextflow

Check prerequisites

Java 8 or later is required

1

Make sure 8 or later is installed
on your computer by using the command:
`java -version`

Note: version numbers "1.8.y_z" and "8" identify the same
[Java release](#).

Set up

Dead easy to install

2

Enter this command in your terminal:
`curl -s https://get.nextflow.io | bash`
(it creates a file `nextflow` in the current dir)

Note: it can also be downloaded from [GitHub](#) or installed by
using [Bioconda](#) package manager.

Launch

Try a simple demo

3

Run the classic *Hello world*
by entering the following command:
`./nextflow run hello`

Problem: no
containerization 😱

Dependencies

- BBmap
- QIIME
- MetaPhlAn2 (Bowtie2)
- HUMANn2

Bowtie2



Alex Chacon 12:20 AM

I hope all of you are doing well, if you need some support I will keep tracking this channel :)

3 1



Ioannis Valasakis 12:41 AM

@Alex Chacon

Yes if you feel like not sleeping, I have a nice task for you 😊



Ioannis Valasakis 1:01 AM

@Alex Chacon seems you've done some work on `bowtie2`; I followed the instructions over there <https://gitlab.com/arm-hpc/packages/wikis/packages/bowtie2#build-details-for-version-v0717-arm> but still can't get it to compile, I am getting:

```
simde/x86/sse2.h:181:1: note: in expansion of macro 'HEDLEY_STATIC_ASSERT'
    HEDLEY_STATIC_ASSERT(16 == sizeof(simde__m128d), "simde__m128d size incorrect");
    ^
simde/x86/../../hedley.h:1135:65: error: expected string-literal before ')' token
    # define HEDLEY_STATIC_ASSERT(expr, message) static_assert(expr)
                                ^
simde/x86/sse2.h:181:1: note: in expansion of macro 'HEDLEY_STATIC_ASSERT'
    HEDLEY_STATIC_ASSERT(16 == sizeof(simde__m128d), "simde__m128d size incorrect");
    ^
Makefile:340: recipe for target 'bowtie2-align-s' failed
make: *** [bowtie2-align-s] Error 1
```

QIIME



Alessia 9:30 AM

@Jun Aruga

Untitled ▾

```
1 Command error:  
2   Traceback (most recent call last):  
3     File "/home/team2/hackathon18/gogut/local/src/qiime/cheat/usr/lib/qiime/bin/alpha_diversity.py", line 14, in  
<module>  
4       from qiime.util import make_option, parse_command_line_parameters  
5     File "/usr/lib/python2.7/dist-packages/qiime/util.py", line 42, in <module>  
6
```



Jun Aruga 9:34 AM

```
team2@bicho-1:~/hackathon18/gogut/local/src$ python -c 'import biom; print(biom.__version__)'  
2.1.6
```



Jun Aruga 9:45 AM

Memo:

```
$ pip2 uninstall biom-format  
$ pip2 install biom-format==1.3.1 --user
```

Ref: <https://pypi.org/project/biom-format/>

It works.

```
$ python -c 'from biom.table import DenseTable'  
$ echo $?  
0
```

Concluding...

Take-home message #1



alesssia @_alesssia · Jul 3

#BioDataHack: YAMP almost ready to run on @Arm, thanks to the amazing contribution of @wizofe and Jun Aruga. Must say @nextflowio was the easiest bit: it worked out-of-the-box, as usual 😎

Take-home message #2

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ACROSS CLOUDS AND CLUSTERS

AND MOBILE DEVICES

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Evan Floden

22 November 2018

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Acknowledgements

GoGut Team

Jun Aruga - Oliver Giles - Ioannis Valasakis - Chen Zhang

CRG

Paolo di Tommaso - All the organisers



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Questions?