Nix for genetics

Powering a bioinformatics pipeline

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Next-generation sequencing

Bioinformatics: 1 million -> 1 000 candidates
Bioinformatics pipeline

align → call variant → annotate → filter

Database 1,2... → annotate → Database 5,6...

Nix?

- Reproducible dependencies: ok! (it’s the law)
- High Performance Computing: ok!
- Manage workflow?
- Manage databases?
Nix: excellent community
Thank you!

And to:

Besançon Hospital

Mésocentre de calcul de Franche-Comté

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