# An Open Framework for Extensible Multi-Stage Bioinformatics Software

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# This talk

- New principles for bioinformatics software
- The Scala programming language
- The Friedrich framework

# Bioinformatics software today

# Bioinformatics software

- Software development for data-intensive experimental science is very difficult

- However, we have inadequate tools, frameworks, common practices and developer skills

# Bioinformatics software development is special

- One of the main sources difficulty is change
  - Technology and data formats (for example, sequencing)
  - Scientific methods
  - Availability and nature of data sources (databases etc) being used
- But there's also scale
  - Enormous data sets, constantly growing larger
  - Need for parallelism

# Additional problems

- R and Perl were good choices 10-15 years ago - not anymore!
    - But there's still a huge repository of bioconductor and CPAN packages - massive network effect, hard to leave old technology
- What about big data and concurrency?
    - There's a need for accessible solutions that anybody can program, making use of all the idle CPU cores that are around us in our labs
    - Concurrency is very hard with Perl and C but much easier with modern languages

# New principles

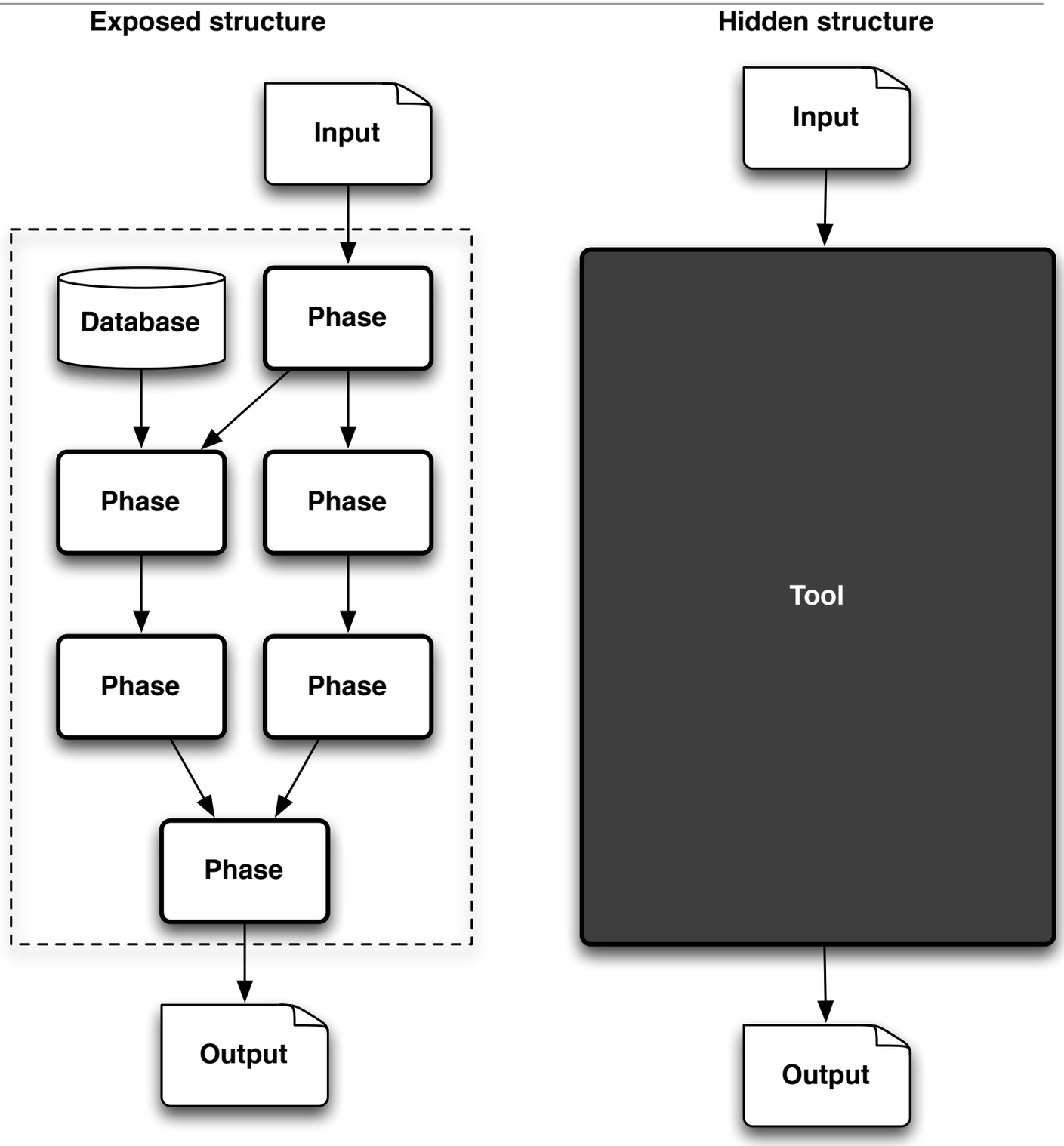
- In the following, we make a set of **observations** about the current situation and as a result, recommend **a new set of principles**
  - The principles were arrived at while developing a de novo genome assembler

# Monolithic software

- When we optimise for performance at any cost, software can become difficult to change - *“monolithic”*
- Monolithic software resembles a black box that cannot be changed or is very difficult to change
- Encapsulation may not be well suited to bioinformatics
- Principle: expose internal structure

# Principle: Expose internal structure

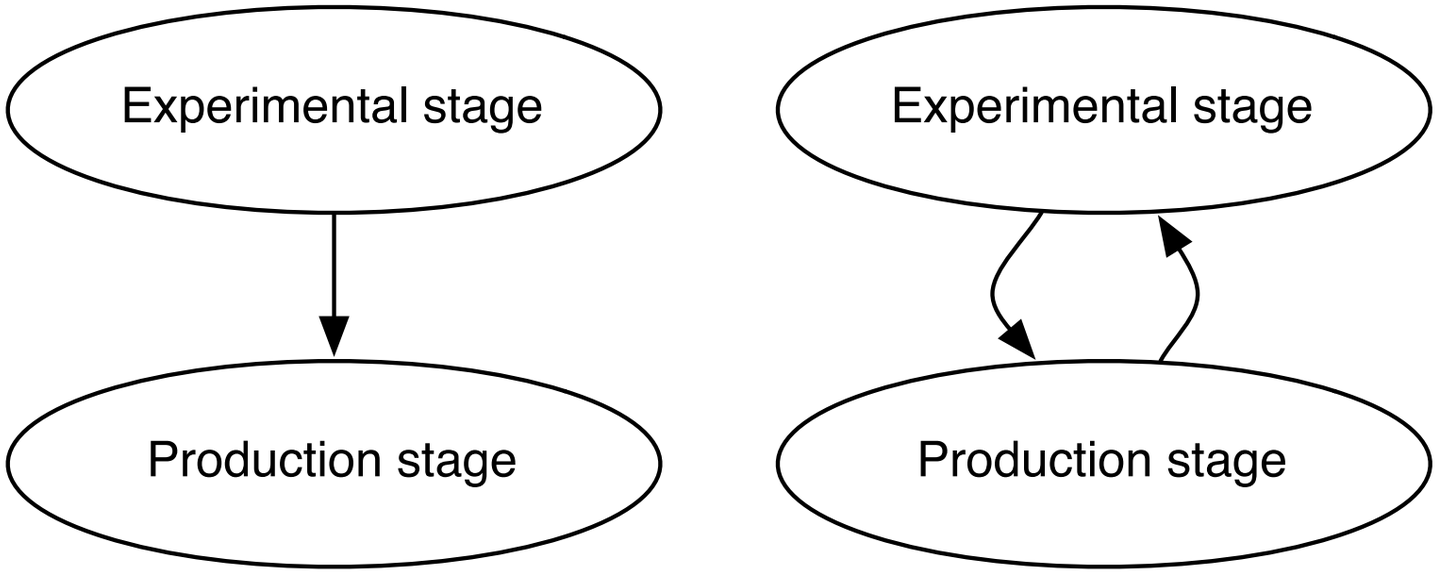
- Software tools should expose each internal processing step
- Allow for manipulation and inspection of each one independently
- Allow for reconfiguration of data flow



# Multiple stages

- Conventional view: software is a product (scientific tool) that is delivered to a customer (a researcher)
  - First method development (experimentation), then method usage (production)
- Realistic view: scientific software is never finished, and needs to evolve along with the research
  - Moving from experimentation to production, and back again (multi-stage software)

# Multi-stage software




- Avoid designing for either the experimental stage (flexible, slow) or for the production stage (inflexible, fast).

- Assume that we have to move back and forth continuously between **applying** the method and **modifying** the method!

# Finality

- Software developers often make various final assumptions about input formats, users' intentions, and so on, and hardcode them throughout the software

- Avoid a final design or final assumptions about how the software is to be used ultimately: minimal finality

# Loss of intermediate data

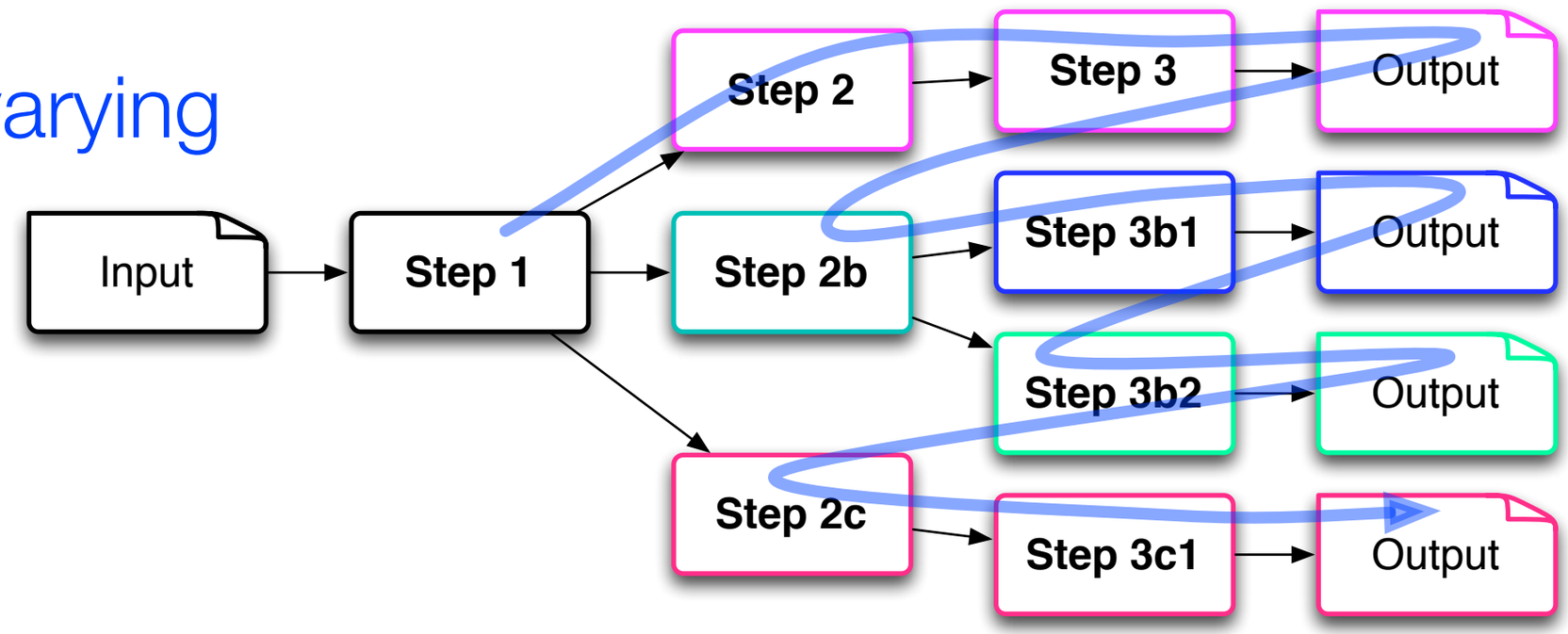
- Many tools naturally perform computation in multiple stages
- However, after each stage has been computed, data is discarded and it is impossible to go back to the previous stage
- Principle: retain intermediate data maximally, so that it is efficient to go back and explore previous stages with other parameters
  - Mathematically: preserve dimensionality maximally

# Preserving intermediate data

## Traditional: start to finish


## With preservation


## Enables efficient exploration with varying parameters



# Performance bias OR flexibility bias

- Traditionally, bioinformatics programmers tend to write either very flexible software (experimental stage) or very fast software (production stage)

- Instead of optimising **max(*f, p*)**, optimise ***f*** • ***p*** !

  - Aim for acceptable performance and acceptable flexibility

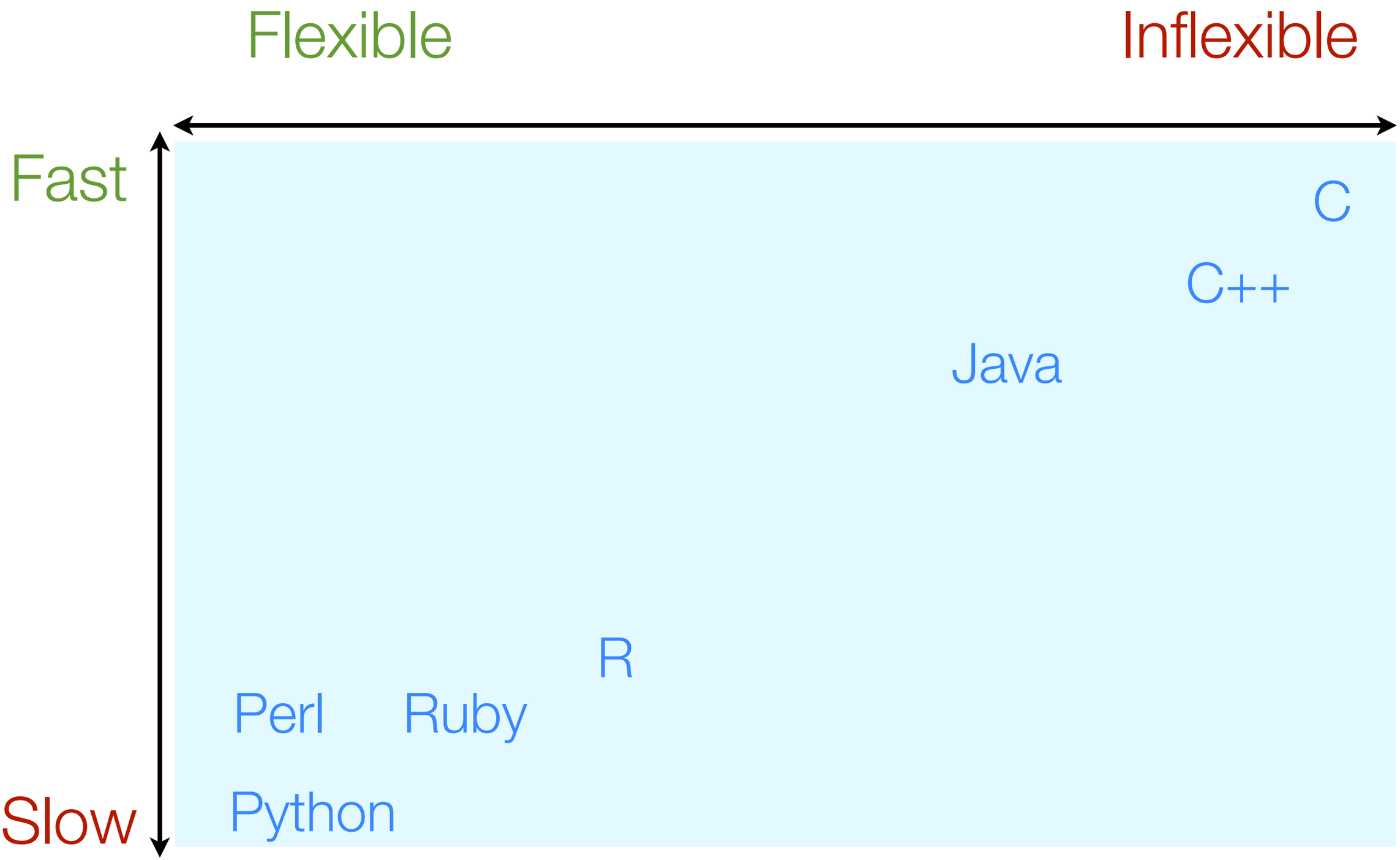
| Context | Performance | Flexibility | Monolithic | Examples |
|---|---|---|---|---|
| **Experimentation** | Low | Very high | No | BioPerl, BioPython |
| **Production** | Very high | Low | Possibly | Velvet, Abyss, BioJava |
| **Proposed ideal** | High | High | No | |

# Principles for bioinformatics software: summary

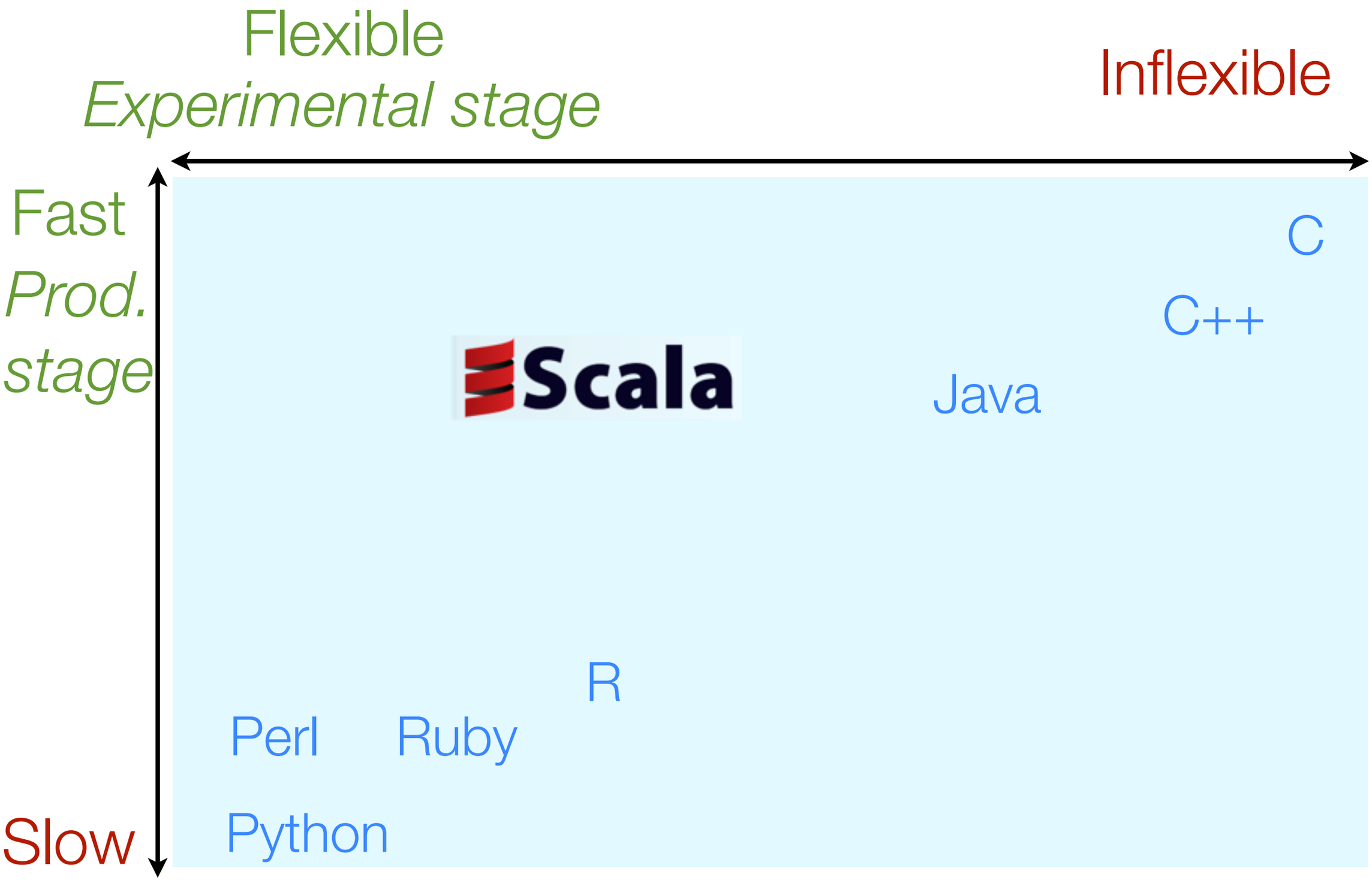
- Expose internal structure
- Multi-stage applications
- Conserve dimensionality maximally
  (retain intermediate data)
- Minimal finality
- Flexibility with performance
- (Ease of use)

# The Scala programming language

# Programming languages



# A new kind of compromise?



# Scala


- Hybrid functional/object-oriented language for the Java VM
- In development for the last 10 years or so, now becoming popular and widely used in academia, industry
- Very easy to combine with Java code and libraries
- Based on **modern computer science**
    - Simple, efficient concurrency and parallelism (Erlang-style model with actors)
- www.scala-lang.org

# Scala (2)


- Industrial users include The Guardian, LinkedIn, Xerox, Twitter, Siemens, ...
- Code is very compact, flexible style, often 3x smaller than Java
- Interactive console (like python, perl etc) (“REPL”)
- The performance of Java and the compactness of Python/Perl!

# Scala in bioinformatics


- **BioScala** - 2 year old project, now dormant, by Pjotr Prins (https://github.com/bioscala/bioscala)
- (**BioJava**) - substantial, can be used very easily from Scala (http://biojava.org)
- **Scabio** - small bioinfo algorithms collection, by Markus Gumbel (http://www.mi.hs-mannheim.de/gumbel/en/forschung/scabio)
- **Friedrich** - our contribution in this talk
- Also: use any maths/visualisation/DB etc library you want from Java

# Bioinformatics needs Scala


- Several small libraries and projects exist, but none has become very big yet - hopefully this will change soon

- Scala may be the best language to support the experimental stage and the production stage simultaneously: good fit for scientific research

- *Why everyone in bioinformatics should learn Scala* by Pjotr Prins (http://blog.thebird.nl/?p=26)

# Friedrich: A software framework

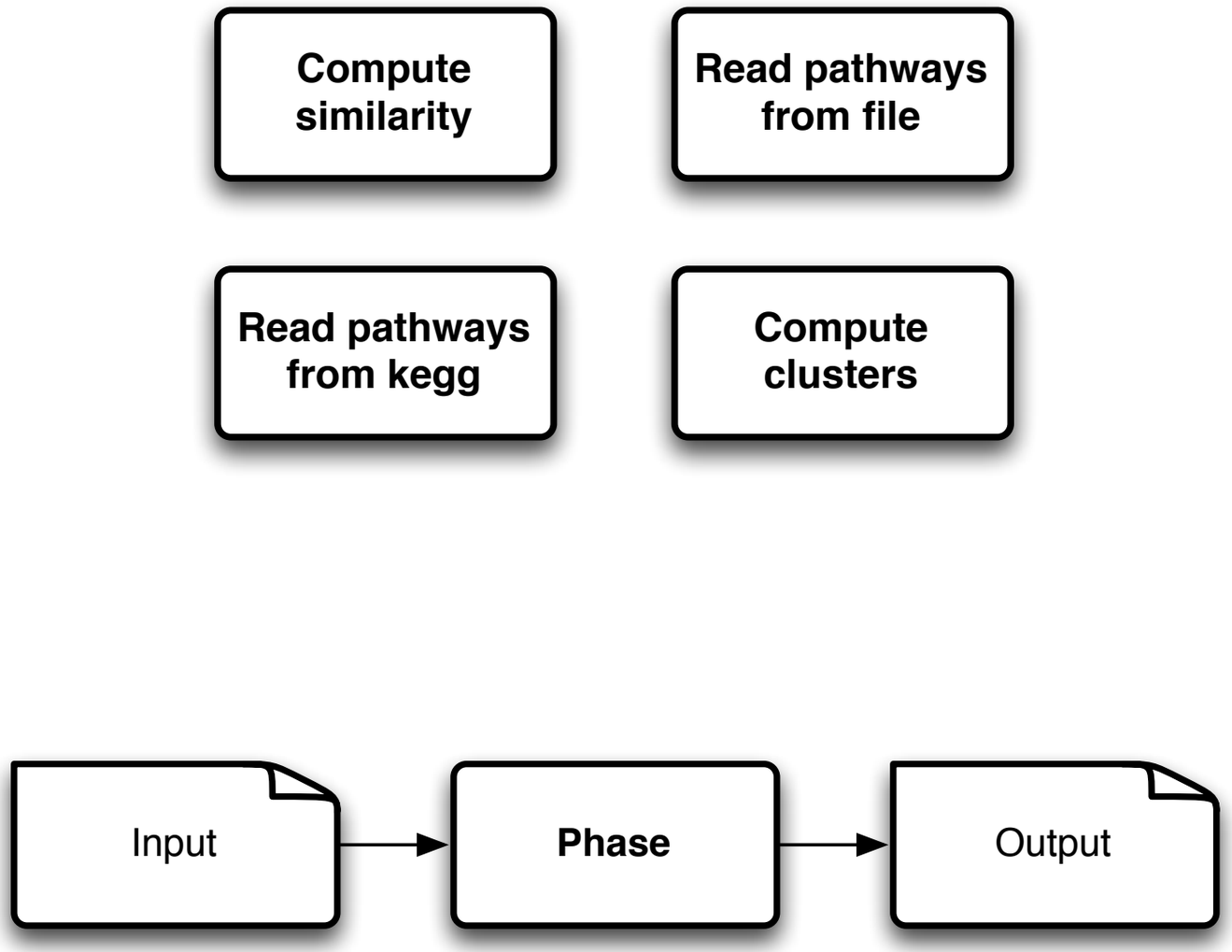
# Friedrich

- A framework that supports bioinformatics software development in Scala according to the principles we have outlined (“The Friedrich principles”)

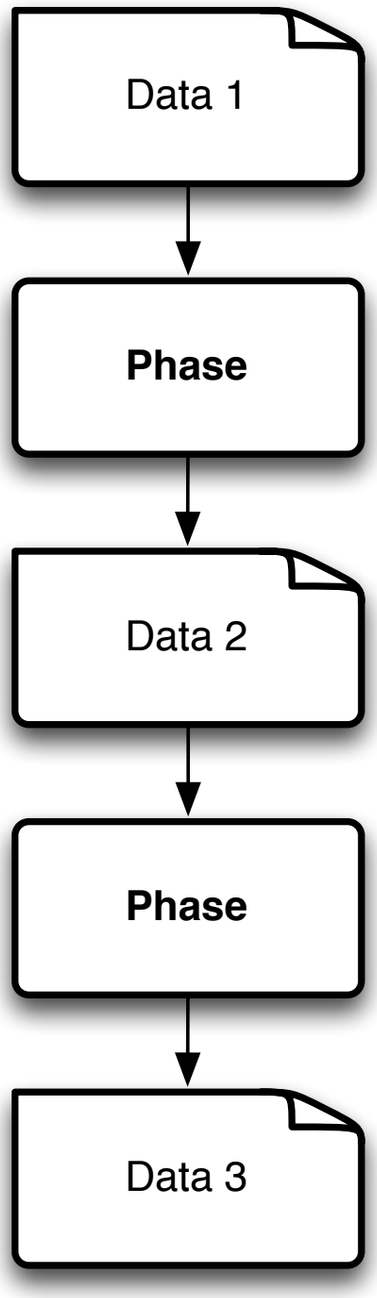
# Friedrich features (current)

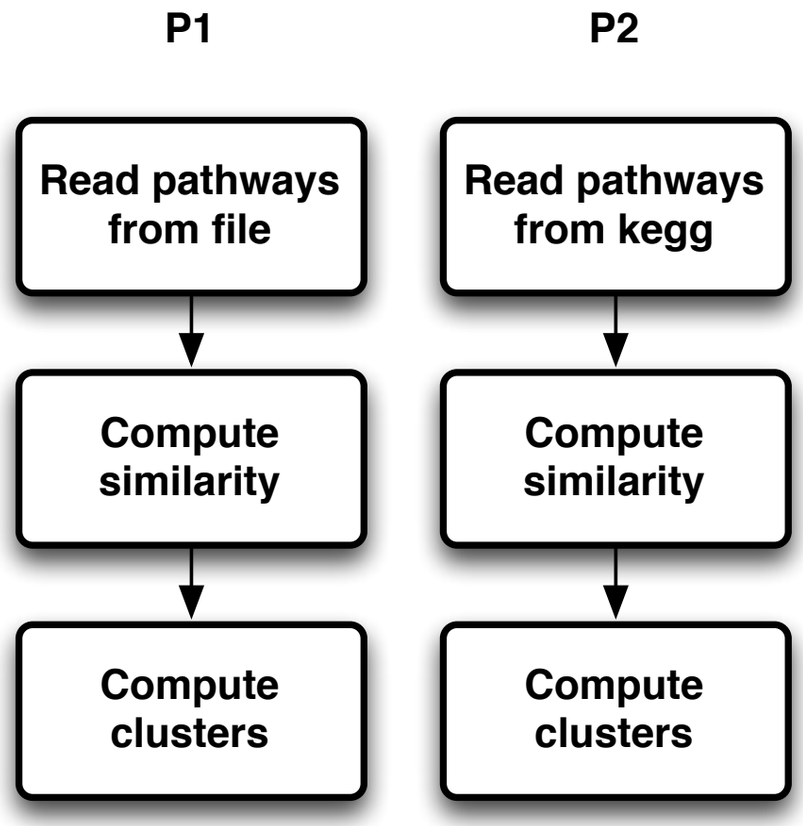
- Phases
  - An “application” is structured as a set of phases that operate on data
  - Just as in Scala, there is support for both **mutable** and **immutable** data
- Pipelines
  - A pipeline is a sequence of phases that can process data
- Configuration management

# Phases


Compute similarity
Read pathways from file
Read pathways from kegg
Compute clusters
Input
Phase
Output

# Pipelines


Data 1
Phase
Data 2
Phase
Data 3


P1
P2
Read pathways from file
Read pathways from kegg
Compute similarity
Compute similarity
Compute clusters
Compute clusters

# Supporting the principles

- Because phases can be rearranged, **minimal finality** is supported, and **internal structure is exposed**

- Immutable data supports **conservation of intermediate results** (work in progress)

- Scala supports **flexibility with performance**

# Friedrich applications

- A simple but functional de novo genome assembler is available
    - Can handle approx. 20 million *k*-mers using 2 GB RAM
- Internal applications at NIBIO, not ready for release

- Feel free to develop your own!
- Get Friedrich: http//bitbucket.org/jtnystrom/friedrich

# Comparison with...

- Task running frameworks, for example Galaxy and Yabi are focussed on providing a high level interface to existing components
  - User-developer separation
- “Toolkits” e.g. SAMTools, Picard: multiple binaries
  - Not flexible enough, no true interactive experimentation

# Ongoing and future work


- Currently in progress
  - Akka, a framework for distributed/concurrent *actor-based* programming
    - Model is similar to Erlang
      - Goal: transparent, location-agnostic concurrency
  - Integration with BioScala/BioJava
- Future goals
  - Downloadable package/module system

# Summary

- Bioinformatics software development faces unique challenges, and collectively we are not up to scratch

- New principles show the way to more natural and efficient software development in BI

- Scala may be the language we need next; Perl, R and C++ are not good enough

- Friedrich is a framework that supports our new principles, and you are welcome to use and contribute to it

*“Everyone who has ever built anywhere a new heaven*
*first found the power thereto in his own hell.”* - F. W. Nietzsche

# Thank you !

We would very much appreciate comments and collaboration.
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gabriel7@gmail.com (Gabriel)