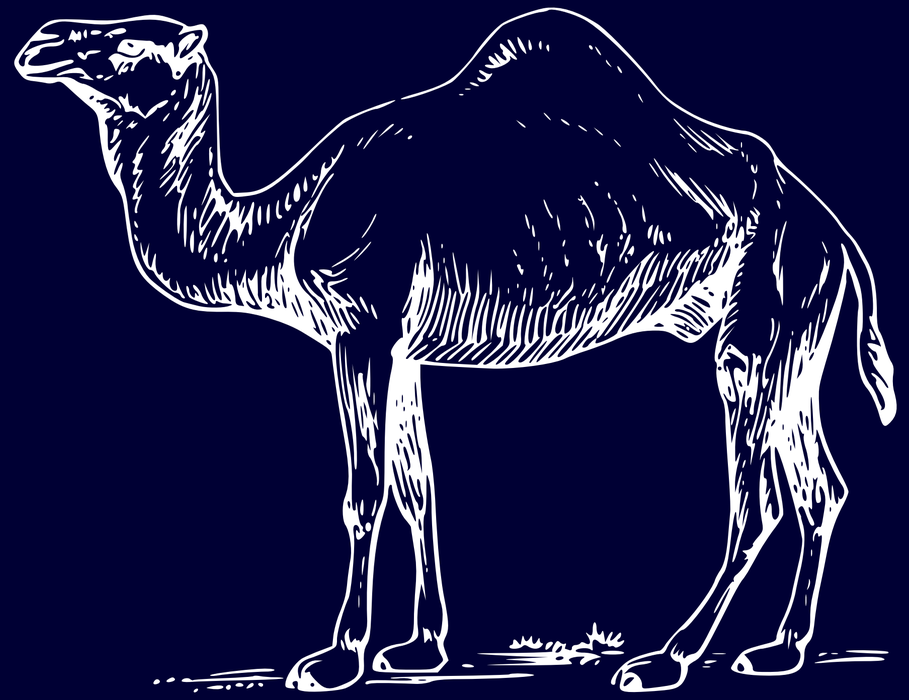
Miniconda can be a valuable channel to deliver your Perl packages and modules



`conda install perl-module`

ANDREA TELATIN, QUADRAM INSTITUTE BIOSCIENCE

TPC

How did I get here?

- I'm **not** a developer (I'm a molecular biologist)
- I learned Perl 💙 in 2004, when it was the most popular scripting language in **bioinformatics**

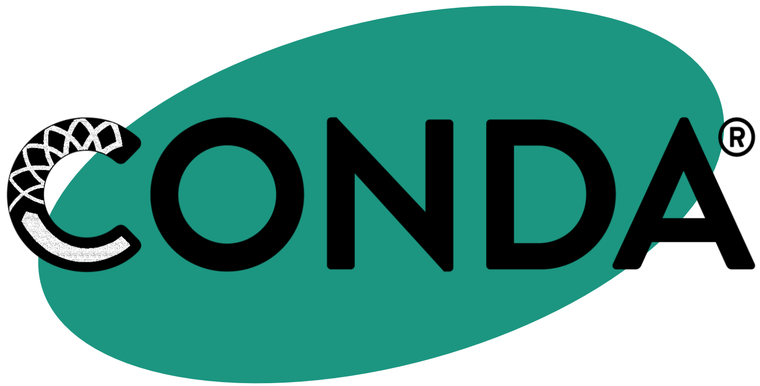
- Slides and example code on GitHub
  https://github.com/telatin/learnperl/tree/master/TPRCiC

The problem

- For **BIOINFORMATICIANS**:
  - Our analyses rely on a vast number of software tools
  - Sometimes incompatible versions of tools / modules etc.

- For **Perl programs**:
  - Non developers would struggle installing modules (and cpanm…)

The solution



https://anaconda.org

- **PACKAGE MANAGER**:
  - Will install packages and their dependencies picking the right versions
  - `conda install` **`package-name`**
- **ENVIRONMENT MANAGER**:
  - Allows to use different versions of modules/ tools in isolated “environments”
  - `conda create -n` **`environment_1`**
  - `conda activate` **`environment_1`**

Conda “channels”

- **CONDA CHANNELS**
  - Conda channels are the locations where packages are stored
  - Any user signing up can create their own channel
  - e.g. `conda install -c my_channel perl=5.22`
- **The BioConda channel** (https://bioconda.github.io/)
  - >7000 packages (of which >700 Perl modules)
  - e.g. `conda install -c bioconda perl-capture-tiny`

Devon Ryan
@dpryan79

The “recipe”

- **INGREDIENTS**
  - **`meta.yaml`** Metadata (package name, URL, dependencies)
  - **`build.sh`** Compilation / installation script (not needed for Python)
  - **`test.sh`** Optional test script (basic tests can be added in meta.yaml)
  - All inside a `package-name` directory

  - Fork `bioconda-recipes`, add the new recipe and make a PR

```
{% set name = "perl-module-name" %}
{% set version = "0.01" %}
{% set sha256 = "de31386013dc32f46f4c00d19230eeecca0c33ed1f1b13403a08e087a0278a05" %}

package:
  name: {{ name }}
  version: {{ version }}

source:
  url: https://cpan.metacpan.org/authors/id/X/XY/XYNICKNAME/Module-Name-{{ version }}.tar.gz
  sha256: {{ sha256 }}

build:
  noarch: generic
  number: 0

requirements:
  host:
    - perl
    - perl-module-build
    - perl-test-more

  run:
    - perl

test:
  imports:
    - Module::Name
```

meta.yaml

- **CONDA MAGIC**
  - When you release a new version of the module on CPAN, the BioConda Bot will automatically fetch it and make it available

build.sh

```
#!/bin/bash

# If it has Build.PL use that, otherwise use Makefile.PL
if [ -f Build.PL ]; then
    perl Build.PL
    perl ./Build
    perl ./Build test
    # Make sure this goes in site
    perl ./Build install --installdirs site
elif [ -f Makefile.PL ]; then
    # Make sure this goes in site
    perl Makefile.PL INSTALLDIRS=site
    make
    make test
    make install
else
    echo 'Unable to find Build.PL or Makefile.PL. You need to modify build.sh.'
    exit 1
fi
```

We can finally have Python serving the **Perl community**

Thanks for your attention