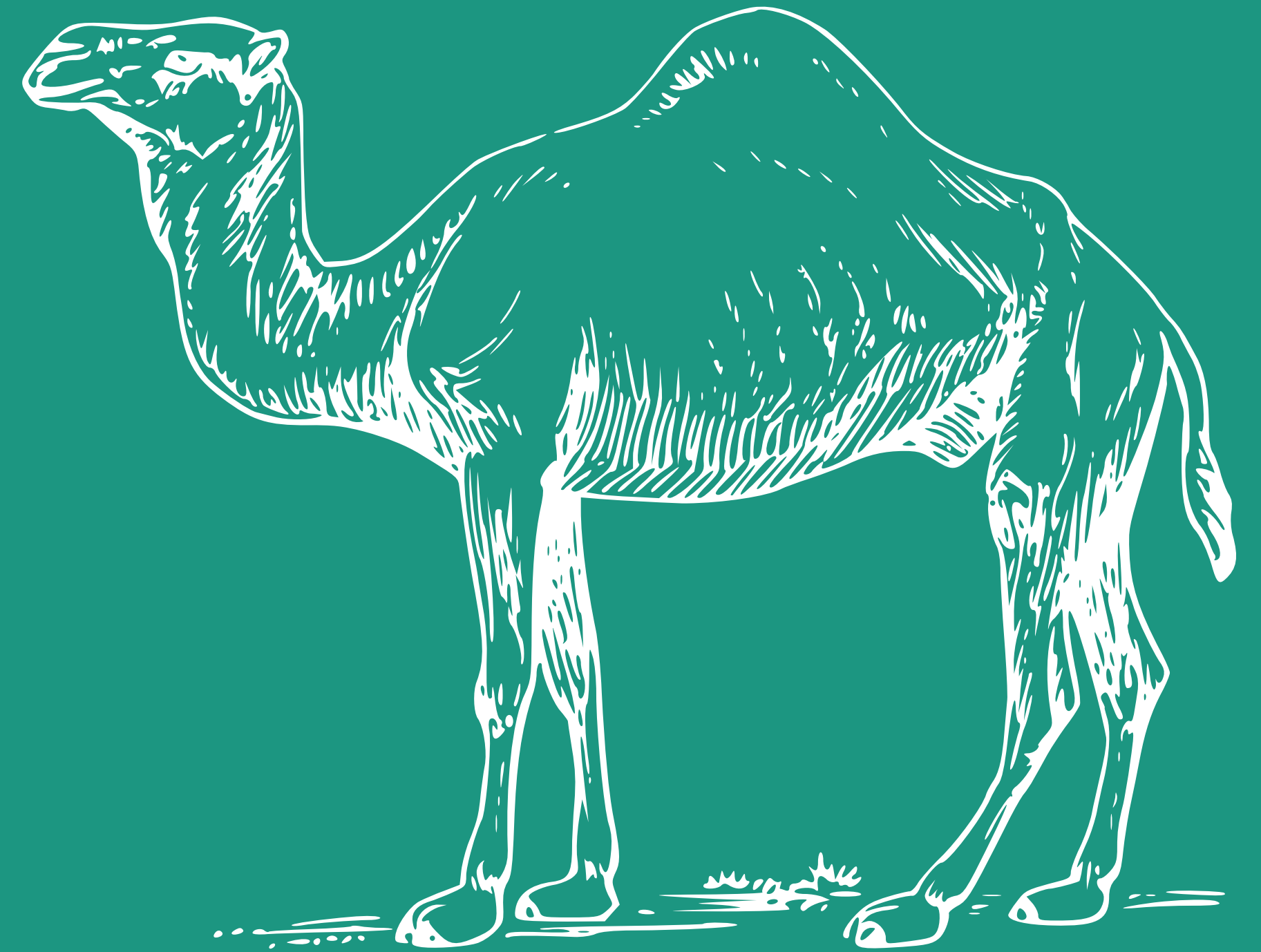


Miniconda can be a valuable channel to deliver your Perl packages and modules



conda install perl-module

How did I get here?

Andrea Telatin
twitter: **@telatin**
CPAN: **PROCH**



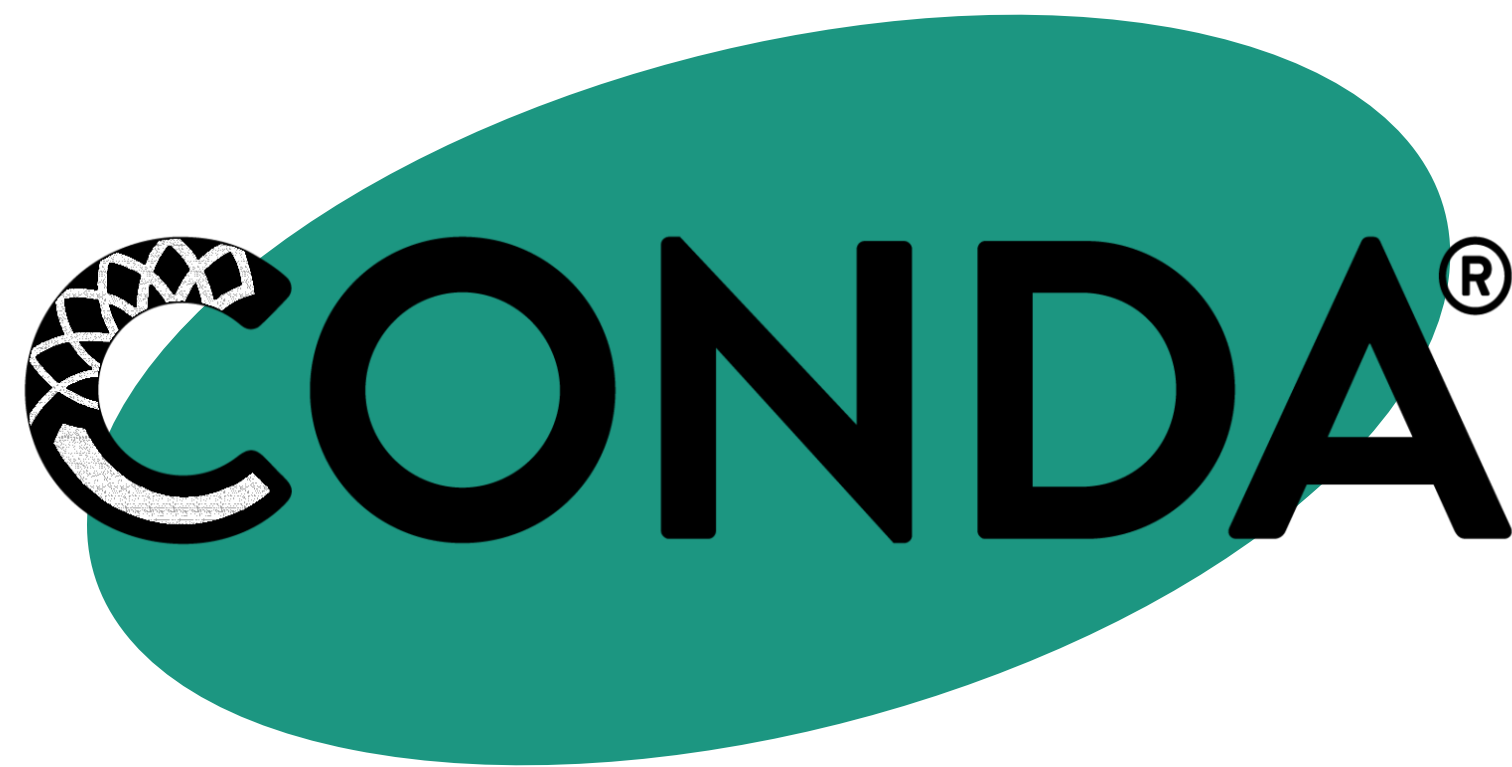
- I'm **not** a developer (I'm a molecular biologist)
- I learned Perl ❤️ in 2004, when it was the most popular scripting language in **bioinformatics**
- Slides and example code on GitHub
<https://github.com/telatin/learnperl/tree/master/TPRCiC>

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 = "de31386013dc32f46f4c00d19230eecca0c33ed1f1b13403a08e087a0278a05" %}
```

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

Andrea Telatin
twitter: **@telatin**
CPAN: **PROCH**