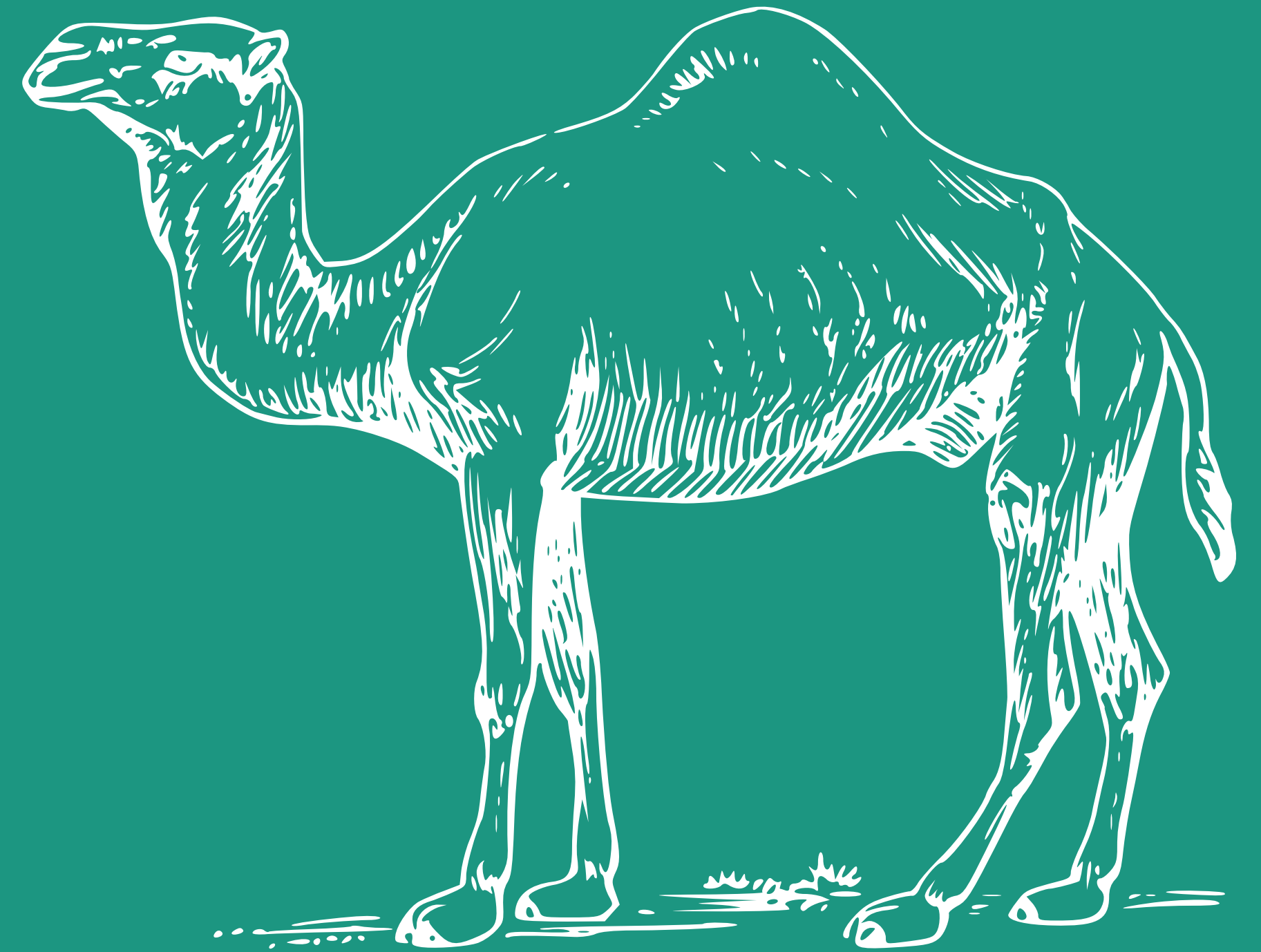


**Miniconda** can be a valuable channel to deliver your Perl packages and modules



---

**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>

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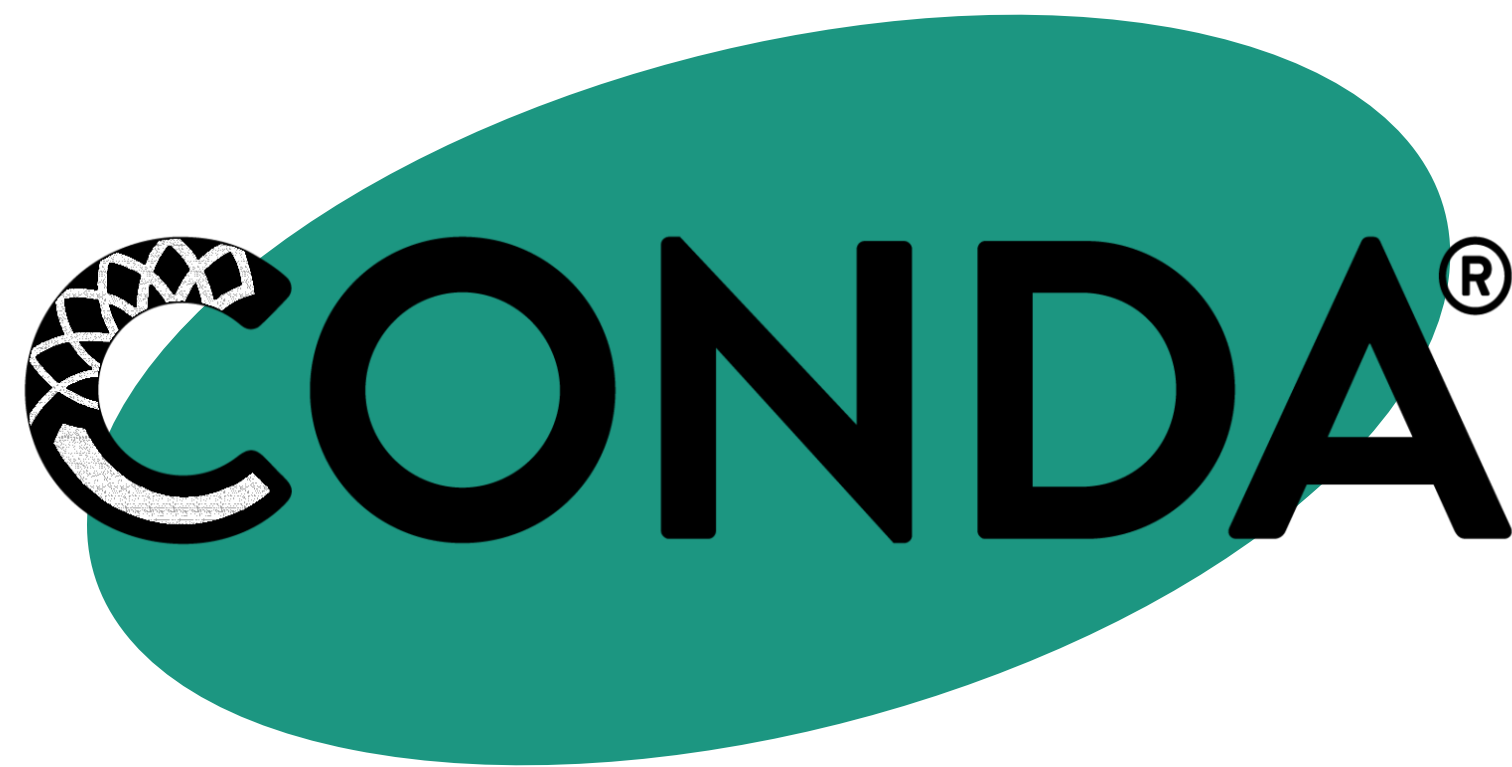
# The problem

- 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 conda-forge htop=2.2.0`

- **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.'
```

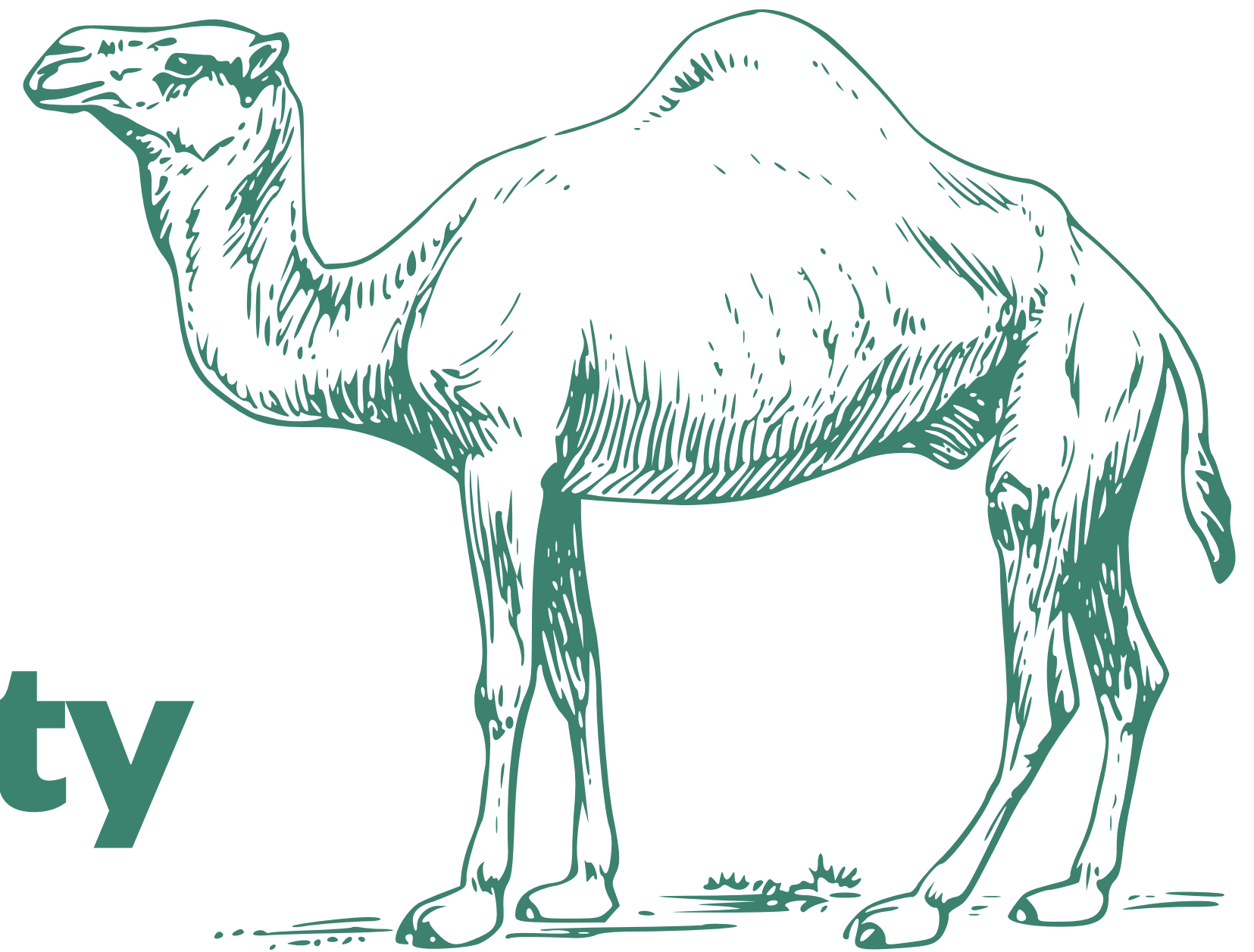
```
    exit 1
```

```
fi
```



---

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







**Thanks for  
your attention**

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