INTRODUCTION

conda install hell

SOLUTION

pixi

- extremely fast
- clever isolation

BIT OF HISTORY

Scripting language support extensions in lower-level languages

For example for Python and R

Python has Cython to do that very easily

Great idea ->

Heavy lifting in typed performant language ->

Easily script around it

Numpy/Pandas/Scipy/Tensorflow do this

DATA SCIENCE BOOM

2010 big boom in data science

However, practically impossible to install numpy on Windows
(pip just arrived in 2008)

That was the hole Anaconda filled with conda packages (2012).

Conda packages provides a way to bring Windows binaries to the masses
(to install alongside pypi packages.)

WINDOWS BINARIES

Bringing Windows binaries to the masses is a big problem.

It still is. No big adopted package manager for Windows.

Still no way to bring binaries cross platform to the masses.*

No greatly adopted package manager
(except maybe apt).

So, conda packages is a great vehicle for shipping binaries.

(*The problem for this is someone has to pay the cost of hosting.)

CONDA GOT ADOPTED TO BIOINFORMATICS

So conda and the likes got also adopted by the *bioinformatics* community.

Because bioinformatics packages are often scripts,

But they rely on C++ standalone programs that do the heavy lifting.

Conda packages could just bring these binaries with you and *manage environments*

CONDA ENVIRONMENTS

Conda environments are great for development.

That is the intended use case.

```
conda create -n myenv
conda activate myenv
python ...
conda install ..
```

But bionf people want to run the packages as tools!

Putting everything into one environment creates a big mess.

RUNNING BINARIES WITH CONDA

That was never (and still is not) the intended usecase.

`conda run` works, but it is extremely slow
    (conda is slow in so many regards).

Also the new client (mamba, completely written in C!)
just has a very slow `run` command.

Only micromamba could provide you with "fast" `run` command.
    First below a 1s (0.2s)

CONDA RUN IS JUST USELESS

You now have to call `conda run` everywhere

Not great.

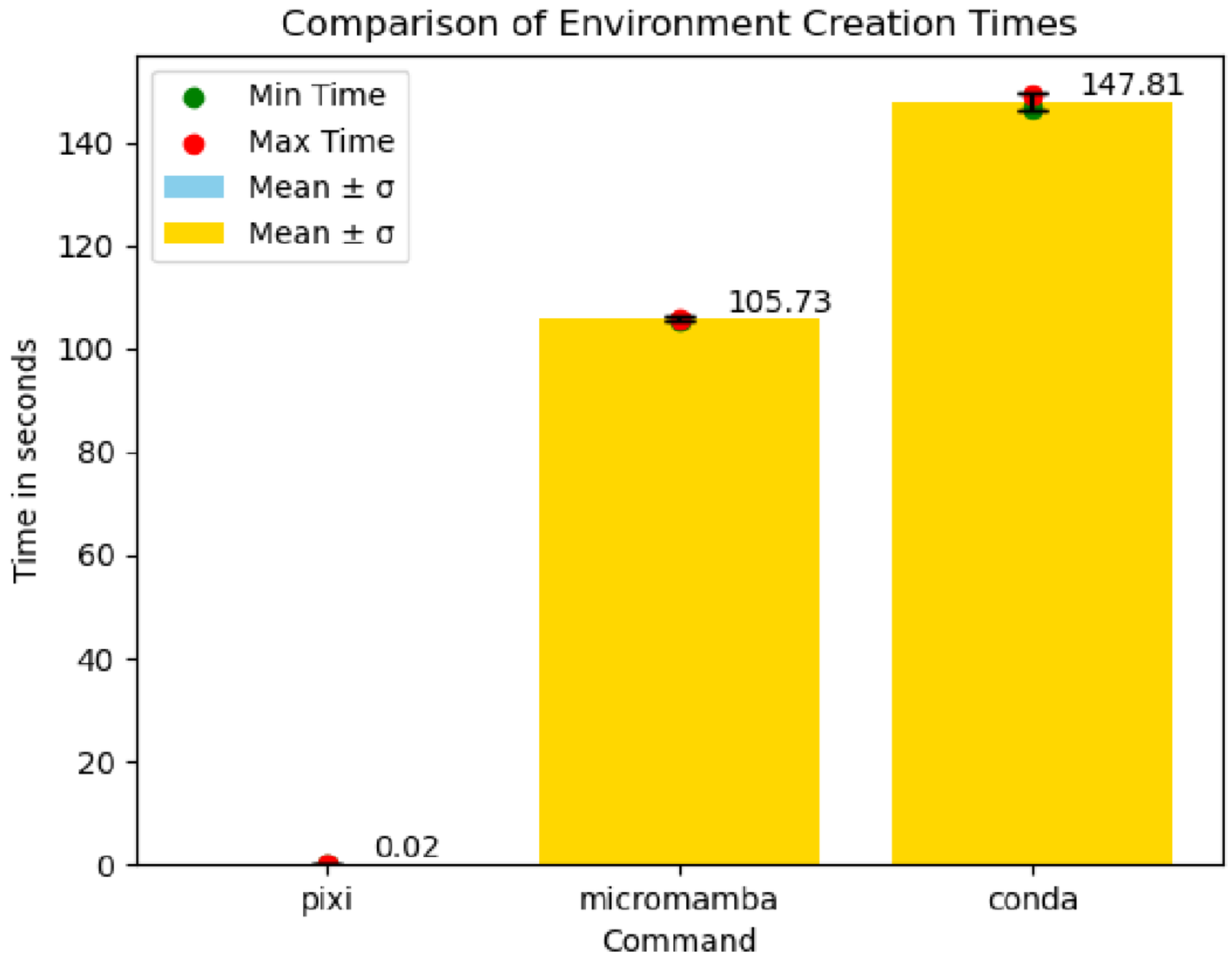
Any other tool just looking the PATH for a binary fails.

Real solution:

Just use conda environments with Snakemake

NOW WE BRING PIXI TO THE TABLE

* Fast (written in Rust) (has written its own solvers as well)
* Project-first, not environment-first
  - So much better idea
  - Deps installed in the same directory
  - Everything for setup in one file: pixi.toml
  - (Optional) Automatic environment activation with direnv
    (enter environment when inside directory)
* A super fast way to run binaries with trampolines
  - basically a very small binary 607KB does the setup before running the main binary
  - Which is now just in your PATH!
* Resolves both conda and pypi
  - This problem was never solved by anaconda,
    the general advice was to minimize pypi dependencies and do the solve in your head I guess
  - With a conda-pypi-map to map packages for both indexes (pixi doing the lords work here)
  - Now it is "conda resolve" -> map remainging packages -> send to "pypi resolve"
  - The holy grail (for pixi) is to have a single resolve for both providers
* Legal to use (if you use conda now you are a criminal)


Comparison of Environment Creation Times
Min Time
Max Time
Mean ± σ
Mean ± σ
Time in seconds
0
20
40
60
80
100
120
140
0.02
105.73
147.81
pixi
micromamba
conda
Command

PIXI INSTALLATION

```

curl -fsSL https://pixi.sh/install.sh | sh
```

That is it. A portable binary in your `$PATH`.

No base environment. No bootstrapping another conda tool with another conda tool.

TOOL INSTALLATION

```

pixi global install <package>
```

```

pixi global install -c conda-forge -c bioconda snakemake==7.25.4
```

THE UGLY

channel-priority is on strict by default and cannot be disabled (considered a security problem).

`pixi global install -c bioconda -c conda-forge` will make you cry.

bioconda packages will be preferred here,
    but are often way too old in comparison to conda-forge.

Just use:

`pixi global install -c conda-forge -c bioconda`

Or just

pixi config set default-channels '["conda-forge", "bioconda"]'

The plethora of channels of the conda ecosystem is also a headache sometimes.

Especially considering the fact that there then also exists equivalents which also exist on pypi.

THIS IS THE SIMPLE SOLUTION

Install the tool, and then

```
export PATH="$HOME/.pixi/bin:$PATH"
```

to the top of your script and you are done!

BONUS:

The complete setup is captured in ~/.pixi/manifests/pixi-global.toml

Can be put on another machine and repeat the whole setup exactly.

ADVANCED USAGE

Adding more dependencies to the environment:

pixi global install jupyter --with polars

Or later

pixi global install -e jupyter polars

Misc: Using a fixed PATH (if you are really afraid of module PATH changes)

export PIXI_BASE_PATH=$PATH

VERSIONS - EXPOSING

pixi global install -c conda-forge -c bioconda -e snakemake-9 --expose snakemake-9=snakemake snakemake==9.*
snakemake-9 --version

OR

pixi global expose remove snakemake
pixi global expose add snakemake -e snakemake-9

NB. `expose` is pretty slow

THE BAD - SINGLE USER ORIENTED

Problem: Using `pixi global expose`,
we just changed the snakemake version for everybody using this pixi install!

No easy solution, but fear not, I will have a working workflow.

ONTO THE TRAMPOLINE

`~/.pixi/bin/program` is where all the programs execution start.

`~/.pixi/bin/trampoline_configuration/trampoline_bin` can be hardlinked to anything.

Which then loads the configuration found in ~/.pixi/bin/trampoline_configuration/program.json

This will load the environment configuration and run the main binary in it.

Provided the conda package does nothing weird, this can be considered a working binary from your PATH. No magic required.

This has to be in that place. The binary cannot move. It relies on the directory structure.

You can still make soft links to it.

Trampolines are still a new technology, but should be equivalent to

```bash
(
  conda activate myenv
  program ...
)
```

NOW: PROPOSAL FOR VERSION MANAGEMENT

Pixi is not replacing module load

First, module load and easybuild sometimes provide a perfectly fine solution

Second, because some packages are just not available on conda.

Third, module load provides the better multi user version managing.

Pixi is just a better way to "install something", better than conda!

A PROBLEMATIC MODULE FILE

multiqc
```
prepend_path("PATH","/appdata/users/service-hgn/miniconda3/envs/multiqc-1.30/bin/")
prepend_path("PYTHONPATH","/appdata/users/service-hgn/miniconda3/envs/multiqc-1.30/lib/python3.13/site-packages")
```
conda bin folder are filled with other programs

PYTHONPATH is just very problematic

Easily breaks with other modules

```
module load multiqc
module load snakemake
python -c 'import numpy'  # breaks already!
```

PATH

KaleidoApp	fc-list	libpng16-config	psicc	tiffcrop
bunzip2	fc-match	linkicc	pydoc	tiffdither
bzcat	fc-pattern	makeconv	pydoc3	tiffdump
bzcmp	fc-query	markdown-it	pydoc3.13	tiffinfo
bzdiff	fc-scan	markdown_py	pygmentize	tiffmedian
bzegrep	fc-validate	mathjax-path	python	tiffset
bzfgrep	freetype-config	multiqc	python3	tiffsplit
bzgrep	genbrk	natsort	python3-config	tificc
bzip2	gencfu	ncurses6-config	python3.1	tjbench
bzip2recover	gencnval	ncursesw6-config	python3.13	toe
bzless	gendict	normalizer	python3.13-config	tput
bzmore	genrb	nspr-config	raw2tiff	tqdm
c_rehash	humanfriendly	nss-config	rdjpgcom	transicc
captoinfo	icu-config	numpy-config	reset	tset
certutil	icuexportdata	openssl	rich-click	unzstd
cjpeg	icuinfo	opj_compress	sqlite3	wish
clear	idle3	opj_decompress	sqlite3_analyzer	wish8.6
coloredlogs	idle3.13	opj_dump	tabs	wrjpgcom
derb	infocmp	pal2rgb	tclsh	x86_64-conda-linux-gnu-ld
djpeg	infotocap	pip	tclsh8.6	xmlwf
dotenv	jpegtran	pip3	tic	zstd
f2py	jpgicc	pk12util	tiff2bw	zstdcat
fax2ps	jsonschema	pkgdata	tiff2pdf	zstdgrep
fax2tiff	kaleido	plotly_get_chrome	tiff2ps	zstdless
fc-cache	libdeflate-gunzip	png-fix-itxt	tiff2rgba	zstdmt
fc-cat	libdeflate-gzip	pngfix	tiffcmp	
fc-conflist	libpng-config	ppm2tiff	tiffcp	

PYTHONPATH
MarkupSafe-3.0.2.dist-info
PIL
PySocks-1.7.1.dist-info
PyYAML-6.0.2.dist-info
README.txt
__pycache__
_brotli.cpython-313-x86_64-linux-gnu.so
_cffi_backend.cpython-313-x86_64-linux-gnu.so
_plotly_utils
_yaml
annotated_types
annotated_types-0.7.0.dist-info
attr
attrs
attrs-25.3.0.dist-info
brotli-1.1.0.dist-info
brotli.py
certifi
certifi-2025.7.14.dist-info
cffi
cffi-1.17.1.dist-info
charset_normalizer
charset_normalizer-3.4.2.dist-info
click
click-8.2.1.dist-info
colorama
colorama-0.4.6.dist-info
coloredlogs
coloredlogs-15.0.1.dist-info
coloredlogs.pth
colormath
colormath-3.0.0.dist-info
conda-site.pth
dotenv
h2
h2-4.2.0.dist-info
hpack
hpack-4.1.0.dist-info
humanfriendly
humanfriendly-10.0.dist-info
humanize
humanize-4.12.3.dist-info
hyperframe
hyperframe-6.1.0.dist-info
idna
idna-3.10.dist-info
importlib_metadata
importlib_metadata-8.7.0.dist-info
jinja2
jinja2-3.1.6.dist-info
jsonschema
jsonschema-4.25.0.dist-info
jsonschema_specifications
jsonschema_specifications-2025.4.1.dist-info
kaleido
kaleido-0.2.1.dist-info
markdown
markdown-3.8.2.dist-info
markdown_it
markdown_it_py-3.0.0.dist-info
markupsafe
mdurl
mdurl-0.1.2.dist-info
multiqc
multiqc-1.30.dist-info
narwhals
narwhals-2.0.0.dist-info
natsort
natsort-8.4.0.dist-info
networkx
networkx-3.5.dist-info
numpy
numpy-2.3.2.dist-info
packaging
packaging-25.0.dist-info
pillow-11.3.0.dist-info
pip
pip-25.1.1.dist-info
plotly
plotly-6.2.0.dist-info
polars
polars-1.31.0.dist-info
pyaml_env
pyaml_env-1.2.2.dist-info
pycparser
pycparser-2.22.dist-info
pydantic
pydantic-2.11.7.dist-info
pydantic_core
pydantic_core-2.33.2.dist-info
pygments
pygments-2.19.2.dist-info
python_dotenv-1.1.1.dist-info
referencing
referencing-0.36.2.dist-info
regex
regex-2024.11.6.dist-info
requests
requests-2.32.4.dist-info
rich
rich-14.1.0.dist-info
rich_click
rich_click-1.8.9.dist-info
rpds
rpds_py-0.26.0.dist-info
socks.py
sockshandler.py
spectra
spectra-0.0.11.dist-info
tiktoken
tiktoken-0.9.0.dist-info
tiktoken_ext
tqdm
tqdm-4.67.1.dist-info
typeguard
typeguard-4.4.4.dist-info
typing_extensions-4.14.1.dist-info
typing_extensions.py
typing_inspection
typing_inspection-0.4.1.dist-info
urllib3
urllib3-2.5.0.dist-info
yaml
zipp
zipp-3.23.0.dist-info
zstandard
zstandard-0.23.0-py3.13.egg-info

A BETTER WAY TO DO THIS

```
pixi global install multiqc
ln -s ~/.pixi/bin/multiqc /appdata/bin/1.30/multiqc
```

OR, even better

```
pixi global install -e multiqc-1.30 --expose multiqc-1.30=multiqc multiqc
ln -s ~/.pixi/bin/multiqc-1.30 /appdata/apps/multiqc/1.30/multiqc
```

(exposing the versions directly already)

NOW THE MODULE FILE BECOMES:

```
prepend_path("PATH","/appdata/apps/multiqc/1.30/")
```

It just works! `multiqc` (and only `multiqc`)
    with the correct version is now added to the path.

I believe that this is intended usage for modules also:

Make a single binary available in a versioned folder (just as easybuild).

NB. Keep in mind permissions of course!

Setting `$PIXI_HOME` to something outside of a home folder might help.

MODULE LOAD IS HERE TO STAY

but Pixi is still a full replacement for:

`conda`, `miniconda`, `mamba`, `micromamba`,
`pip`, `poetry`, `uv`, `pdm`, `hatch`, `rey`
`venv`, `virtualenv`, `pipenv`, `pyenv`,
`conda-build`, `setuptools`, `flit`,
and also task running like `npm run` and what not.

PIXI WITH SNAKEMAKE

You still have to use conda with snakemake to activate the environments

Supporting pixi in snakemake is a work in progress.

You can however still just install conda with pixi.

TLDR

Conda packages from conda-forge and bioconda are great!

The conda client is not great.

Pixi is the next-gen replacement for conda and is great!

Especially since, conda was never used for tool installation, pixi has a system

Module load still provides the better multi-user versioned system, and familiar

Pixi is just a quick and sane package manager when easybuild fails you

Next up: Sane next-gen dependency management and task running for projects with pixi

BRAINSTORMING

But I have some more slides as well!

PS. For those that are on the terminal a lot and like speed and ergonomics

Rewrite it in rust (RIIR):

grep -> ripgrep (rg)

find -> fd-find (fd)

cd -> zoxide (z)

uv -> pip (uv included in pixi)

sed -> sd

I practically use all of them

Best of all: Pixi can install most of them!

More RIIR (which I do not use)

du -> dust/dua

tmux -> zellij

ps -> procs

make -> just (task runner, but pixi comes also with a task runner)

Source: https://github.com/j-m-hoffmann/awesome-rewrite-it-in-rust

And some more modern tools I use

man -> tldr (tealdeer is the rust implementation)

du -> ncdu

? -> fzf (fuzzy finder, there is also skim in rust)

And of course let's not forget:

vim -> neovim