



TEXAS ADVANCED COMPUTING CENTER

WWW.TACC.UTEXAS.EDU



# A Notebook-based Platform for Computational Chemistry and Materials Science

Chun-Yaung Lu  
alu@tacc.texas.edu

# Jupyter Notebook

The Jupyter Notebook is an open-source web application that allows you to create and share documents that contain **live code**, **equations**, **visualizations** and **narrative text**. Uses include: data cleaning and transformation, numerical simulation, statistical modeling, data visualization, machine learning, and much more.



<https://jupyter.org/>

# TACC Visualization Portal

<https://vis.tacc.utexas.edu>

**TACC Visualization Portal** TACC/cylu [logout](#)  
Resource: Stampede2 (Job 3809941)  
Time left: 2:40:11

Home Jobs Help

Welcome to the TACC Visualization Portal  
Simple access to TACC's Vis Resources

You are already logged in as **cylu**. [Logout](#)

**Features:**

- + Remote, interactive, web-based visualization
- + iPython / Jupyter Notebook integration
- + R Studio integration
- + Run on Stampede2 and Wrangler
- + Visualization job submission and monitoring
- + Current resource usage and allocation view

**Job Submission**

**VNC Visualization Session**

**Jupyter/iPython Notebook**

**RStudio**

TACC's Visualization Resources  
TACC User Portal XSEDE User Portal

- Use your **TACC** or **XSEDE** User Portal username and password to log in
- Run VNC, iPython/Jupyter Notebook, R Studio on Stampede2 or Wrangler
- Available Stampede2 queues for iPython/Jupyter: *development*, *skx-dev*, *normal*, *skx-normal*, ...
- One compute node each time  
KNL: **68** cores, SKX: **48** cores

# TACC Visualization Portal

<https://vis.tacc.utexas.edu>

The screenshot shows the 'Start a Job' form in the TACC Visualization Portal. The form includes fields for Resource (Stampede2), Project (A-ccsc), Session type (iPython/Jupyter Notebook), Reservation ID (optional), and Job runtime (optional). A dropdown menu for Queue is open, showing options: development (checked), skx-dev, normal, skx-normal, large, skx-large, and flat-quadrant. A 'Start Job' button is at the bottom left.

The screenshot shows the TACC Visualization Portal dashboard. At the top, it says 'Your iPython Notebook session is running on Stampede2.' with buttons for 'Open In Browser' and 'Terminate Jupyter'. Below, it displays 'Stampede2 load and queue state.' with a refresh button and a pie chart. The pie chart shows 95.5% of nodes are in use (red) and 4.5% are available (blue). The text above the chart says 'Nodes: 268 available out of 5936 total.'

The screenshot shows the Jupyter file browser interface. It displays a list of files and folders in the '/notebook/examples' directory. The files are listed with their names, last modified times, and file sizes.

Name	Last Modified	File size
..	seconds ago	
ase	3 months ago	
hoomd	7 months ago	
lammps	6 months ago	
nglview	3 months ago	
octave	5 months ago	
rdkit	a month ago	
sympy	7 months ago	

# Running LAMMPS

On Stampede2:

```
$module load lammops
```

will load default version 16Mar18.

The latest version 5Jun19 is also available

In Python3

```
c455-043[knl](1001)$ python3
Python 3.7.0 (default, Feb 6 2019, 21:24:19)
[GCC Intel(R) C++ gcc 6.3 mode] on linux
Type "help", "copyright", "credits" or "license" for more information.
>>> from lammops import IPyLammps
>>> L = IPyLammps()
LAMMPS (22 Aug 2018)
  using 1 OpenMP thread(s) per MPI task
LAMMPS output is captured by PyLammps wrapper
>>> █
```

Command line: `Imp_stampede < input`

```
c455-043[knl](1017)$ cp $TACC_LAMMPS_EXAM/melt/in.melt .
c455-043[knl](1018)$ Imp_stampede < in.melt
LAMMPS (22 Aug 2018)
  using 1 OpenMP thread(s) per MPI task
Lattice spacing in x,y,z = 1.6796 1.6796 1.6796
Created orthogonal box = (0 0 0) to (16.796 16.796 16.796)
  1 by 1 by 1 MPI processor grid
Created 4000 atoms
Time spent = 0.00205088 secs
Neighbor list info ...
```

In Jupyter

```
In [1]: from lammops import IPyLammps
        L = IPyLammps()
```

LAMMPS output is captured by PyLammps wrapper

```
In [2]: from lammops import PyLammps
        L = PyLammps()
```

LAMMPS output is captured by PyLammps wrapper

[https://lammops.sandia.gov/doc/Python\\_head.html](https://lammops.sandia.gov/doc/Python_head.html)

# More Packages

There are many many other packages that you can install and use in Jupyter

Many packages can be installed simply by using pip:

```
$pip install myPackage --user
```

Some jupyter-friendly chemistry packages that I installed and tested on Stampede2 (not a full list)

Name	Version	Function
gpaw	1.5.1	Quantum DFT
lammps	22Aug18	Classical MD
hoomd-blue	2.3.5	Classical MD, CGMD
ase	3.17.0	Simulation interface
tsase	master	Transition state library for ASE
rdkit	2018_03_4	Cheminformatics, ML
mdtraj	1.9.2	Analysis tool
pytraj	2.0.3	Analysis tool
cpptraj	18.00	Analysis tool
parmed	3.03	Analysis tool
OpenKIM	1.9.7	Force field database
libxc	4.2.3	XC library
libvdwxc	0.3.2	XC-VDW library
nglview	1.1.7	Visualizer

# Atomic Simulation Environment (ASE)

## Supported Software



Name	Description	ST2
<b>Asap</b>	Highly efficient EMT code	
<b>GPAW</b>	Real-space/plane-wave/LCAO PAW code	<b>YES</b>
<b>Hotbit</b>	DFT based tight binding	
<b>abinit</b>	Plane-wave pseudopotential code	
<b>amber</b>	Classical molecular dynamics code	<b>YES</b>
<b>castep</b>	Plane-wave pseudopotential code	
<b>cp2k</b>	DFT and classical potentials	
<b>demon</b>	Gaussian based DFT code	
<b>dftb</b>	DFT based tight binding	
<b>dmol</b>	Atomic orbital DFT code	
<b>QE</b>	Plane-wave pseudopotential code	<b>YES</b>
<b>exciting</b>	Full Potential LAPW code	
<b>aims</b>	Numeric atomic orbital, full potential code	
<b>fleur</b>	Full Potential LAPW code	

Name	Description	ST2
<b>gaussian</b>	Gaussian based electronic structure code	<b>YES</b>
<b>gromacs</b>	Classical molecular dynamics code	<b>YES</b>
<b>gulp</b>	Interatomic potential code	<b>YES</b>
<b>jacapo</b>	Plane-wave ultra-soft pseudopotential code	
<b>lammps</b>	Classical molecular dynamics code	<b>YES</b>
<b>mopac</b>	Semiempirical quantum chemistry code	
<b>nwchem</b>	Gaussian based electronic structure code	<b>YES</b>
<b>octopus</b>	Real-space pseudopotential code	
<b>onetep</b>	Linear-scaling pseudopotential code	
<b>siesta</b>	LCAO pseudopotential code	<b>YES</b>
<b>turbomol</b>	Fast atom orbital code	
<b>VASP</b>	Plane-wave PAW code	<b>YES</b>
<b>dftd3</b>	DFT-D3 dispersion correction calculator	

<https://wiki.fysik.dtu.dk/ase/ase/calculators/calculators.html#module-ase.calculators>

# LAMMPS + Jupyter + HPC

TACC Vis Portal lets you run Jupyter Notebook on ONE compute node (KNL: 68 cores, SKX: 48 cores)

- LAMMPS's USER-OMP package (provides optimized and multi-threaded version of many LAMMPS functions)

```
In [18]: L.clear()
          L.package("omp 4")

Out[18]: ['set 4 OpenMP thread(s) per MPI task',
          'using multi-threaded neighbor list subroutines']
```

- Run LAMMPS on multiple processors (use ipyparallel + mpi4py)

## MPI4Py:

MPI for Python provides bindings of the Message Passing Interface (MPI) standard for the Python programming language, allowing any Python program to exploit multiple processors.

<https://mpi4py.readthedocs.io/en/stable/>

## Ipyparalle:

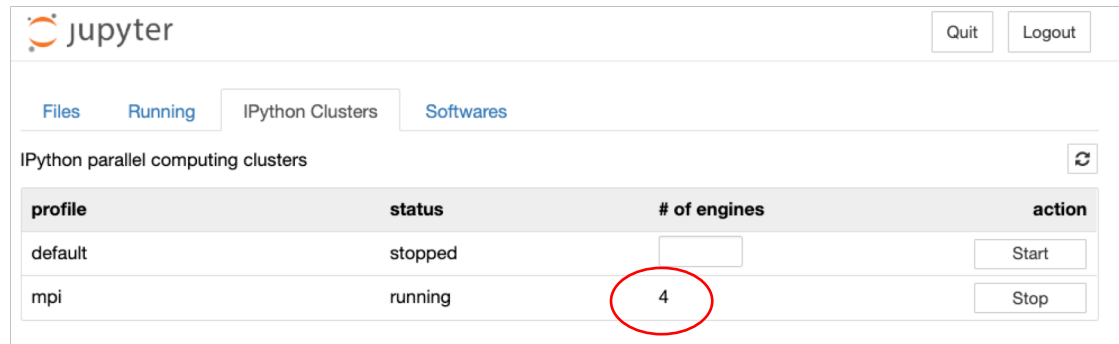
Ipyparallel (formerly IPython parallel) enables all types of parallel applications to be developed, executed, debugged, and monitored interactively.

<https://ipyparallel.readthedocs.io/en/latest/intro.html>



# Parallel Scheme (domain decomposition)

**Step 1**  
Start ipcluster



The screenshot shows the Jupyter IPython Clusters interface. At the top, there are tabs for 'Files', 'Running', 'IPython Clusters', and 'Softwares'. Below the tabs, there is a table titled 'IPython parallel computing clusters'. The table has four columns: 'profile', 'status', '# of engines', and 'action'. There are two rows: 'default' with status 'stopped' and an empty input field for the number of engines; and 'mpi' with status 'running' and the number '4' circled in red. The 'action' column has 'Start' and 'Stop' buttons for each row.

profile	status	# of engines	action
default	stopped	<input type="text"/>	Start
mpi	running	4	Stop

Start with 4 ipython engines

**Step 2**  
Import ipyparalle

```
In [1]: import os
import ipyparallel as ipp
rc = ipp.Client(profile='mpi')
view = rc[:]
print("Total number of MPI tasks =", len(view))

Total number of MPI tasks = 4
```

**Step 3**  
Import mpi4py and  
start LAMMPS

```
In [3]: %%capture
%%px ← Cell magic for executing python
commands on the ipython engines

from mpi4py import MPI
from lammps import IPyLammps

L = IPyLammps(cmdargs=["-log", logfile])
```

# Parallel Scheme (multi-replica)

(Example: lammmps\_neb\_hop1.ipynb)

E.g. 13 replicas, 2 cpus/replica



jupyter

Quit Logout

Files Running IPython Clusters Softwares

IPython parallel computing clusters

profile	status	# of engines	action
default	stopped	<input type="text"/>	Start
mpi	running	26	Stop

Start with 26 iPython engines

```
In [1]: import os
import ipyparallel as ipp
rc = ipp.Client(profile='mpi')
view = rc[:]
print("Total number of MPI tasks =", len(view))
```

Total number of MPI tasks = 26

```
In [4]: %%capture
%%px
from mpi4py import MPI
from lammmps import PyLammmps
# Use 13 images with 2 MPI tasks per image
L = PyLammmps(cmdargs=["-partition", "13x2", "-in", infile, "-log", logfile, "-plog", "none", "-pscreen", "none"])
```

Start LAMMPS with 13 replicas with 2 cores/replica

# Making Workflow: PARSL

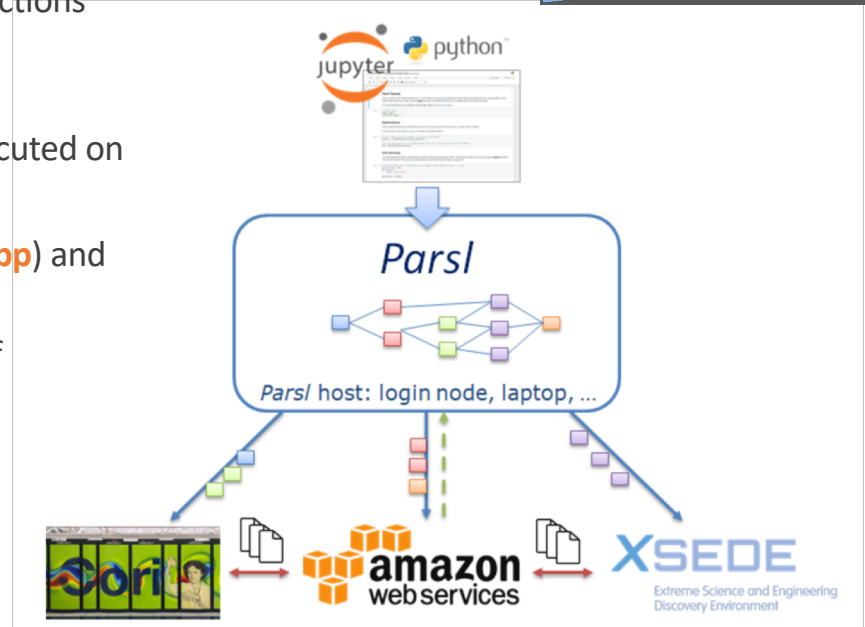


Parsl is a native Python library. It allows you to write functions that execute in parallel and tie them together with dependencies to create workflows.

“App” is a piece of code that can be asynchronously executed on an execution resource

Parsl provides support for pure Python apps (**python\_app**) and also command-line apps executed via Bash (**bash\_app**)

Parsl creates implicit workflows based on the passing of control or data between Apps.



```
@python_app
def hello ():
    return 'Hello World!'
```

```
@bash_app
def echo_hello(stdout='echo-hello.stdout', stderr='echo-hello.stderr'):
    return 'echo "Hello World!"'
```

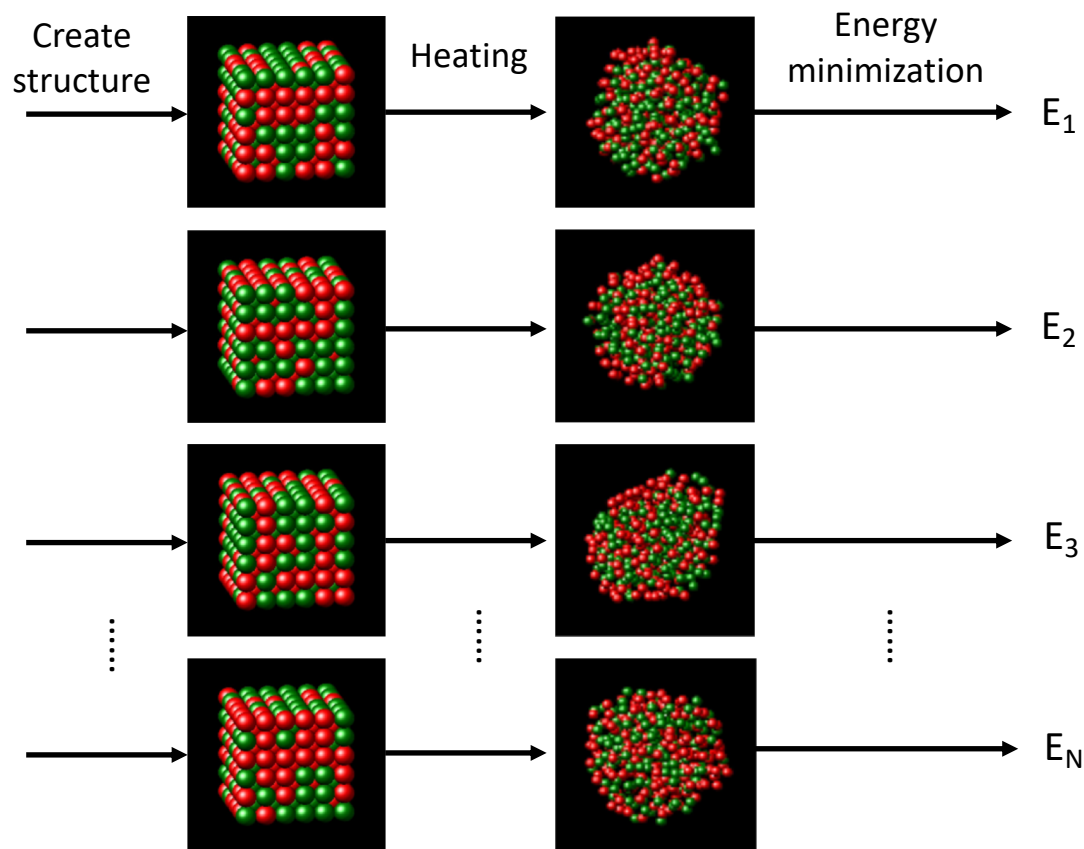
```
@bash_app
def run_lammps(stdout='stdout', stderr='Imp.stderr'):
    return 'Imp_stampede < input'
```

<http://parsl-project.org/>

# Example 1 (Fe/Cr random alloy)

Pure python code

M tasks  
N workers

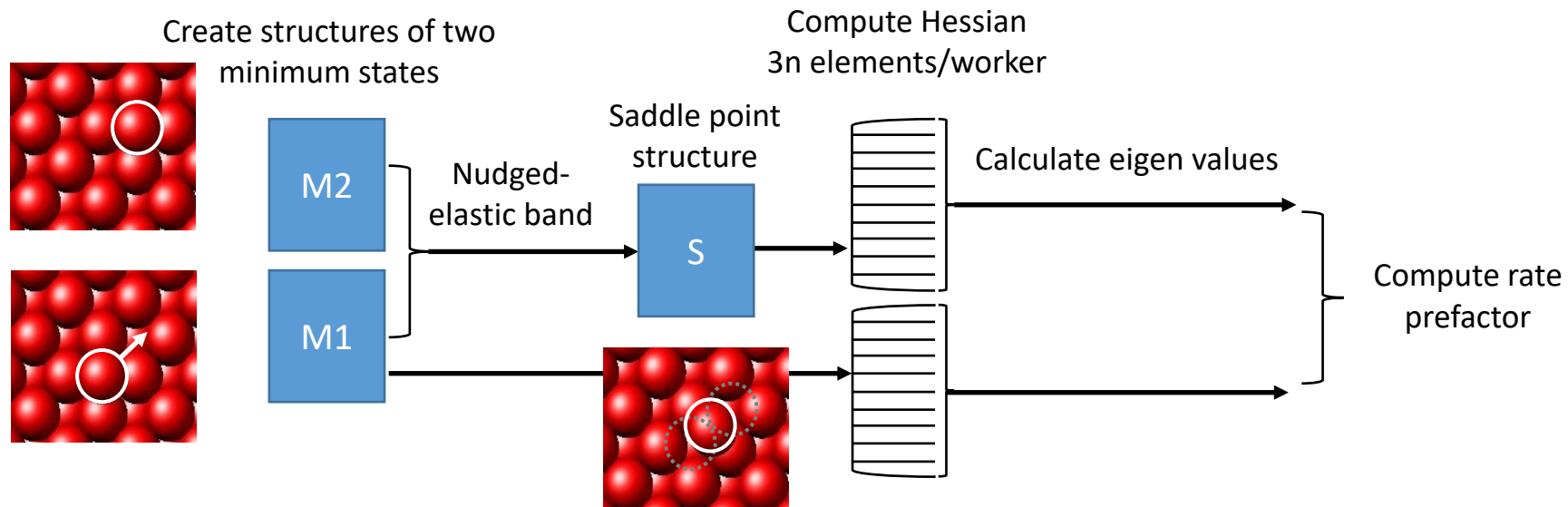


Parallel workflow

# Example 2 (Al surface diffusion, Hessian matrix)

Pure python code

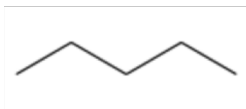
$$H_{3n \times 3n} = \{\partial V / \partial x_i \partial x_j\}$$



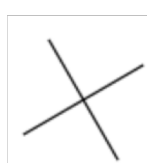
# Example 3 (Alkane C-H Bond dissociation Energy)

Alkane isomers:

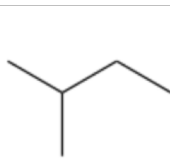
E.g.  $C_5H_{12}$



n-pentane



neo-pentane



i-pentane

Number of isomers:

$C_{10}H_{22}$ : 75

$C_{12}H_{26}$ : 355

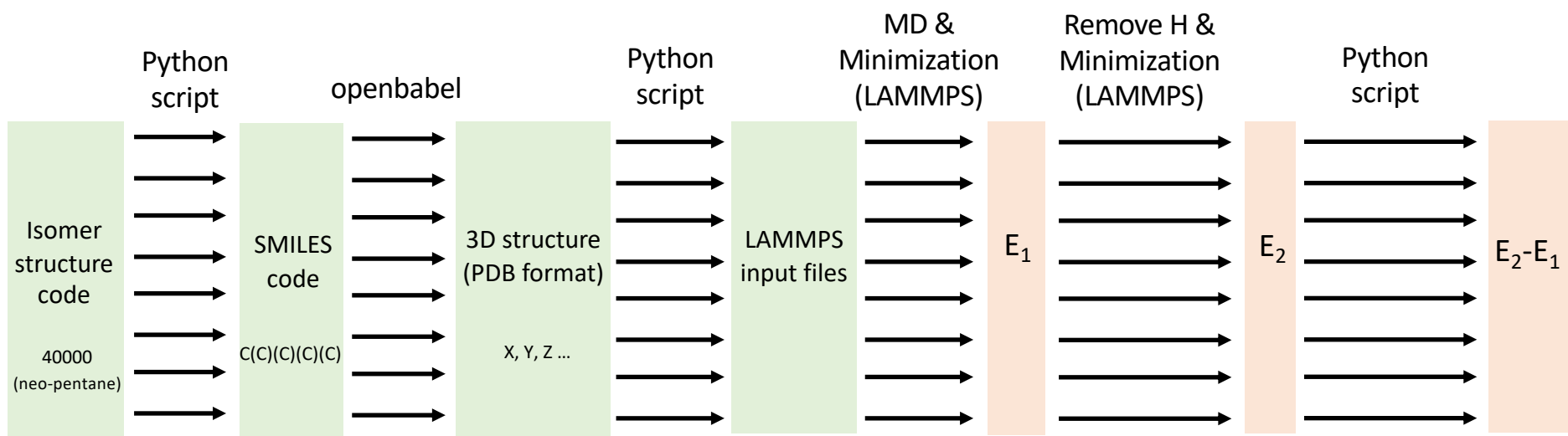
$C_{15}H_{32}$ : 4,347

$C_{18}H_{38}$ : 60,523

$C_{20}H_{42}$ : 366,319

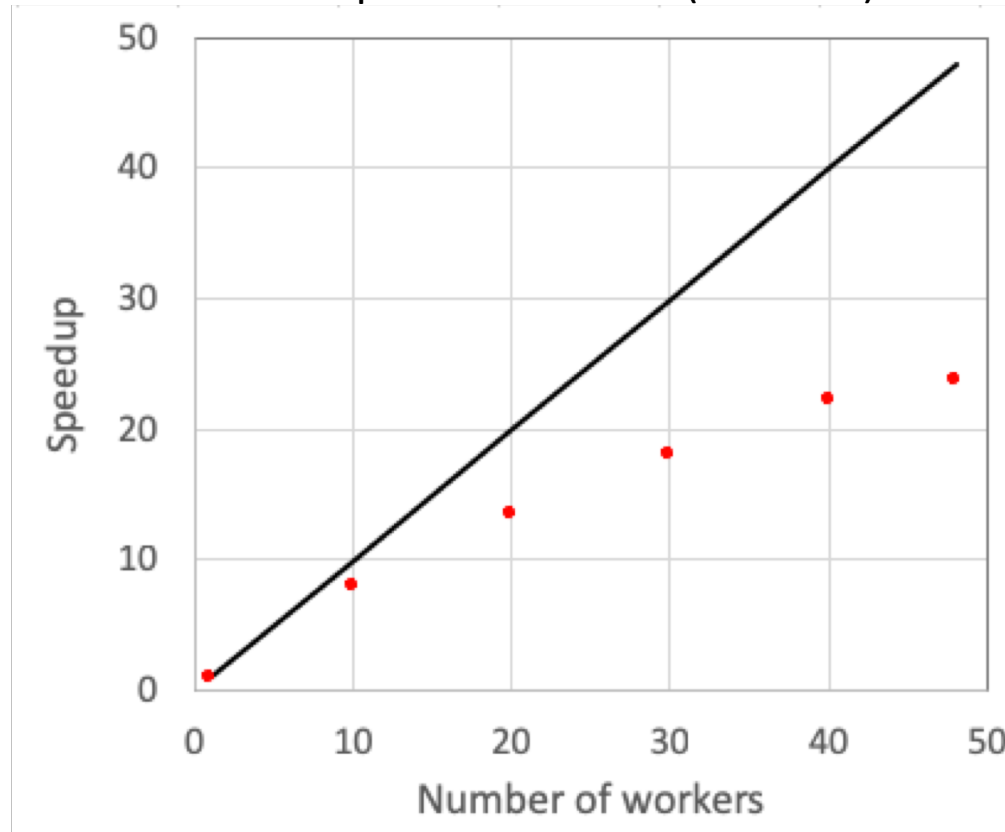
$C_{21}H_{44}$ : 910,726

$C_{24}H_{50}$ : > 14.5M



# Example 3 (performance test)

Stampede2 SKX node (48 cores)



48 workers

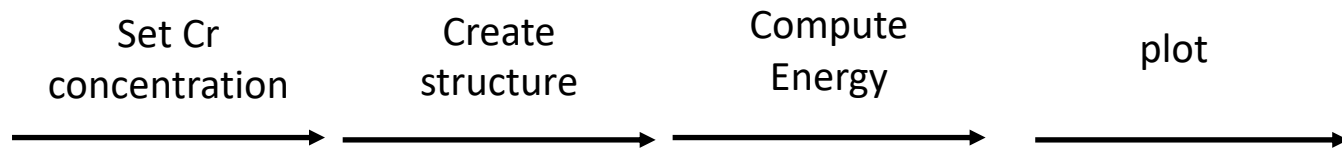
Efficiency ~50%

96 mins → 4 mins

Run directly

```
$time python3 alkane.py
```

# Example 4 (Fe/Cr random alloy, ipywidgets)



```
In [3]: im=interact_manual(Reset)
im.widget.children[0].description = 'Reset'
interactive_plot = interactive(GenStruct, p=(0, 1, 0.1))
output = interactive_plot.children[-1]
output.layout.height = '350px'
interactive_plot
```

Reset

p  0.20

Cr/Fe random alloy  
Cr = 20.0 %  
Energy = -1188.093495 eV

