

## Problem 2: Advanced cooling

### Aims of this exercise

- 1 Understand that writing cooling functions is a mess
- 2 Realize that KROME saves your day

- *Homework: because 7 hours of school wasn't enough*  
(Anonymous)

## Core of part1

Custom cooling functions go into the chemical network file

## Recap for part1

- [http://kromepackage.org/bootcamp/exercises/day1\\_2.tar.gz](http://kromepackage.org/bootcamp/exercises/day1_2.tar.gz)
- NOTE: network is provided in file `network_start`
- TODO: complete the network with custom cooling function
- NOTE: parts for custom cooling are in `code_block` file
- TODO: copy them into the network file
- TODO: add the tokens `@something` listed in the text
- `@var ntot = get_Hnuclei(n(:)) → @var:ntot = ...`
- `@cooling`
- `@cooling_start @cooling_stop`

## 2 things worth knowing

- 1 loop on Tgas
- 2 for each temperature go to equilibrium

## Recap for part1A

- TODO: write a loop on Tgas with log steps from 10 – 10<sup>4</sup> K
- TODO: inside the loop initialize the species
- `krome_scale_Z` helps
- `python list_user_functions.py`
- NOTE: chemical equilibrium = running KROME at constant temperature for 10<sup>8</sup> yr
- TODO: add call `krome_thermo_OFF()`
- call KROME using `-useThermoToggle`

This is easy...

- `-cooling=H2` enables H<sub>2</sub> cooling
- do not forget `-noExample` option!

## 2 more things worth knowing

- 1 LAMDA is an atomic database (rotational)
- 2 file `tools/coolCO.dat` contains rotational data

## Additional option to use

- `-coolFile=` enables cooling from external data

**GOOD WORK!**

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