KROME + RAMSES: Integration of Chemistry with Fluid Dynamics

**KROME Bootcamp, Göttingen, September 2014** 

### Troels Haugbølle

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Centre for Star and Planet Formation
Natural History Museum
University of Copenhagen

#endif

cvar(ivar) = d\*qvar(ivar)

#ifdef know;

else | Make sure effective adiabatic index is just copied over

tvar(ivar) = qvar(ivar)

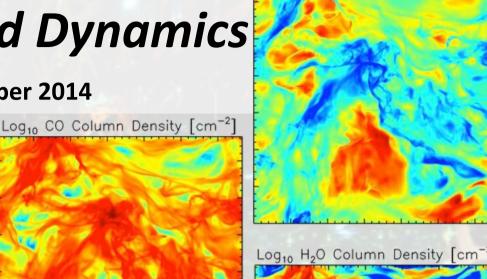
endif

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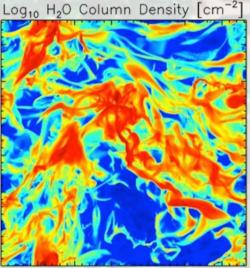
#endif







Adiabatic Index





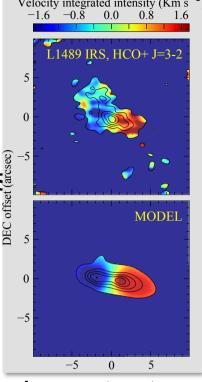
A research centre for cosmochemistry, astrophysics and astronomy



Chemistry + Fluid Dynamics

A Happy Union ?

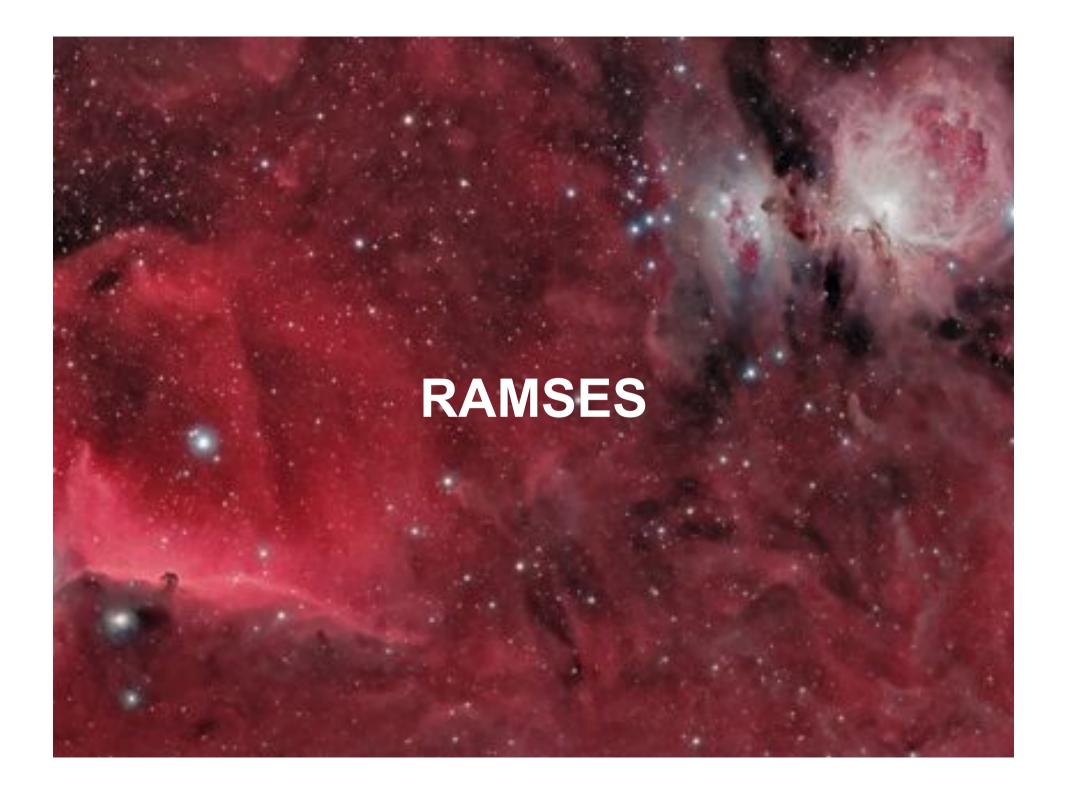




- With the completion of ALMA, precise astrochemistry models are becoming ever more important:
  - Model → Chemical Abundance → Synthetic Observations

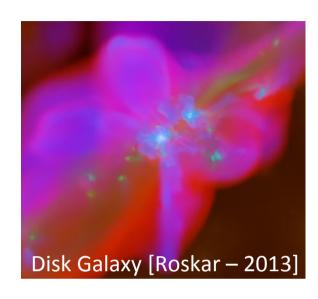
#### But

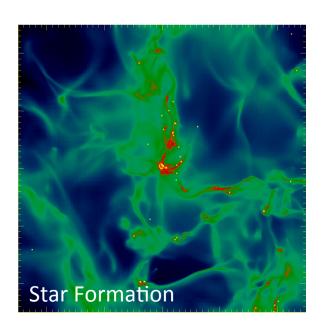
- What are the ingredients in a proper model?
- What are the pitfalls?



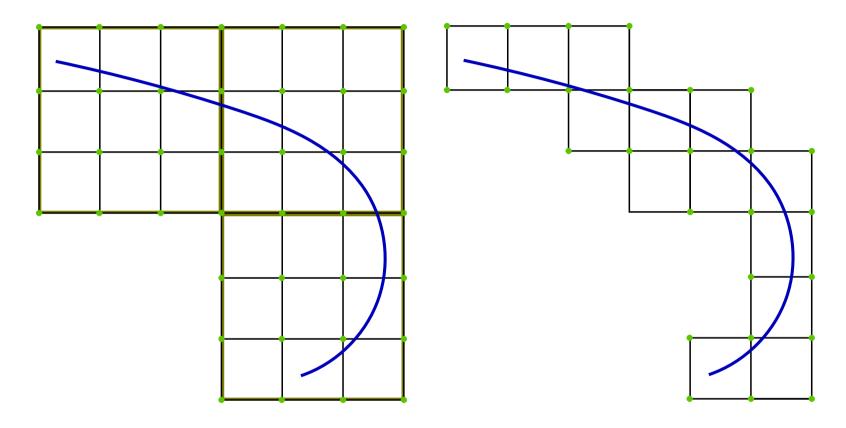
### **RAMSES**

- RAMSES is a well established AMR code originally written for Cosmology, but now applied in many other astrophysical contexts.
- Written by Romain Teyssier in 2002, it is public, and used by a large number of groups.
- https://bitbucket.org/rteyssie/ramses
- The AMR structure is a fully threaded oct-tree.
- The code can model a mixture of cell based fluids and particles. It has many physics modules: MHD, Selfgravity, collisionless particles, sink particles, cooling tables, cosmic rays, radiative transfer, feedback, ...
- Parallelization is (OpenMP)+MPI (public) or OpenMP+MPI (our version), and the code scales to well over 10.000 cores.





### Tree-Based Adaptive Mesh Refinement



- A patch based AMR structure is much better at adapting to complex flows, like turbulence
- CPU overhead is larger; hard to vectorize efficiently due to linked list structure

## Fluid dynamics

- RAMSES includes solvers for HD and MHD with passive scalars
- Implementation based on a second order MUSCL scheme
- Many different Godunov solvers
  - LLF HLL HLLC HLLE HLLD ROE
- Different Slope limiters
  - Minmod, Monotonized central, ultrabee, superbee
- MHD is constrained transport with staggered fields, and 2D Riemann solvers for the EMF
- Recently, non-thermal energy components have been added in to the second-order predictor-corrector time update

## Refinement Criteria

- Jeans / Truelove Criteria
  - If the Jeans length is not resolved, collapse becomes unphysical
- Gradients, in particular it is possible to refine on passive scalar gradients
- Mass Refinement (Quasi-Lagranian)
  - Related to Jeans. F.x. refine every time density goes up with 4 to have same Jeans resolution on all levels
- Geometrical (zoom)
  - Only allow code to refine in specific region

## Godunov and AMR Refinement

- Interpolation to finer meshes
  - Creation of new cells
  - On-the-fly boundary cells
- Averaging to coarser levels
  - Destruction / derefinement
  - Filling of the threaded tree

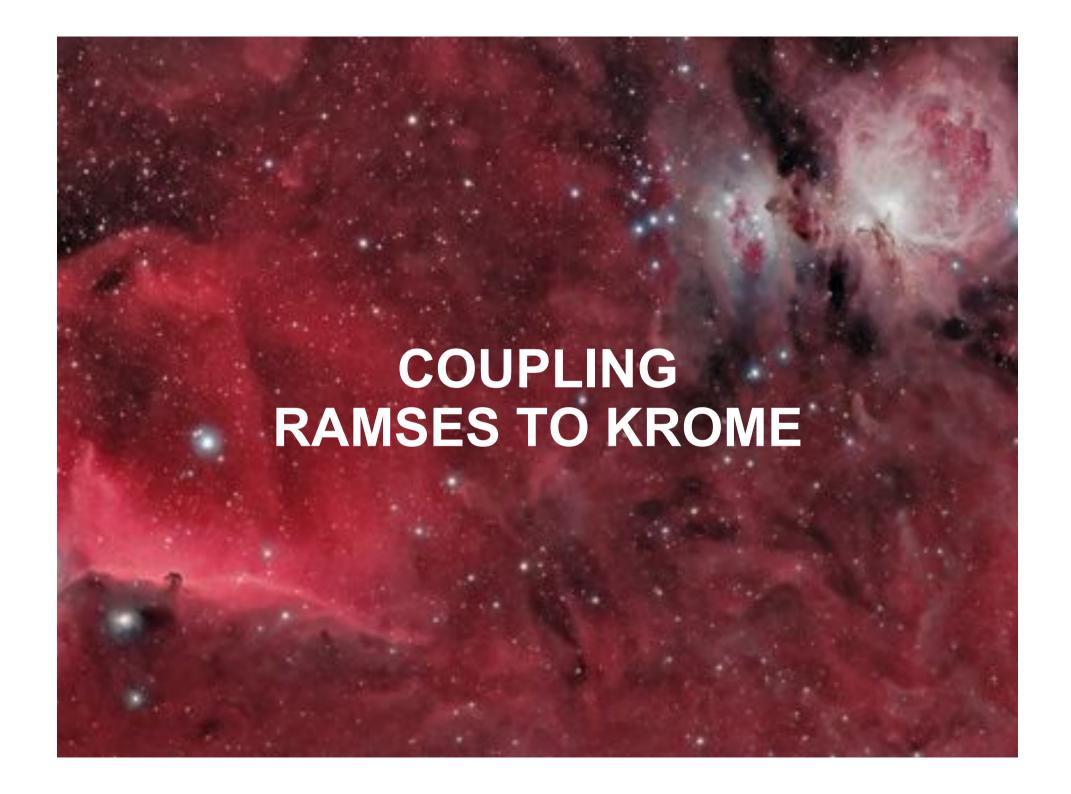


- Flux correction at boundaries
  - Relatively easy for volume fluxes
  - Tricky for EMF at edges
- Different interpolators
  - Conservative / internal energy
  - Apply different slope limiters

(from talk by Romain Teyssier)

## **Physics**

- HD / MHD: State-of-the-art; many solvers
- Self-Gravity: Conjugate gradient or Multigrid methods
- Cooling & Heating:
  - Cooling for cosmology, high-T, implicit solver, UV & cosmic ray heating
  - Moment based radiative transfer. Coupling to energy equation.
- Particles: DM (collisionless), tracers, sinks
- Sink particles: Based on a clump finder algorithm, can feedback on the gas (Supernovae, winds)
- Metals as passive tracers



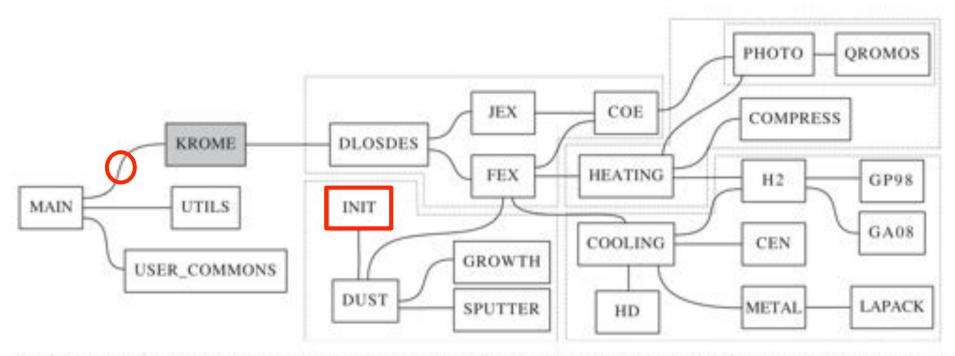


Figure 5. Pictorial view of the graph representing subroutine and modules in the KROME package. MAIN is the framework program, KROME (greyed) is the main module of KROME, while the other modules are explained in detail within the text.

Running KROME with a *framework code* is easy:

./krome -ramses -useN -network ...

the files, ready for integration, are left in ./build

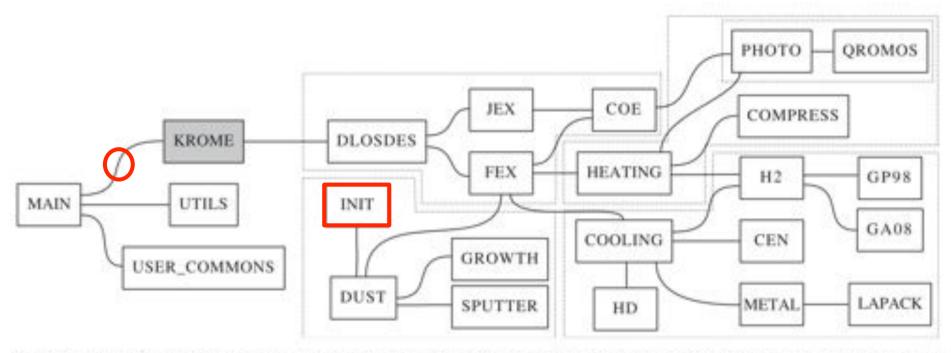


Figure 5. Pictorial view of the graph representing subroutine and modules in the KROME package. MAIN is the framework program, KROME (greyed) is the main module of KROME, while the other modules are explained in detail within the text.

KROME couples through the energy equation as a source term:

$$\frac{\partial \boldsymbol{U}}{\partial t} + \nabla \cdot \boldsymbol{F} = \boldsymbol{S}$$

$$\frac{\mathrm{d}T}{\mathrm{d}t} = (\gamma - 1) \frac{\Gamma(T, \bar{n}) - \Lambda(T, \bar{n})}{k_{\mathrm{b}} \sum_{i} n_{i}}$$

$$\frac{\partial (\rho e)}{\partial t} + \nabla \cdot [(\rho e + P)v] = S_{e}$$

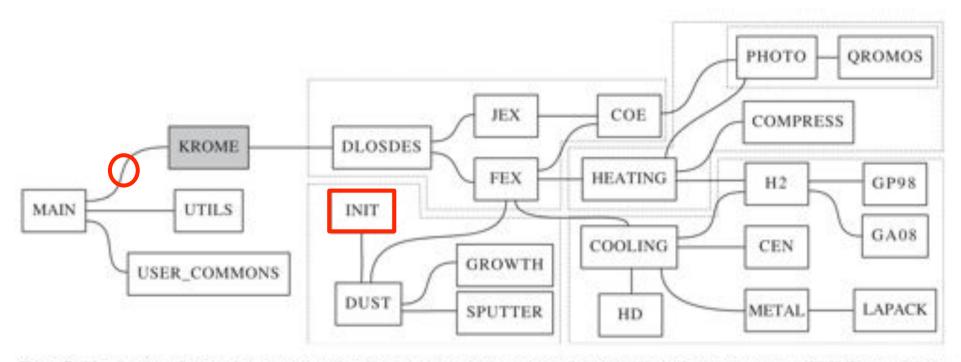


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KROME couples through the energy equation as a source term:

- KROME has to be initialized. This happens in the initialization of cooling and heating in cooling\_module.f90
- Time evolution and cooling and heating due to the chemical composition is calculated in the thermal energy hook: cooling\_fine.f90

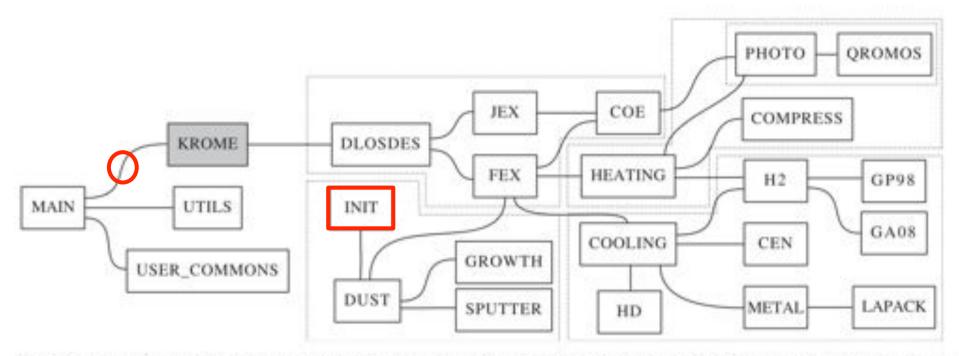


Figure 5. Pictorial view of the graph representing subroutine and modules in the KROME package. MAIN is the framework program, KROME (greyed) is the main module of KROME, while the other modules are explained in detail within the text.

Is that ALL there is to chemistry integration?

In Astro Chemistry

You need to know what you don't know!

applies heavily. You need to know what are the relevant reactions for your physical setup.

- Timescales and thermal conduction
- Adiabatic Index
- Local Conservation of abundances
- Performance and parallelization

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Ionization, MHD, and thermal conduction

$$\frac{\partial n_{i}}{\partial t} + \nabla \cdot (n_{i} \, \mathbf{v}) = f_{i}(n_{j}, N_{j}, T, G_{0})$$

$$\frac{\partial \rho \mathbf{v}}{\partial t} + \nabla \cdot \left( p + \frac{B^{2}}{8 \pi} + \rho \, \mathbf{v} \otimes \mathbf{v} - \frac{B \otimes B}{4 \pi} \right) = 0,$$

$$\frac{\partial e}{\partial t} + \nabla \cdot \left\{ \left( e + p + \frac{B^{2}}{8 \pi} \right) \, \mathbf{v} - \frac{B \cdot \mathbf{v}}{4 \pi} B \right\} = \nabla \cdot \kappa \nabla T - L(n_{i}, N_{i}, T, G_{0}),$$

$$\frac{\partial B}{\partial t} = \nabla \times (\mathbf{v} \times B),$$

$$\rho = \sum_{i} m_{i} n_{i},$$
[Inoue & Inutsuka - 2012]

In Astro Chemistry

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applies heavily. You need to know what are the relevant reactions for your physical setup.

- Timescales and thermal conduction
- Adiabatic Index:
  - Only when  $\gamma < 4/3$  gravitational collapse will proceed
  - Changes in the adiabatic index are crucial for the
    - formation of protostars
    - stability of accretion disks
- The *effective* adiabatic index may be different due to cooling and heating! F.x. ISM has  $\gamma_{eff}$  < 1

In Astro Chemistry

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- Timescales and thermal conduction
- Adiabatic Index

KROME solves: 
$$\frac{\mathrm{d}T}{\mathrm{d}t} = (\gamma - 1) \frac{\Gamma(T, \bar{n}) - \Lambda(T, \bar{n})}{k_{\mathrm{b}} \sum_{i} n_{i}}$$

with the adiabatic index computed according to the KROME "-gamma" switch: constant, FULL, ROT, VIB, EXACT

But what about **YOUR** code? A variable adiabatic index should be implemented, including in the (M)HD solvers, and all places that convert between pressure and internal energy

#### SUBROUTINE find who flux vec(gvar,cvar,ff,vel) II compute the 1D MHD fluxes from the conservative variables !! the structure of gwar is : rho, Pressure, Whormal, Bhormal. !! Vtransversel, Btransversel, Vtransverse2, Btransverse2 INTEGER : 1 . ivar. ib Local variables entho = one/(gamma-one) d->qvar(:,1); P->qvar(:,2); u->qvar(:,3); A->qvar(:,4 y=>qvar(:.5): B=>qvar(:.6): w=>qvar(:.7): C=>qvar(:.8 ecin = half\*(u\*u+v\*v+v\*v)\*d emag = half\*(A\*A+B\*S+C\*C) #ifdef KROME etot = P / (merge(qvar(:\_ichem).gamma.chemistry) - one) + ecin + emag etot = P\*entho+ecin+emag #endi f Ptot = P + emag do = d\*u I Compute conservative variables 10101011 Compute flures ff(:,1) = dudo ivar = 9, nvar #ifdef KROME if (ivar .ne. ichem) them ff(:,ivar) = du\*gvar(:,ivar) else ! Make sure effective adiabatic index has zero flux ff(:.ivar) = zero call trace mpi('find mhd flux vec(over.cvar.ff.vel)', 'exit',3) END SUBROUTINE find mhd flux vec

### Adiabatic Index

Example extract from local CPH version of RAMSES:

- KROME returns adiabatic index as a passive scalar
- All pressures computed from internal energy or vice versa use passive scalar
- Update Godunov solvers to work with changing adiabatic index
- Make sure refinement and interpolation is ok

In Astro Chemistry

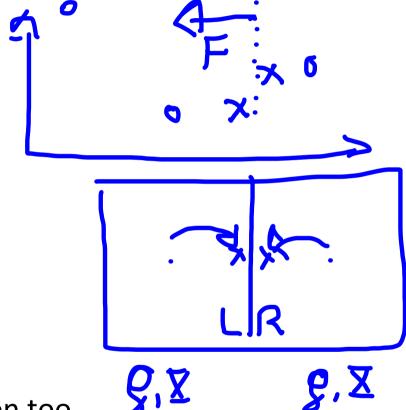
You need to know what you don't know!

applies heavily. You need to know what are the relevant reactions for your physical setup.

- Timescales and thermal conduction
- Adiabatic Index
- Multi-fluid Advection and Conservation of Abundances
   [Plewa and Müller 1999]

# Multi-fluid Advection Conservation of Abundances

- Flux conservation ensures global conservation of species
- Slope limiter induces large local error in species (≈30% errors)
- Simple fix: Renormalize in each step
- Solution: Renormalize interpolated abundances making them sum to 1
- Important at coarse-fine interpolation too



$$\varphi_i^\# = \frac{1}{\sum_{n=1}^{N_X} X_{i,n}^\#} \,, \quad \mathcal{X}_{i,n}^\# = \varphi_i^\# X_{i,n}^\#$$
 [Plewa and Müller 1999]

In Astro Chemistry

 You need to know what you c

 applies heavily. You need to know what are the rele reactions for your physical setup.
 Timescales and thermal conduction
 Adiabatic Index
 Local Conservation of abundances

 1.0

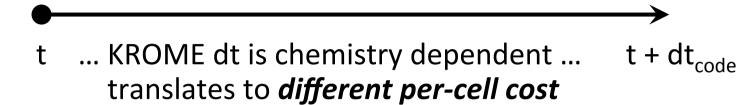
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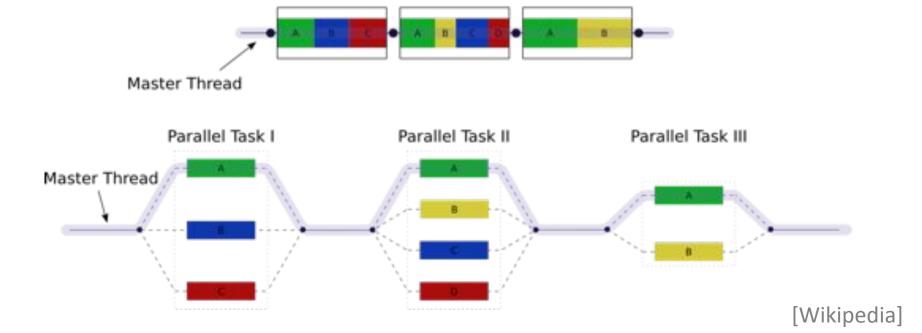
- Performance and parallelization:
  - Traditional parallelization method is MPI
  - Global domain decomposition according to cost of cell or particle updates with e.g. regular domains, or along a space filling curve.
  - Problem: Cost of KROME is highly "non-deterministic"

### KROME + OpenMP

Problem: Cost of KROME is highly "non-deterministic"



 OpenMP can alleviate the imbalance by dynamic load balancing inside a node



Parallel Task I Parallel Task II Parallel Task III

### KROME + OpenMP

Problem: Cost of KROME is highly "non-deterministic"

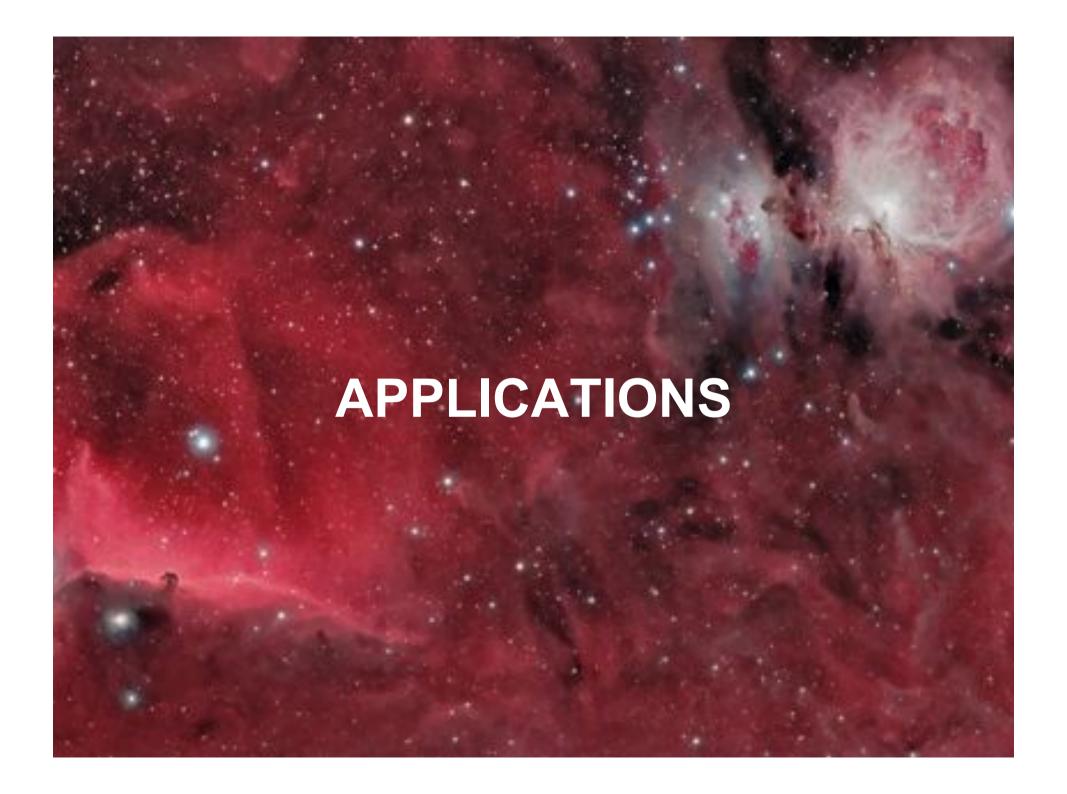
t ... KROME dt is chemistry dependent ... t + dt<sub>code</sub> translates to *different per-cell cost* 

OpenMP can alleviate the imbalance by dynamic load
 balancing inside a node

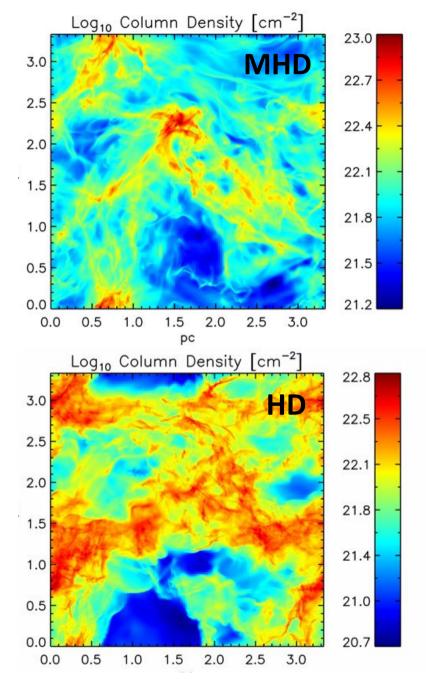
```
From Shock1D

| Somp parallel do private(xx, rhogas, ix) schedule(dynamic,2) ! <- Enable OpenMP do ix = 1, nx
| xx(:) = x(ix,:) !use local array rhogas = rho(ix) !get density call krome(xx(:),rhogas,Tgas(ix),dt) | x(ix,:) = xx(:) !get the updated value back enddo
```

- Read BB Wiki for recommendations of KROME + OpenMP.
- ALWAYS use Intel Inspector or similar before production.

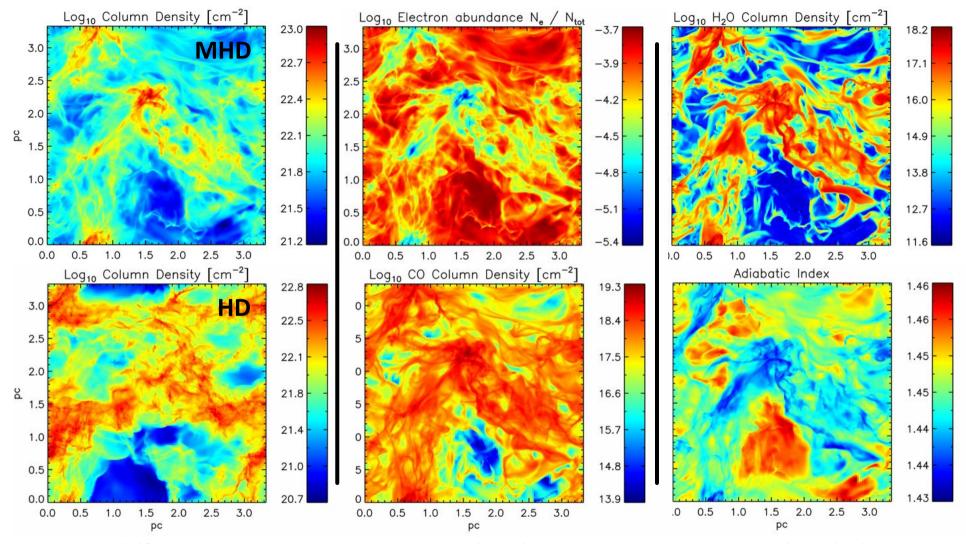


### **Turbulent Molecular Cloud**



- Piece of a molecular cloud: (3.3 pc)<sup>3</sup>
- Running with either HD or MHD
- Driven turbulence to Mach=11 @ 10K
- $<\rho> = 1000 \text{ cm}^{-3}, <B> = 7 \mu\text{G}$
- Root grid: 128<sup>3</sup>
- Refinement on density, and gradients of : ρ, v, P, and B
- More than 18M cells at up to (4096)<sup>3</sup>
- H-C-O chemistry (COthin network), UV,
   CRs, Solar abund. Similar to D. Seifried.
- Approx for  $A_V = (n_{tot} / 1000)^{2/3}$
- Consis. abundance advection, variable γ
- Evolved over 4.7 Myr = 3.5 dyn. times= 4.5 free-fall times

### **Turbulent Molecular Cloud**



■ Large diff. in HD & MHD ■ Most H molecular

Water at threshold density

- ISM is magnetized
- CO effectively formed
- Only small changes in γ

Affects SFR, IMF

- Free ions even @ 10-50K
- Need dust to go further

### Summary

- KROME is ready and viable for complicated chemistry
- It is easy to use KROME with RAMSES, and other framework codes
- If the framework code use a finite volume method, consistent advection should be implemented (simple!), both for fluxes and for interpolation, if AMR.
- A more challenging change is to include a variable adiabatic index. Crucial in combination with self gravity
- We currently only have preliminary results of our molecular cloud models, but first results show promising agreement with literature, but with much higher numerical fidelity and including magnetic fields.
- OpenMP can significantly improve performance of KROME