

APR in Phantom

Live adaptive particle refinement in Phantom

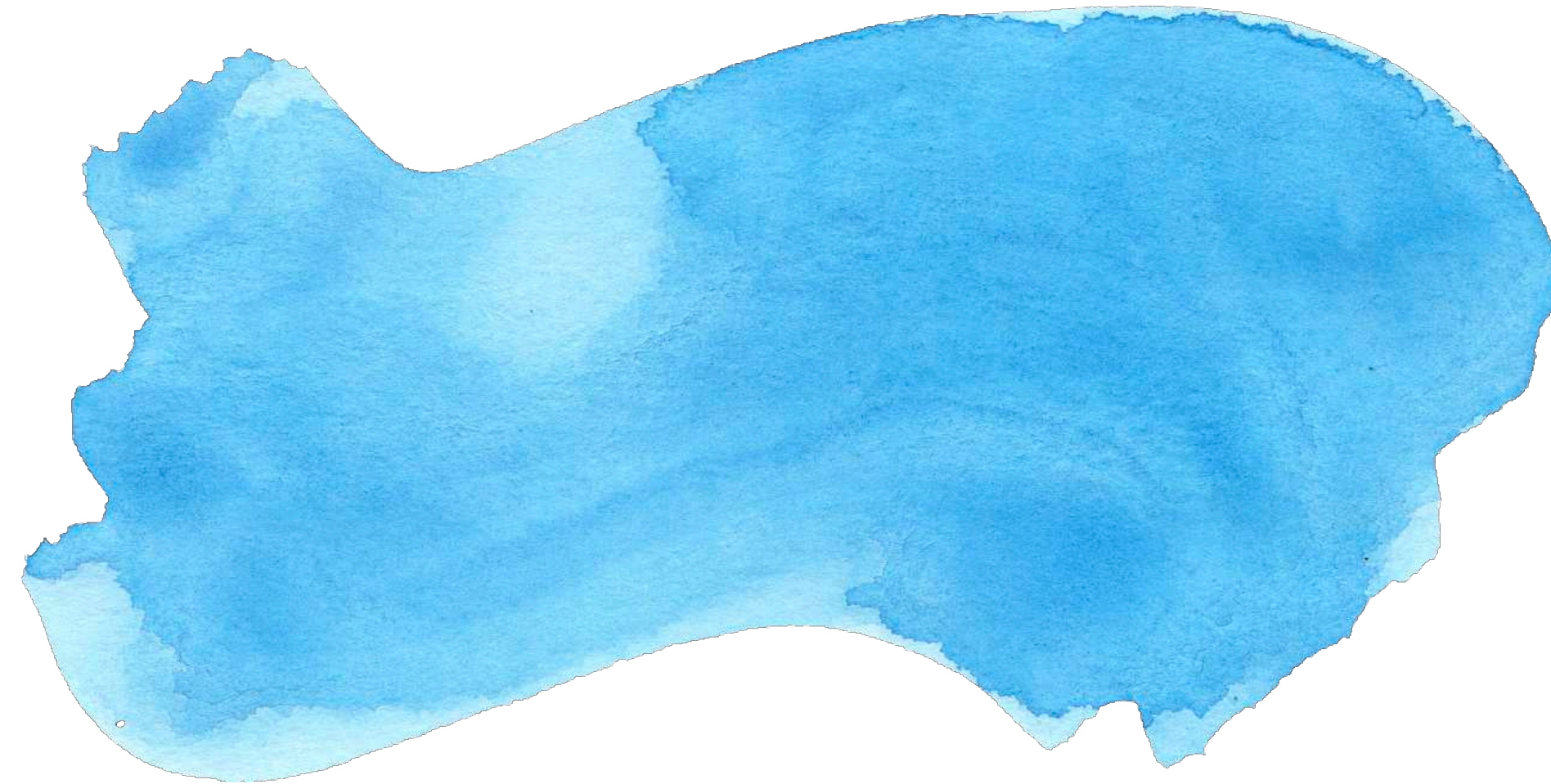
Work in progress!

Rebecca Nealon and Daniel Price
with acknowledgements to James Wurster,
Jeremy Smallwood and Sahl Rowther



MONASH
University

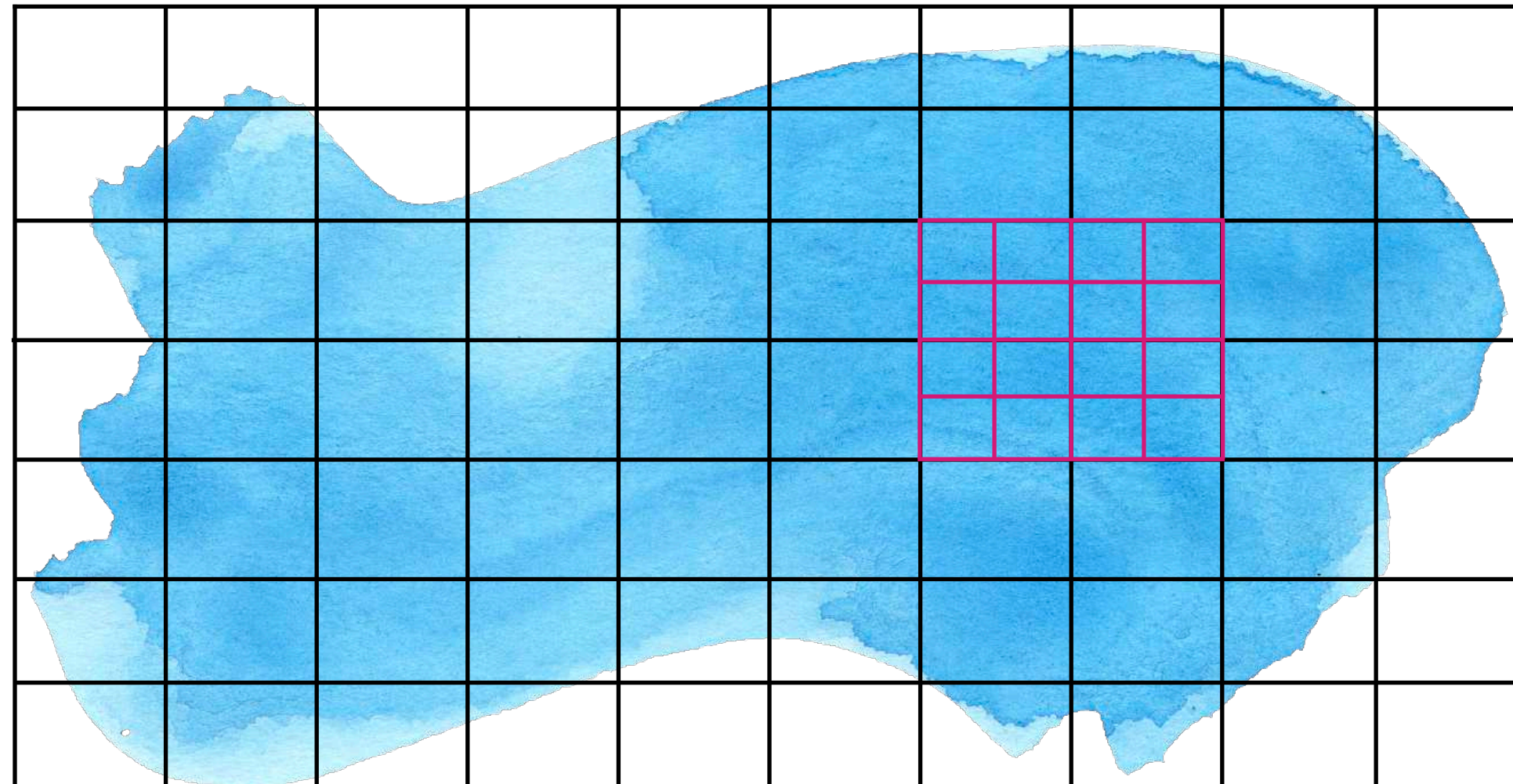




How do we simulate a fluid?

Grid approach

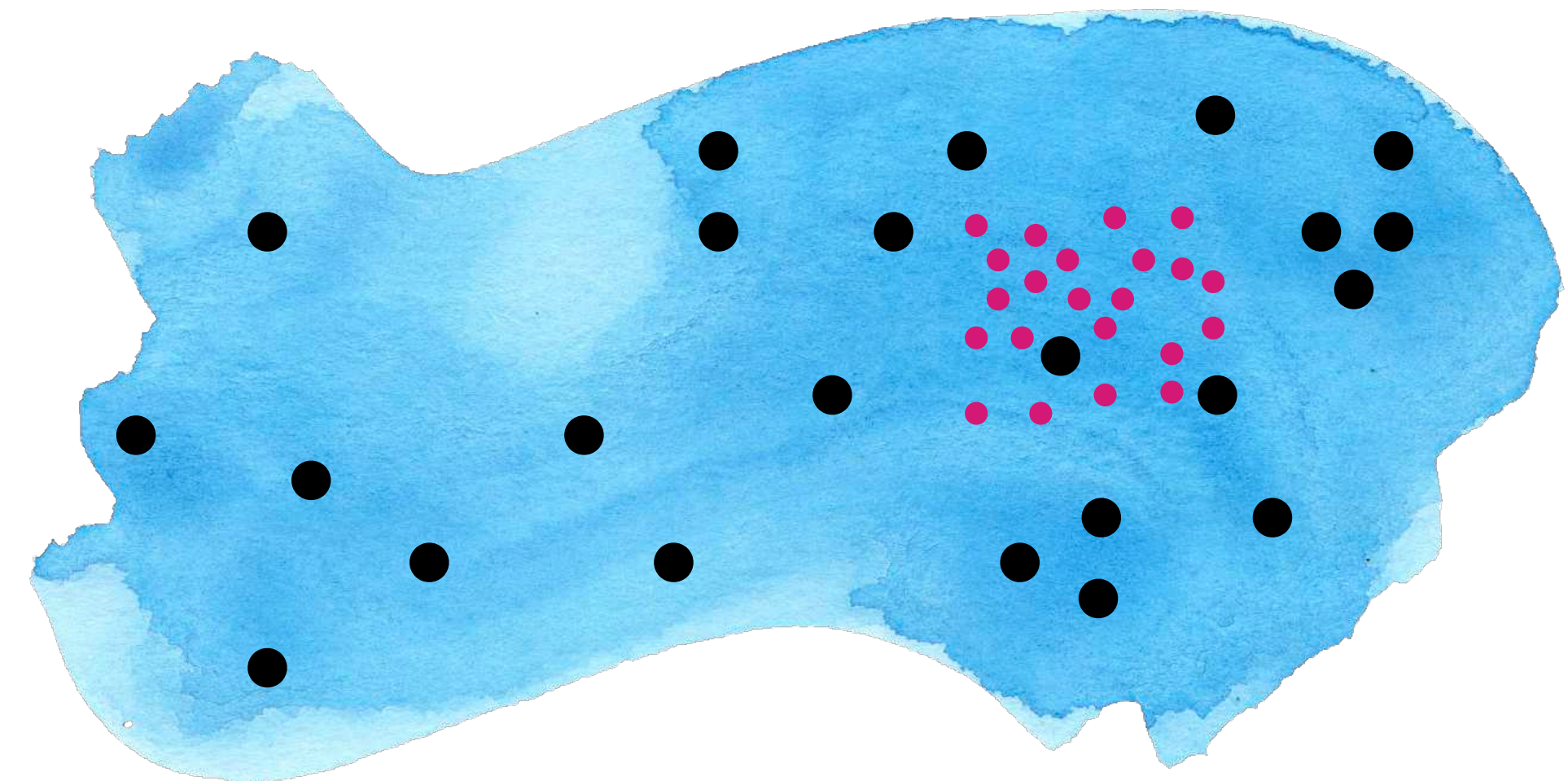
Discretise the domain into a static grid



- Fluid moves through the static boxes
- Easy to parallelise (can be very fast)
- Easy to implement magnetic fields, winds etc.
- Adaptive mesh refinement

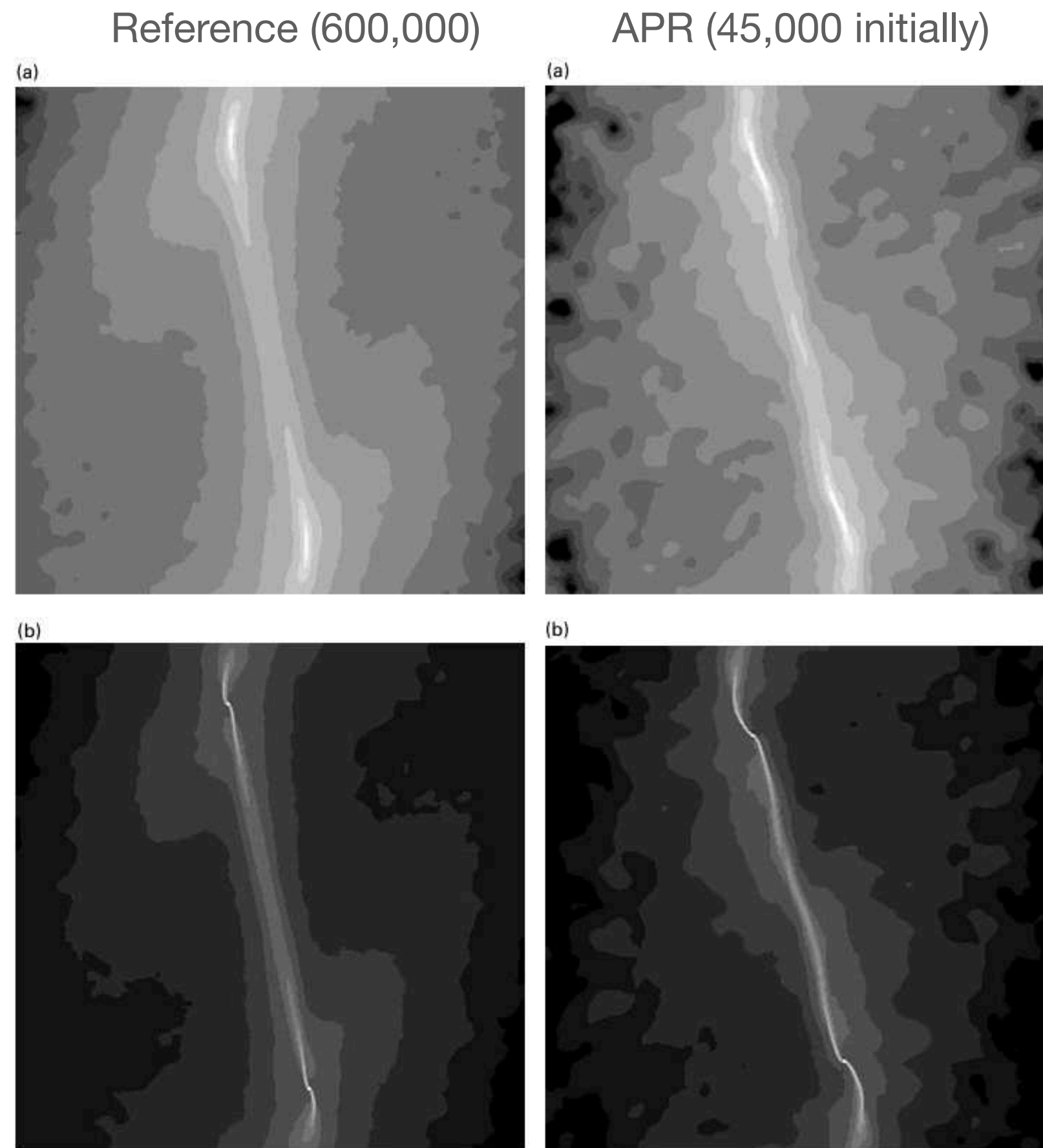
SPH approach

Discretise the fluid onto moving particles



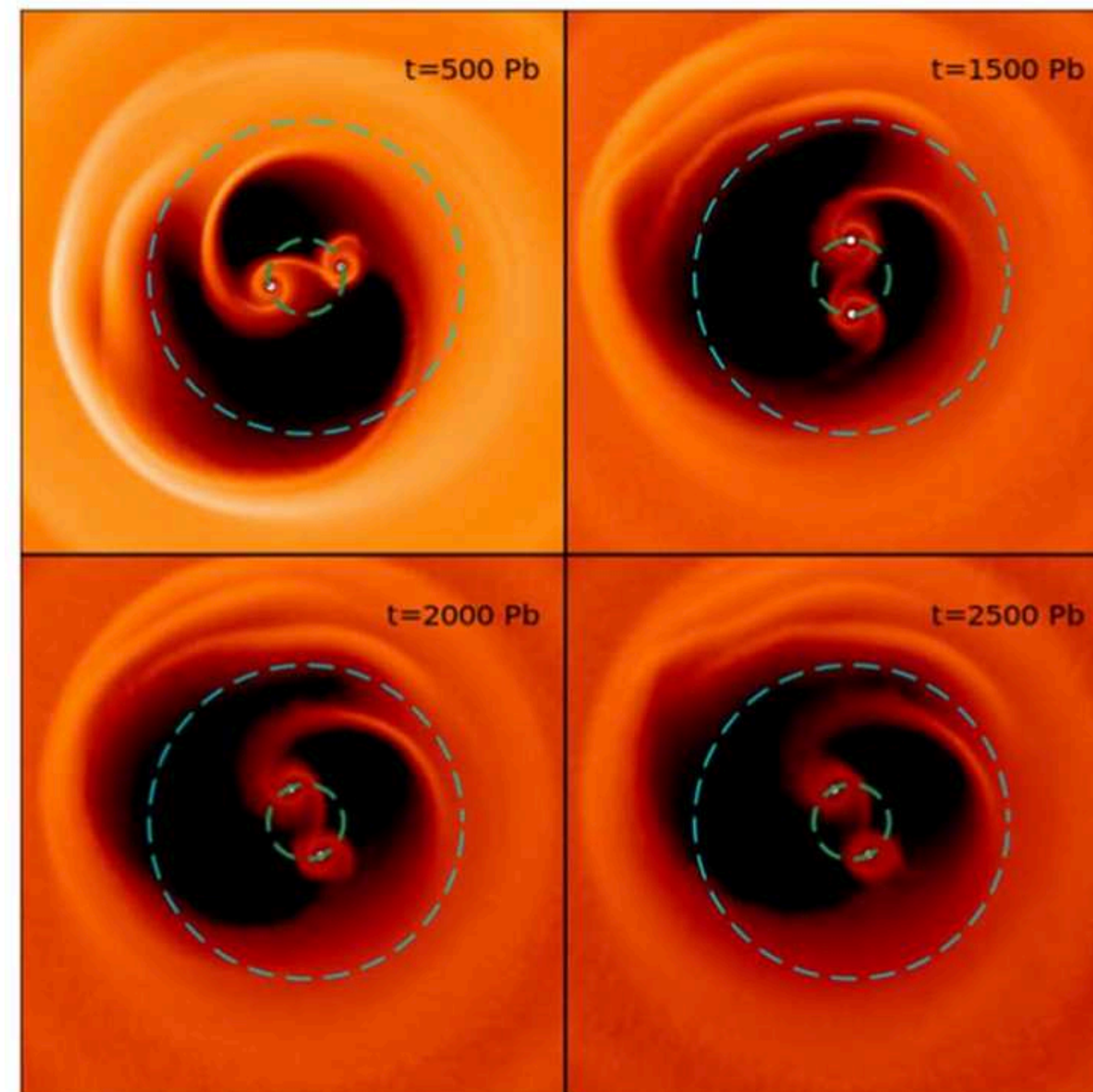
- Particles move with the fluid
- No boundaries or preferred direction
- Exact conservation of mass, linear and total angular momentum
- **Adaptive particle refinement**

It's an old idea ...

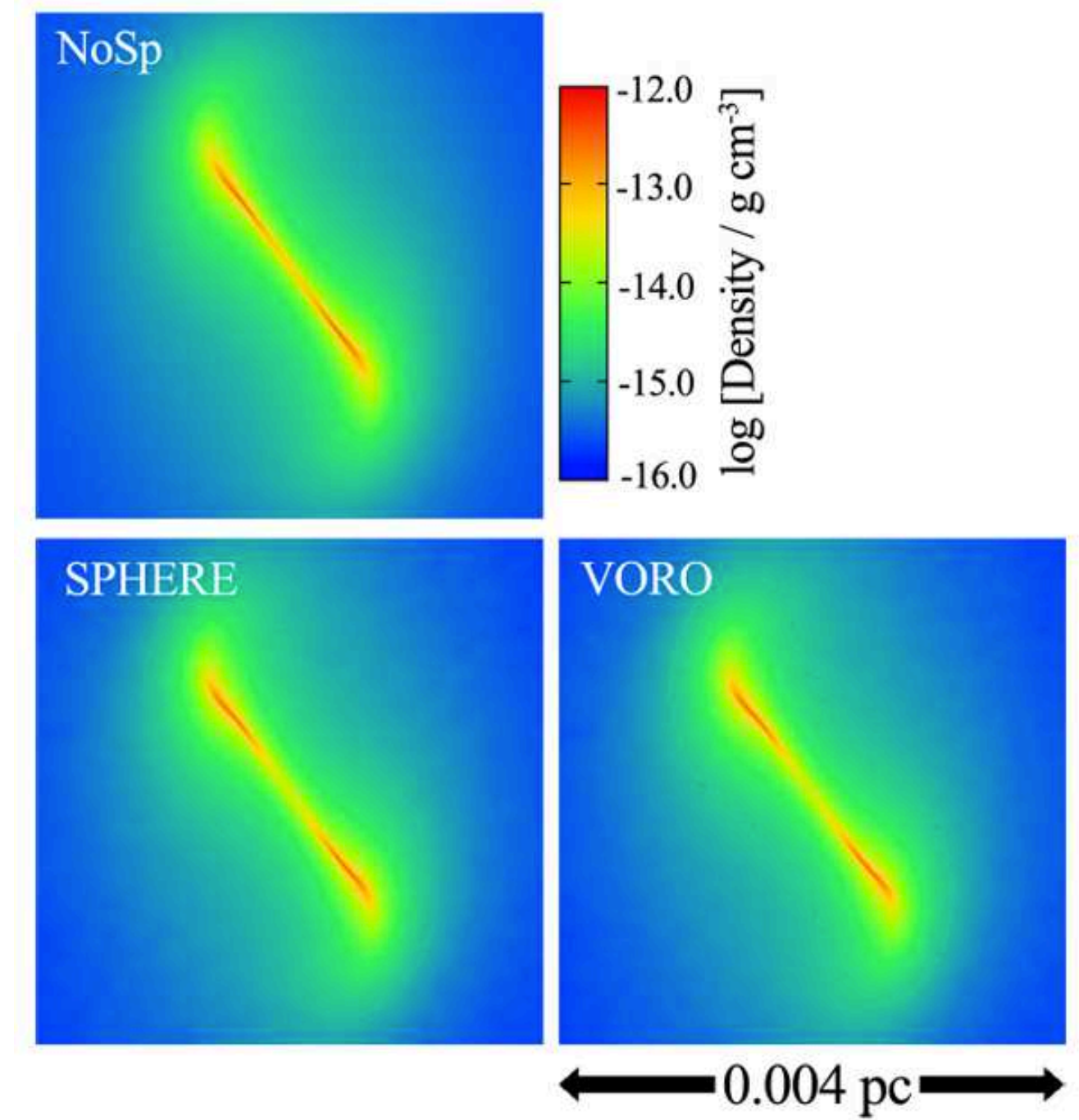


Kitsionas & Whitworth 2002

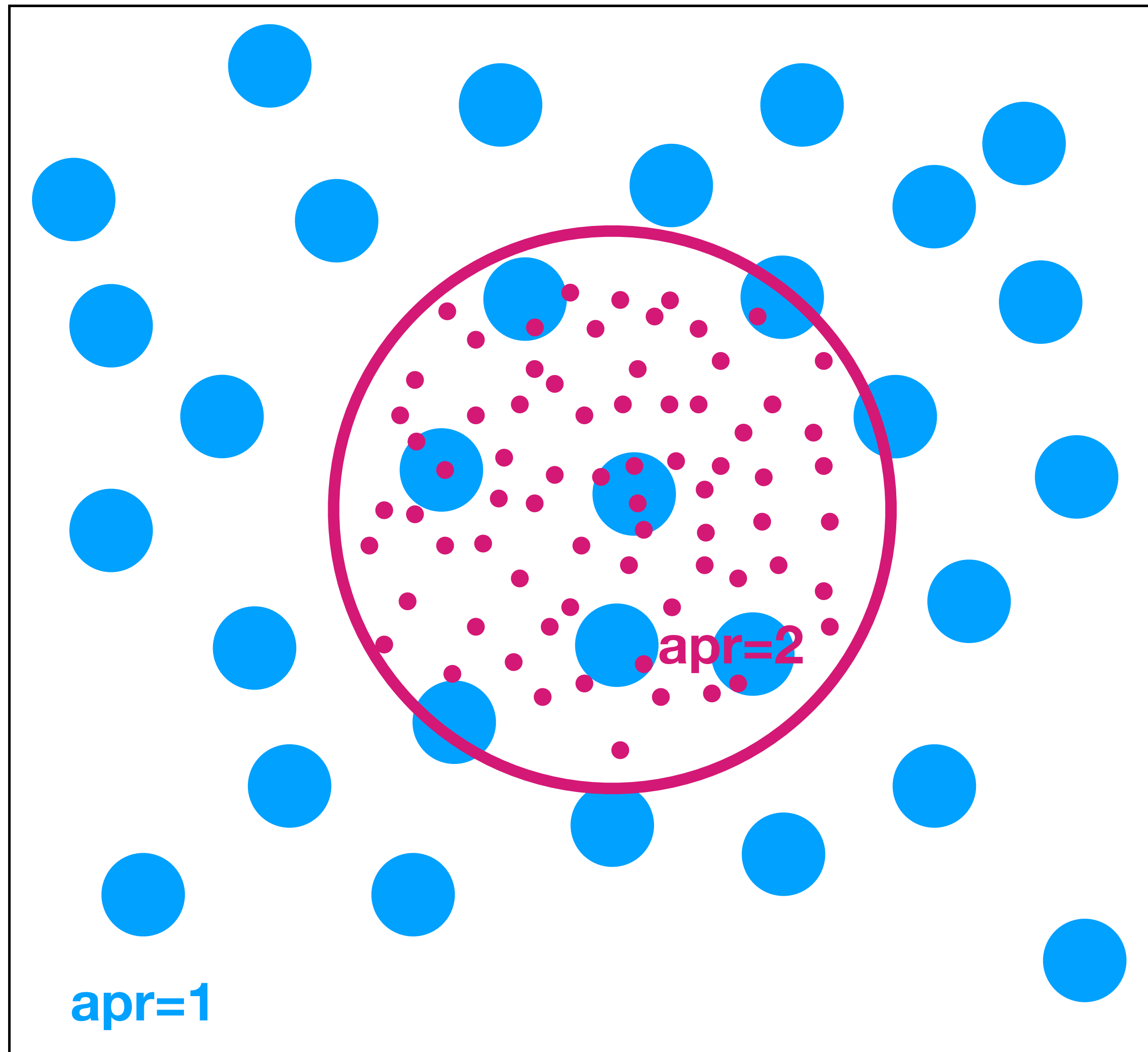
GIZMO: Hopkins 2015, Franchini et al. 2022



Chiaki & Yoshida 2015

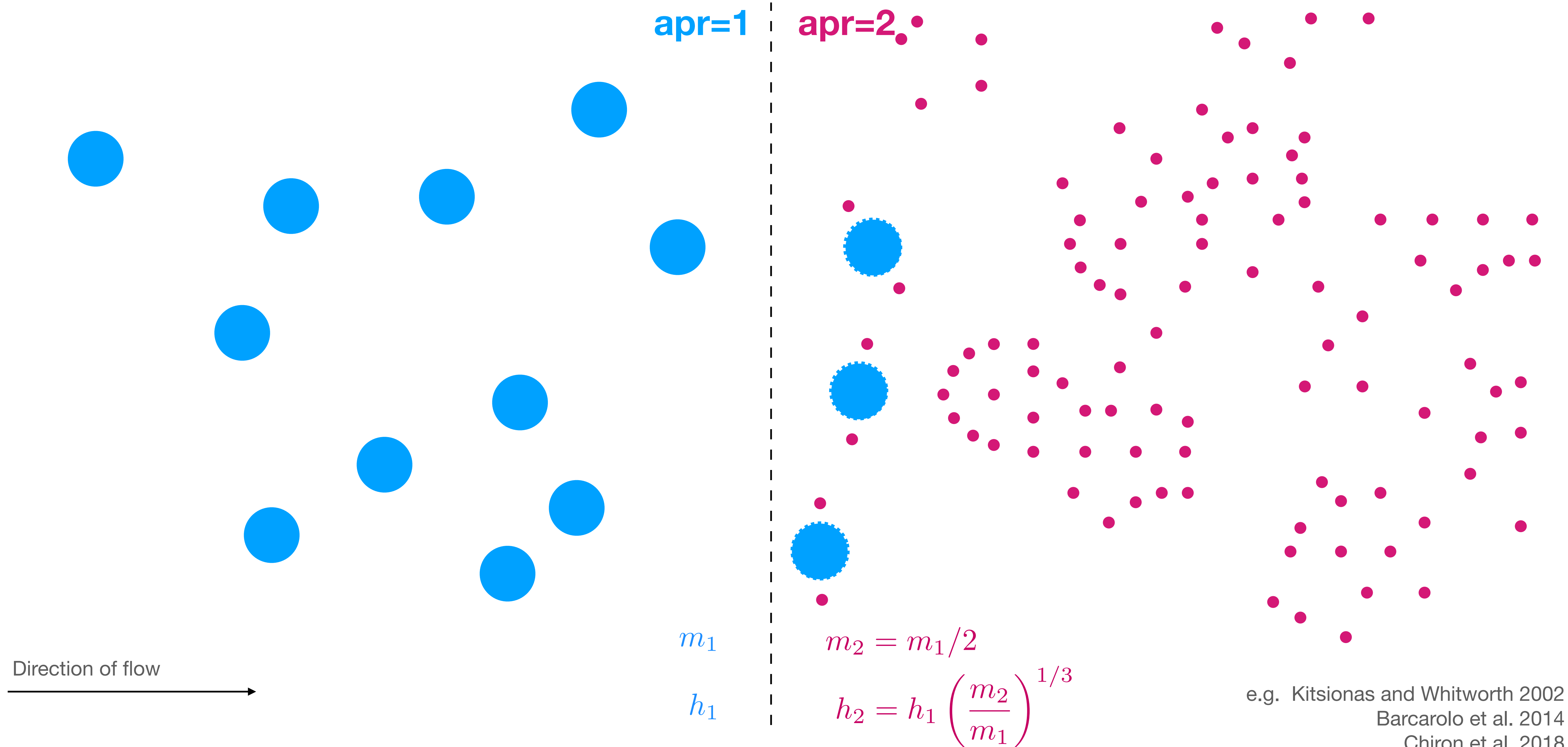


How we do it: refinement levels



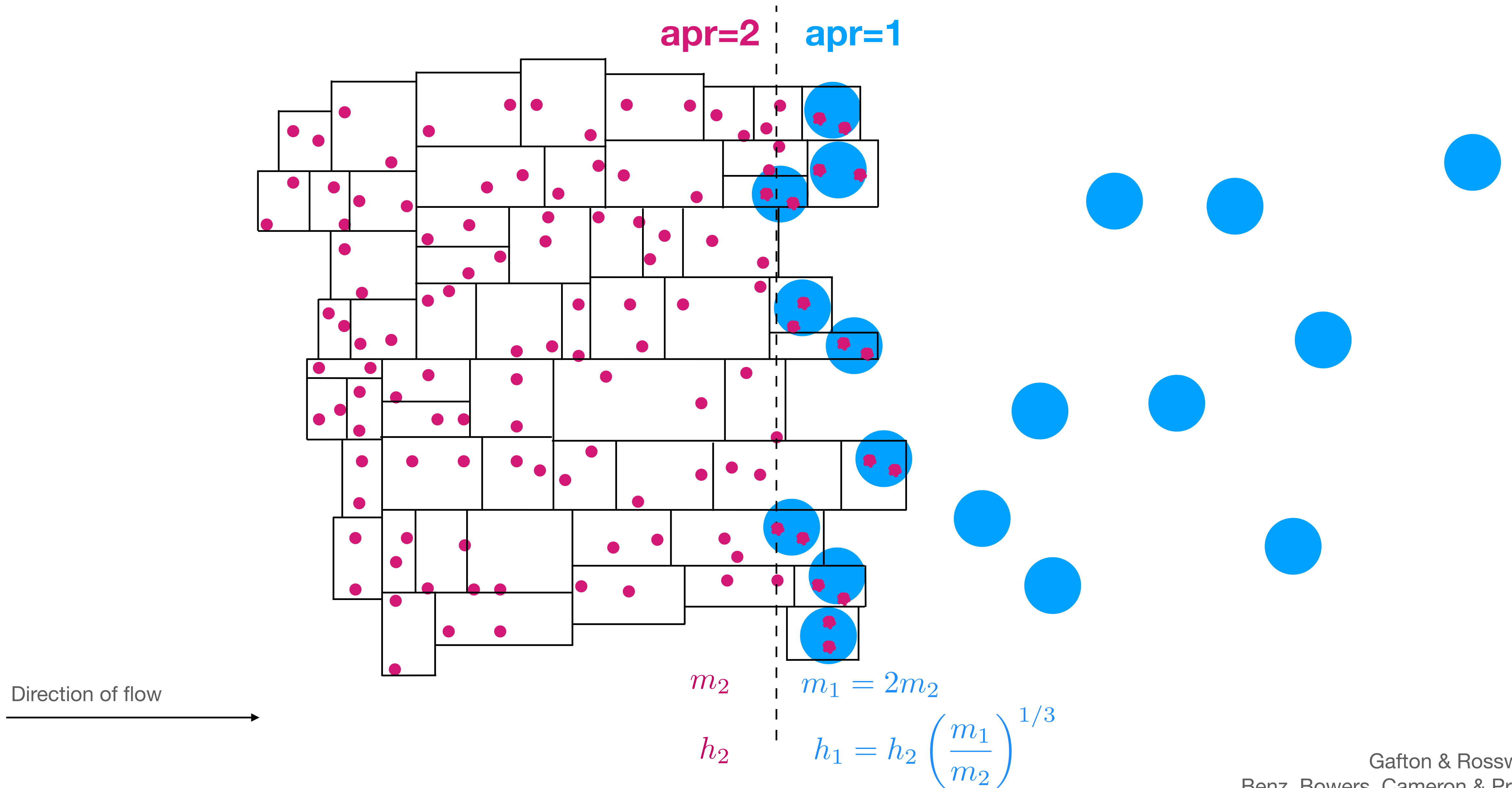
- Decide on a region that we want to increase the resolution in
- Split all the particles inside this region, increasing their refinement level
- Density is decided across both sets of particles
- Particles are able to safely move in and out of the region, transitioning between refinement levels

How we do it: refining



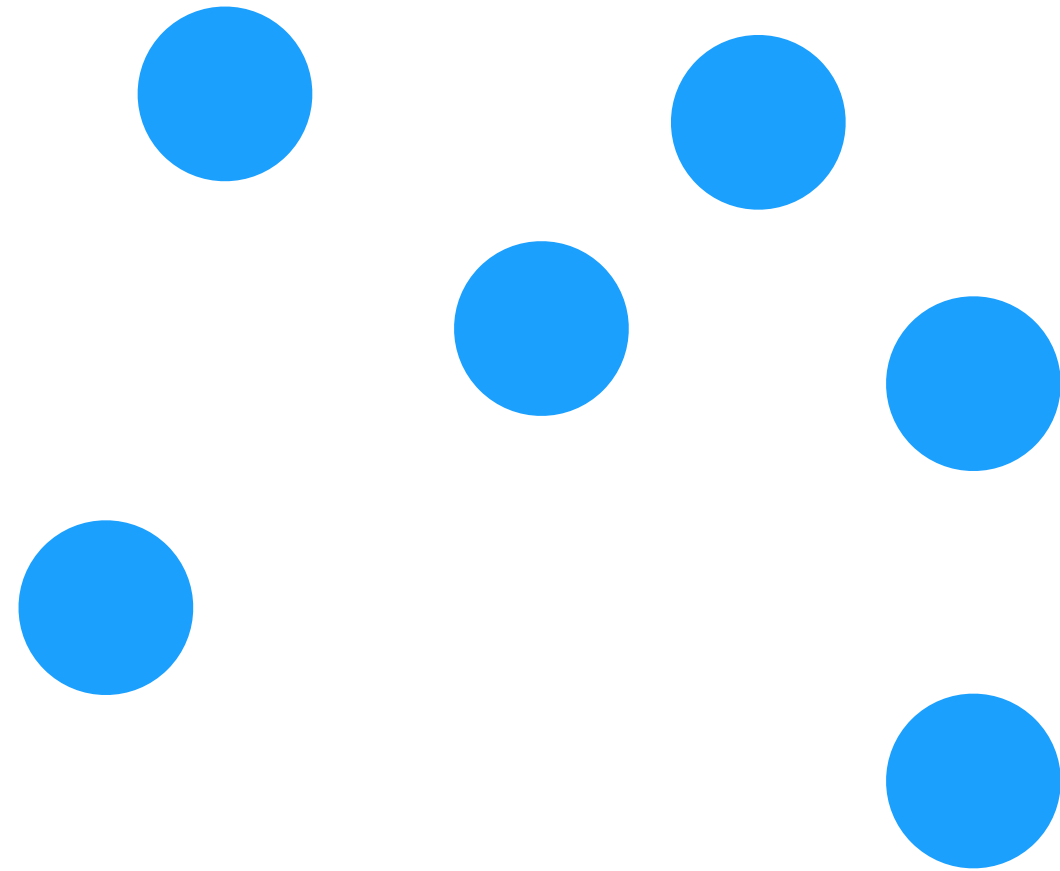
e.g. Kitsionas and Whitworth 2002
Barcarolo et al. 2014
Chiron et al. 2018
Bending et al. 2020

How we do it: de-refining



How we do it: relaxing

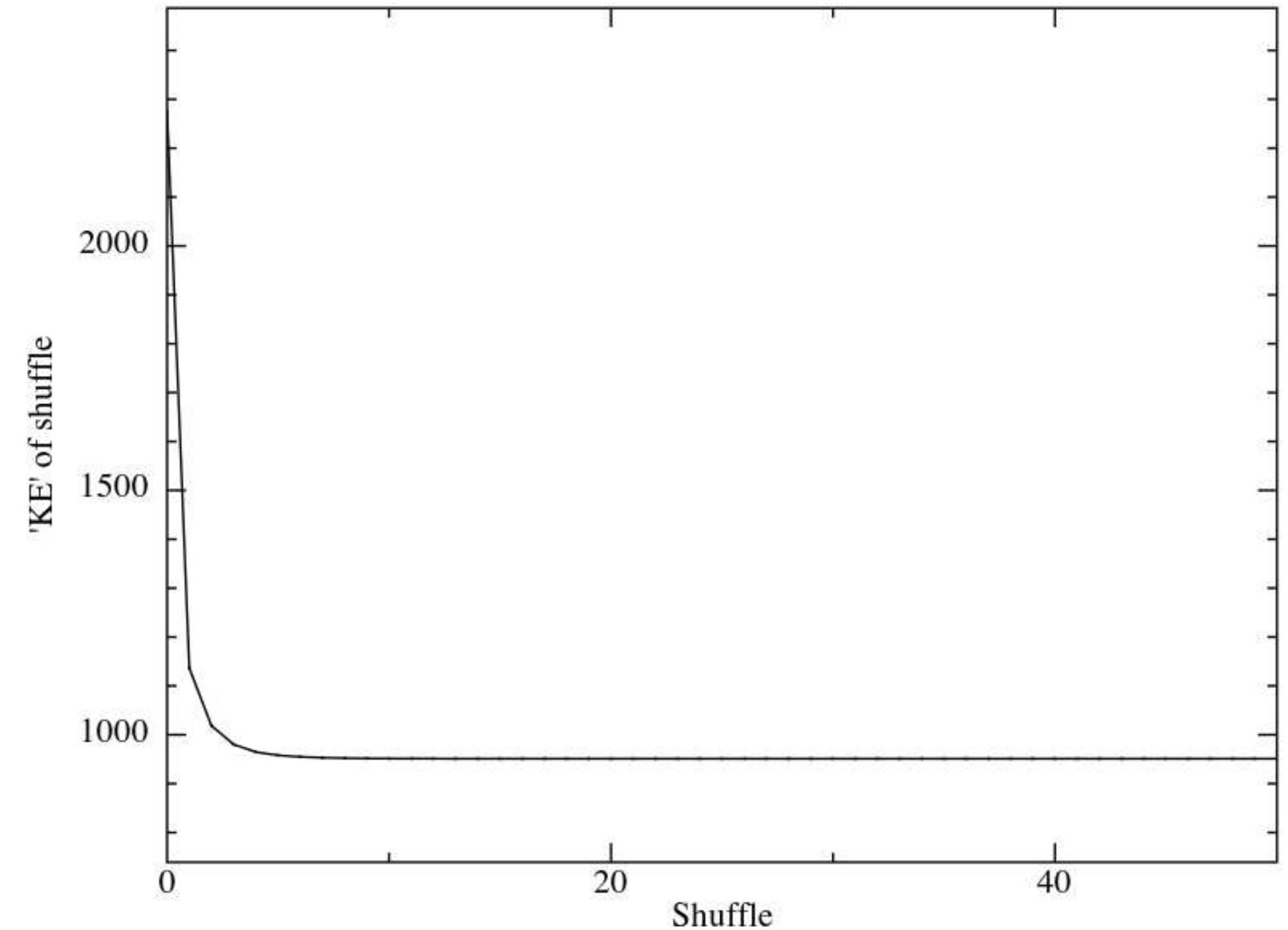
Original arrangement



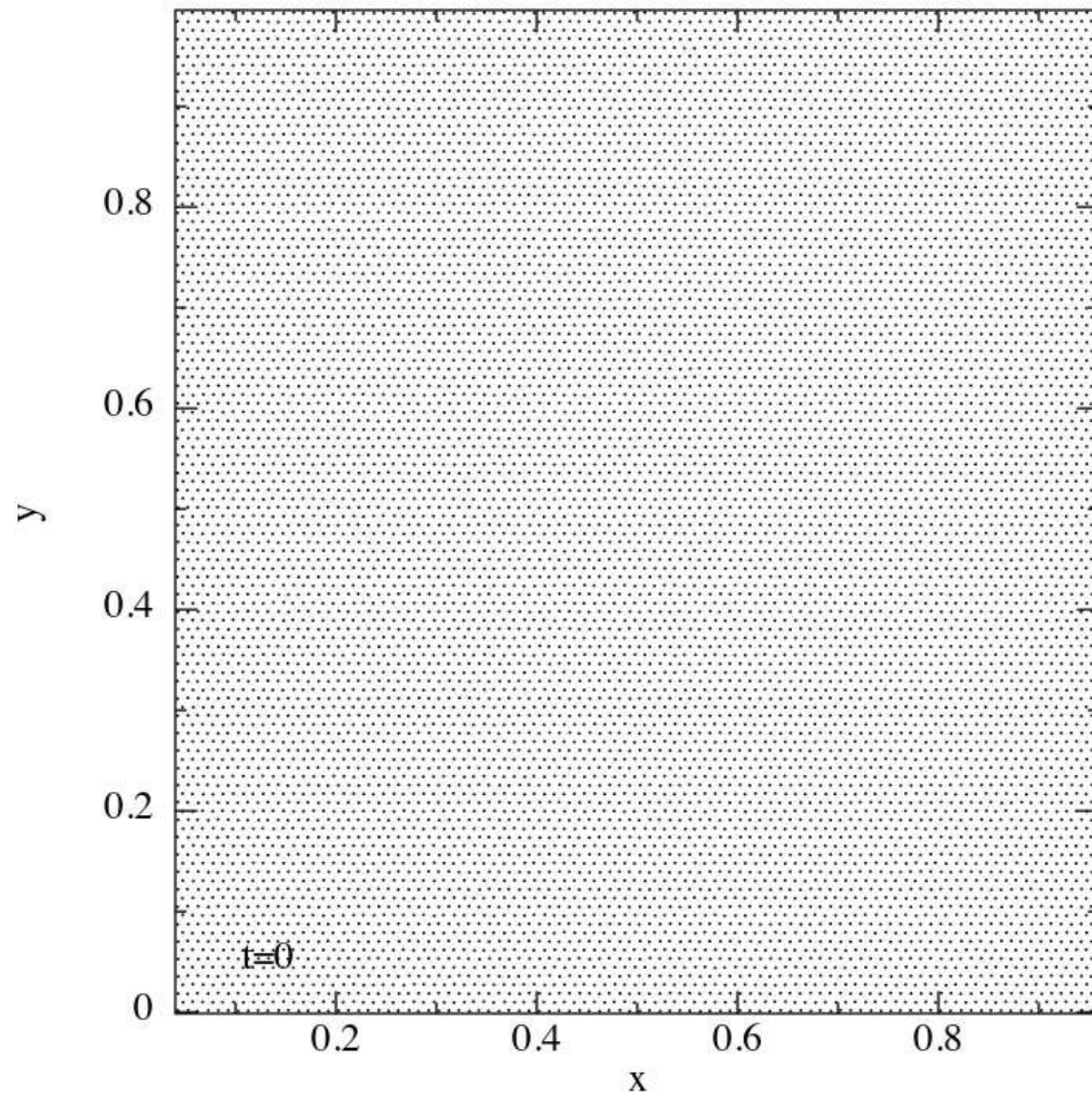
$$\rho(\vec{x}) = \sum_{a=1}^N m_a W_a(\vec{x}, h_a)$$

How we do it: relaxing

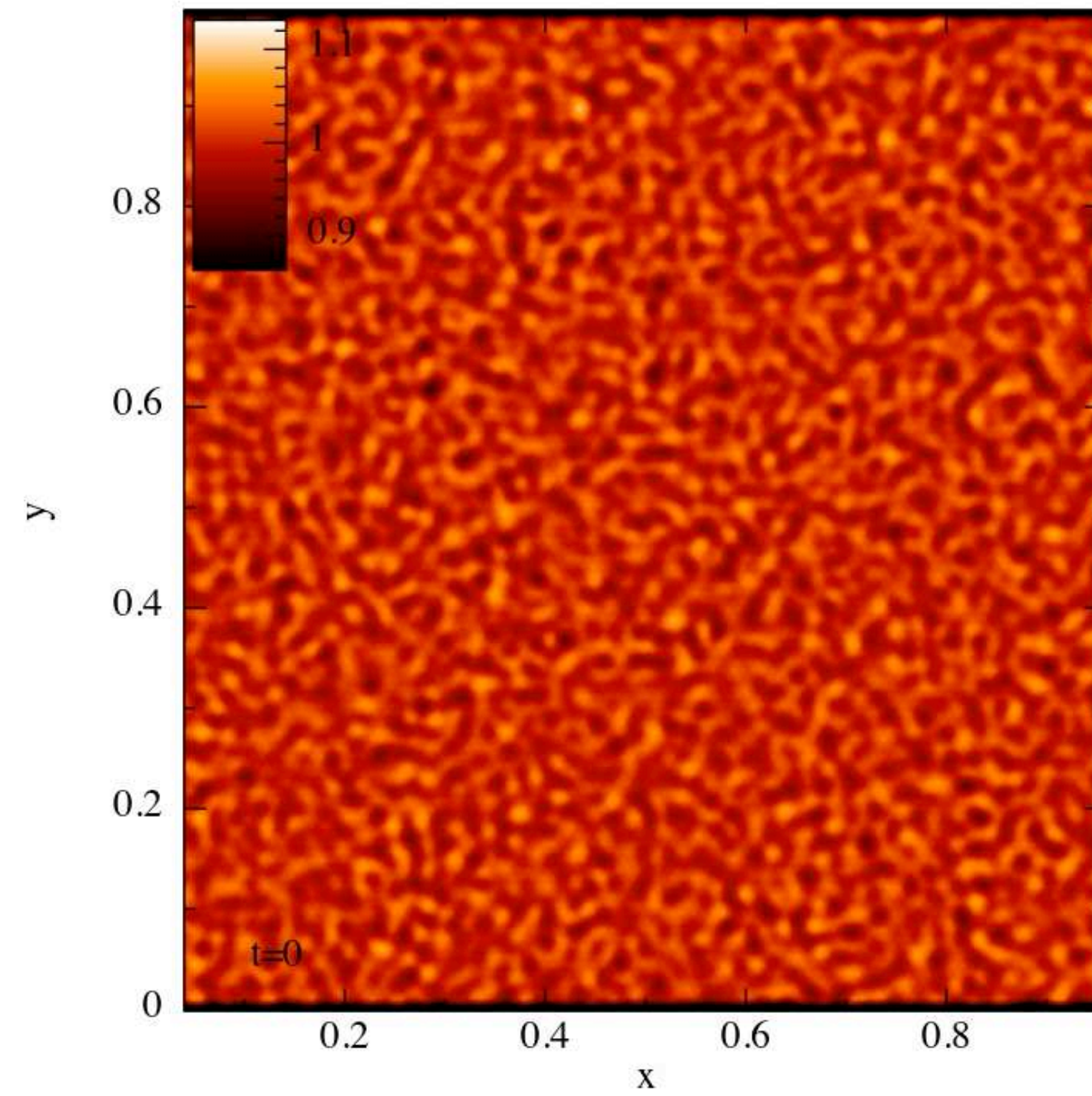
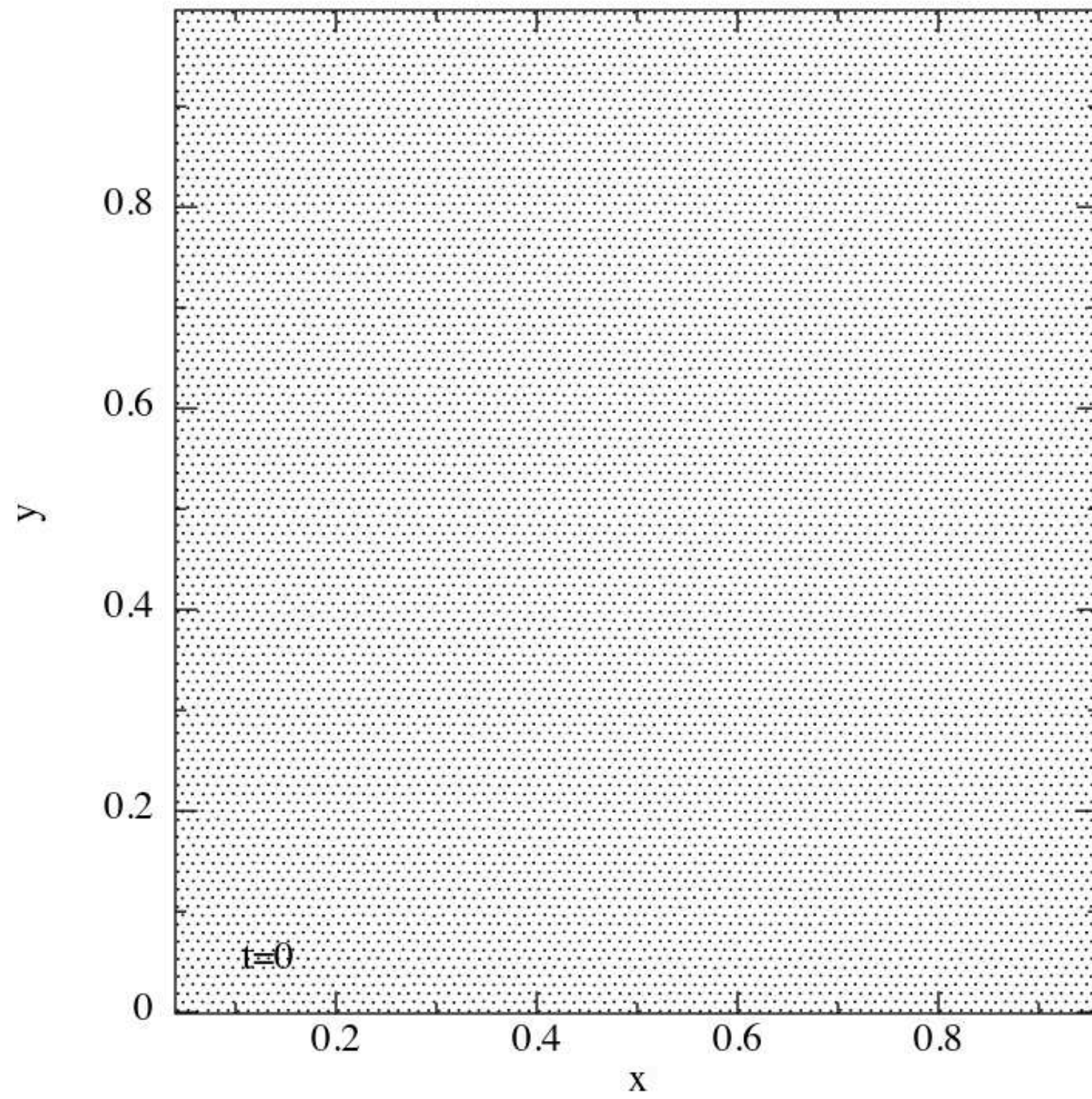
1. Save the properties of all current particles
2. Split/merge as required
3. For new particles:
 - i. Calculate accelerations of new particles at their new locations
 - ii. Interpolate the acceleration at the location of the new particles from the original particles
 - iii. Shift new particles by an amount that is proportional to the difference between these accelerations
- iv. Repeat



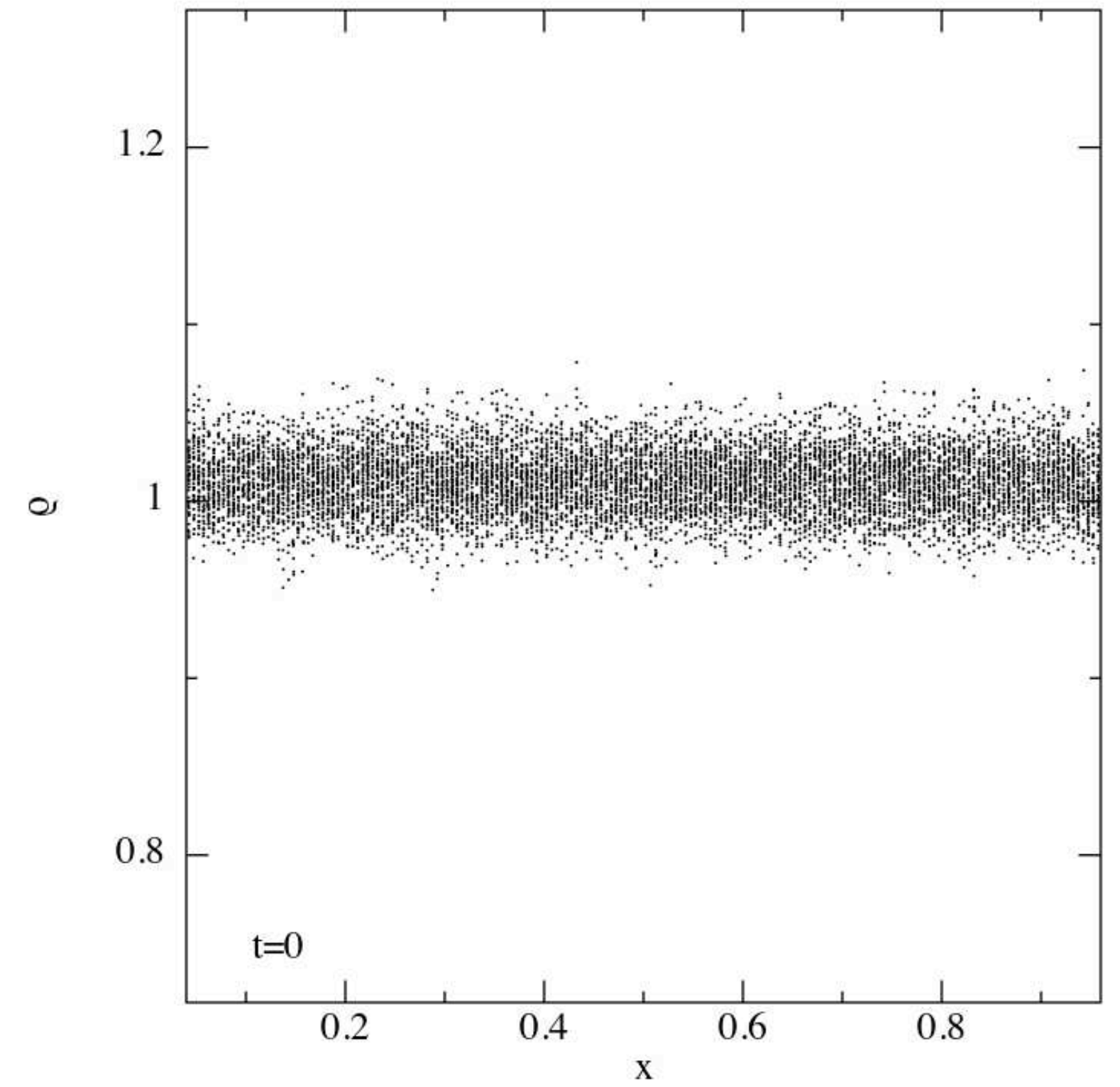
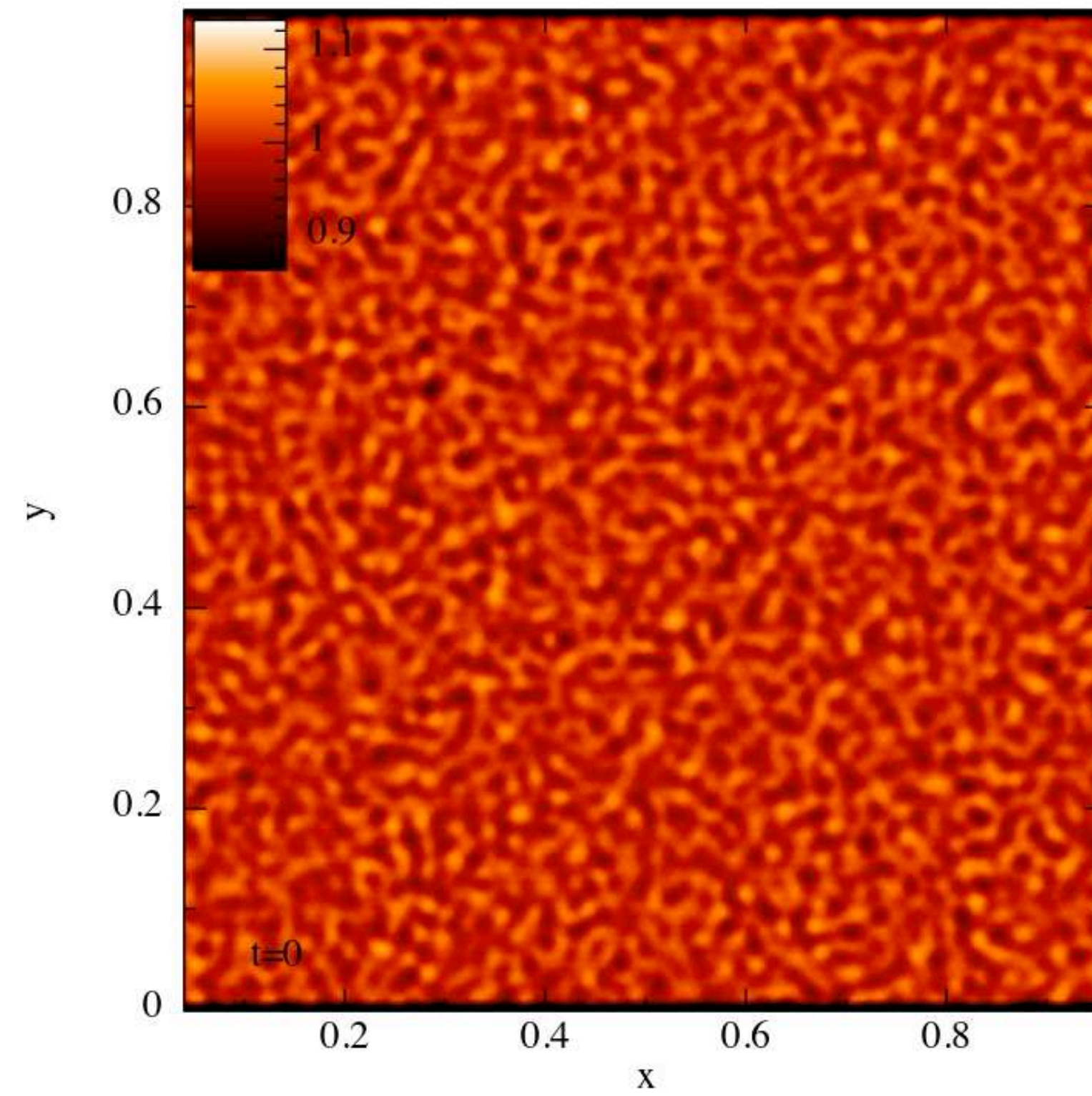
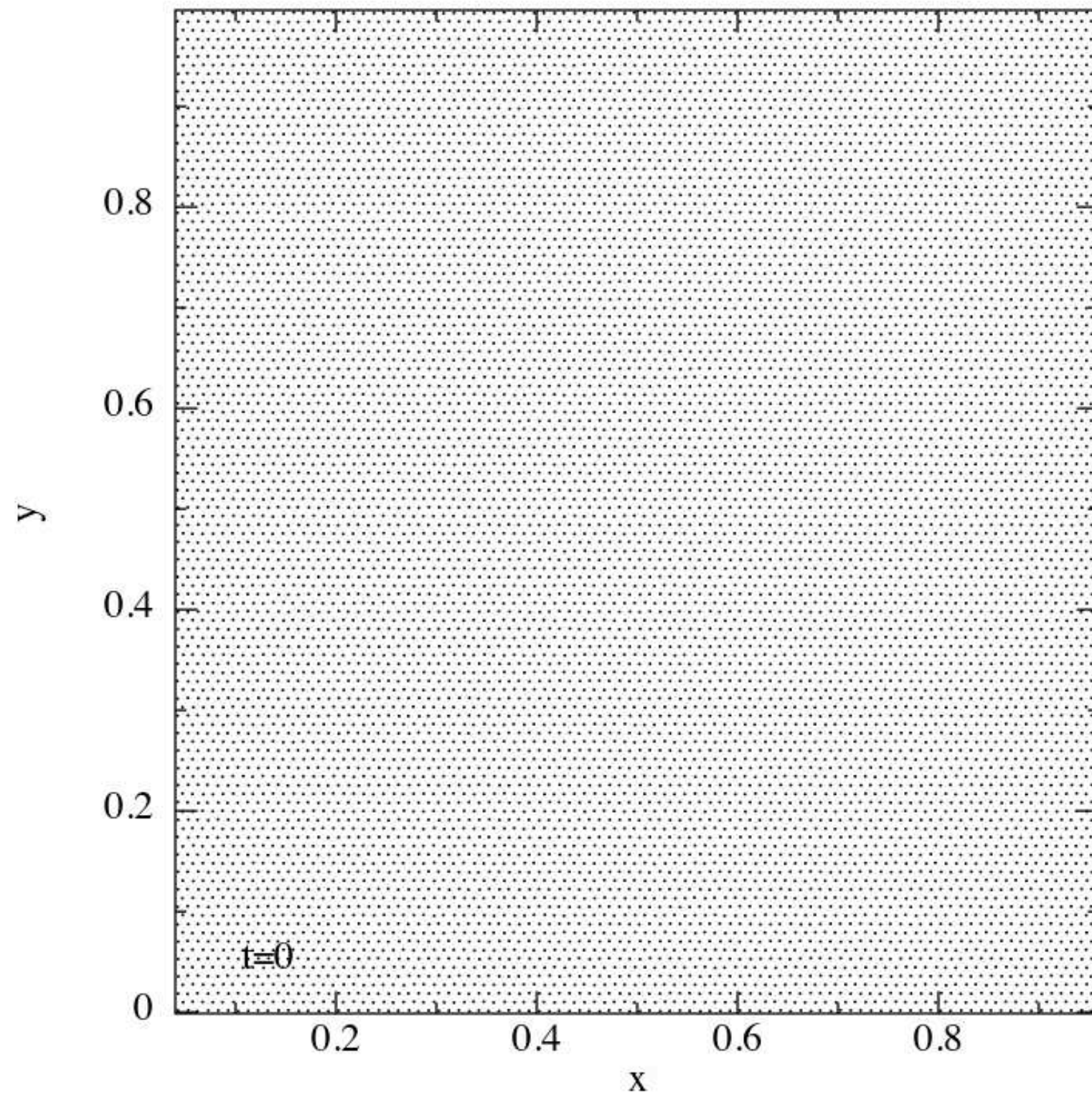
Uniform density box



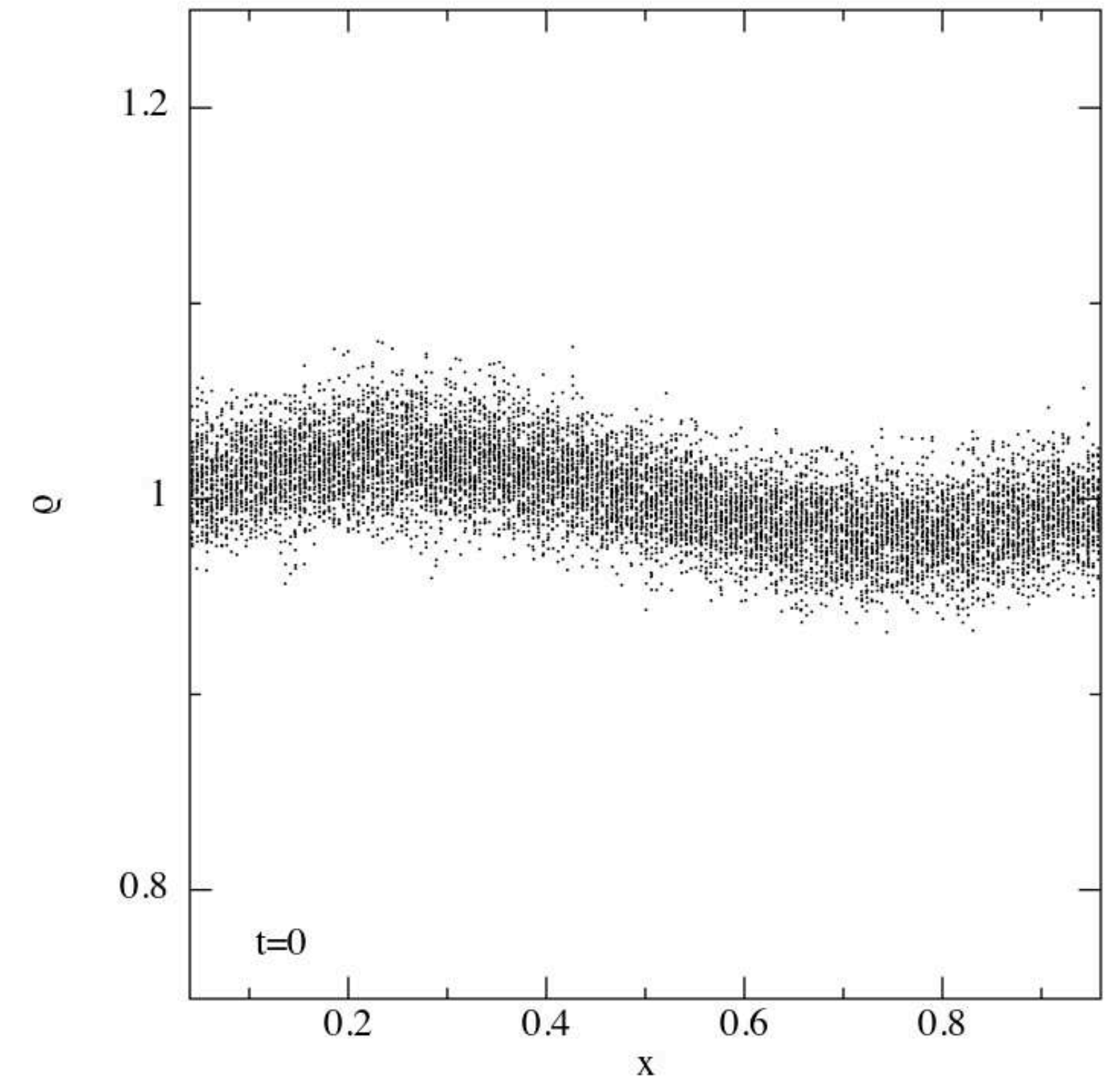
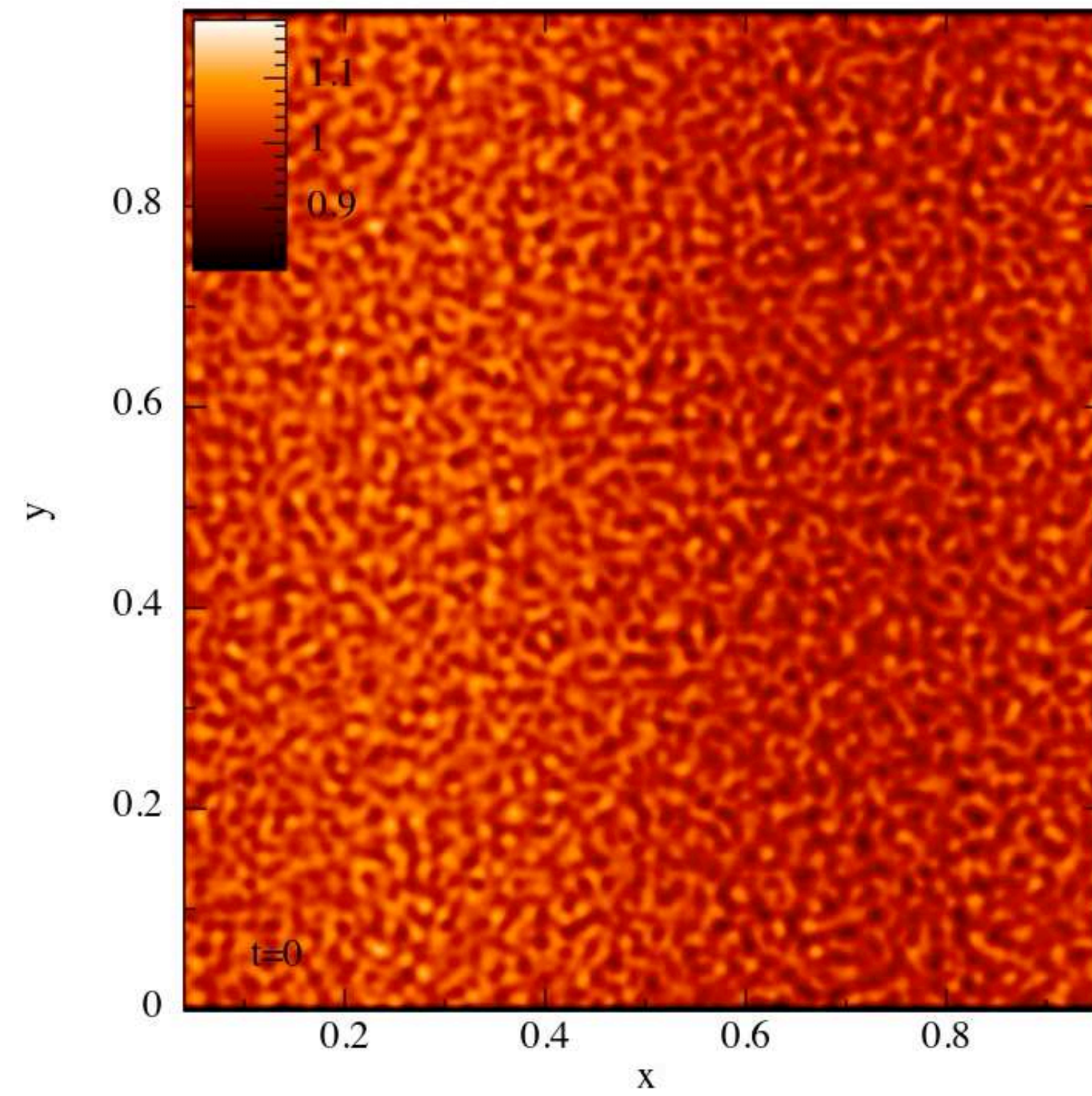
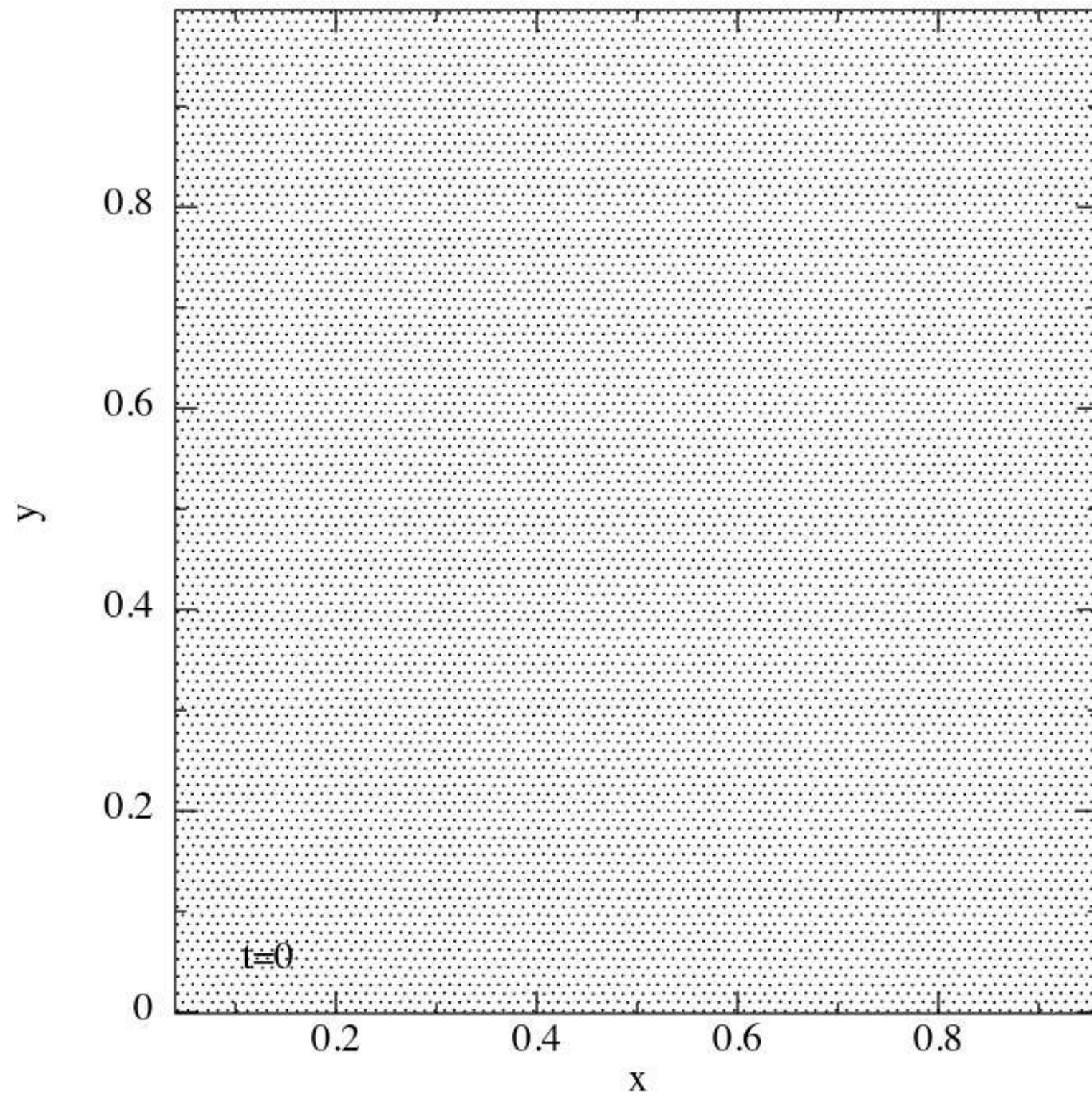
Uniform density box



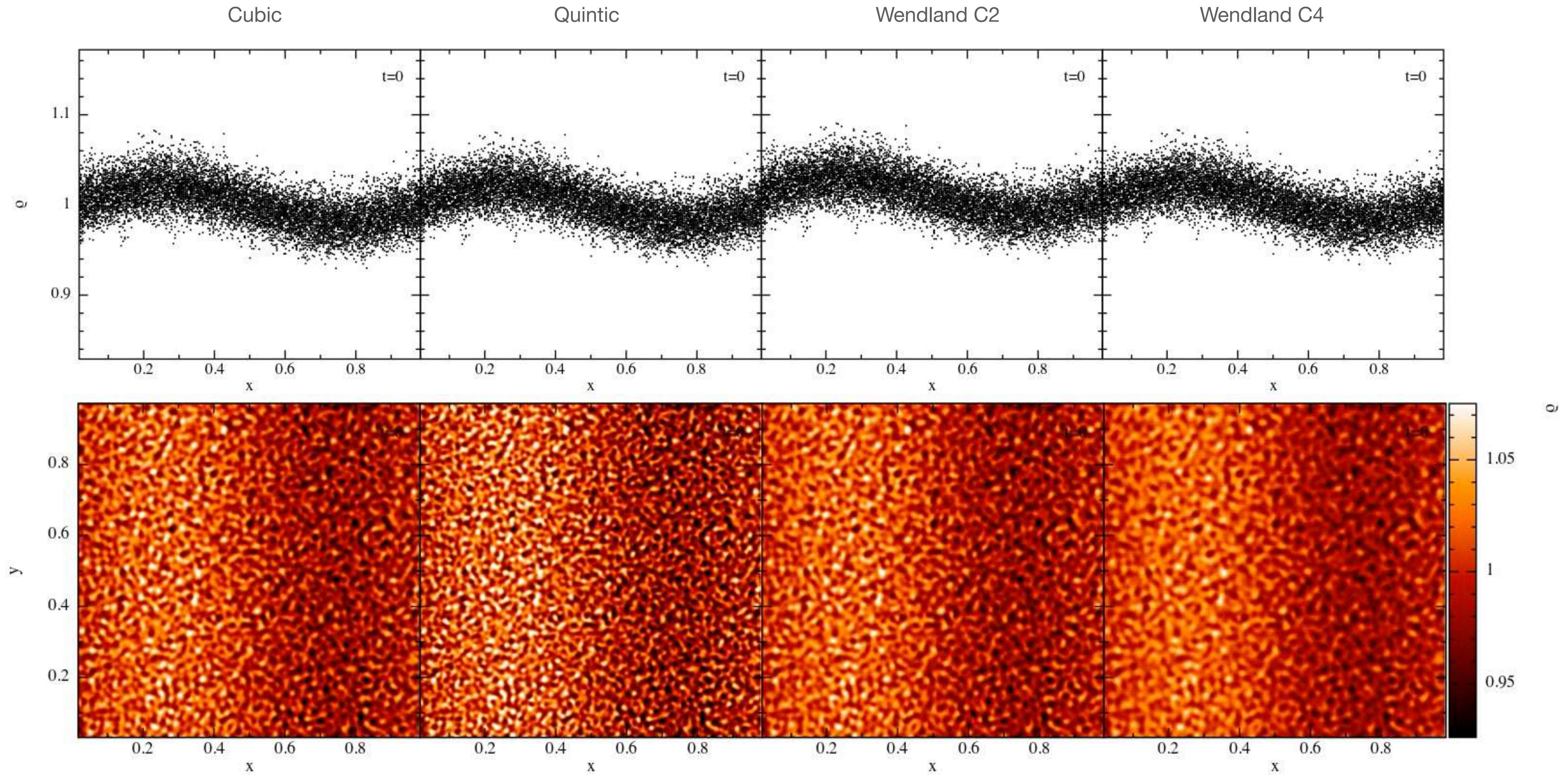
Uniform density box



Wave in a box



Wave in a box: kernels



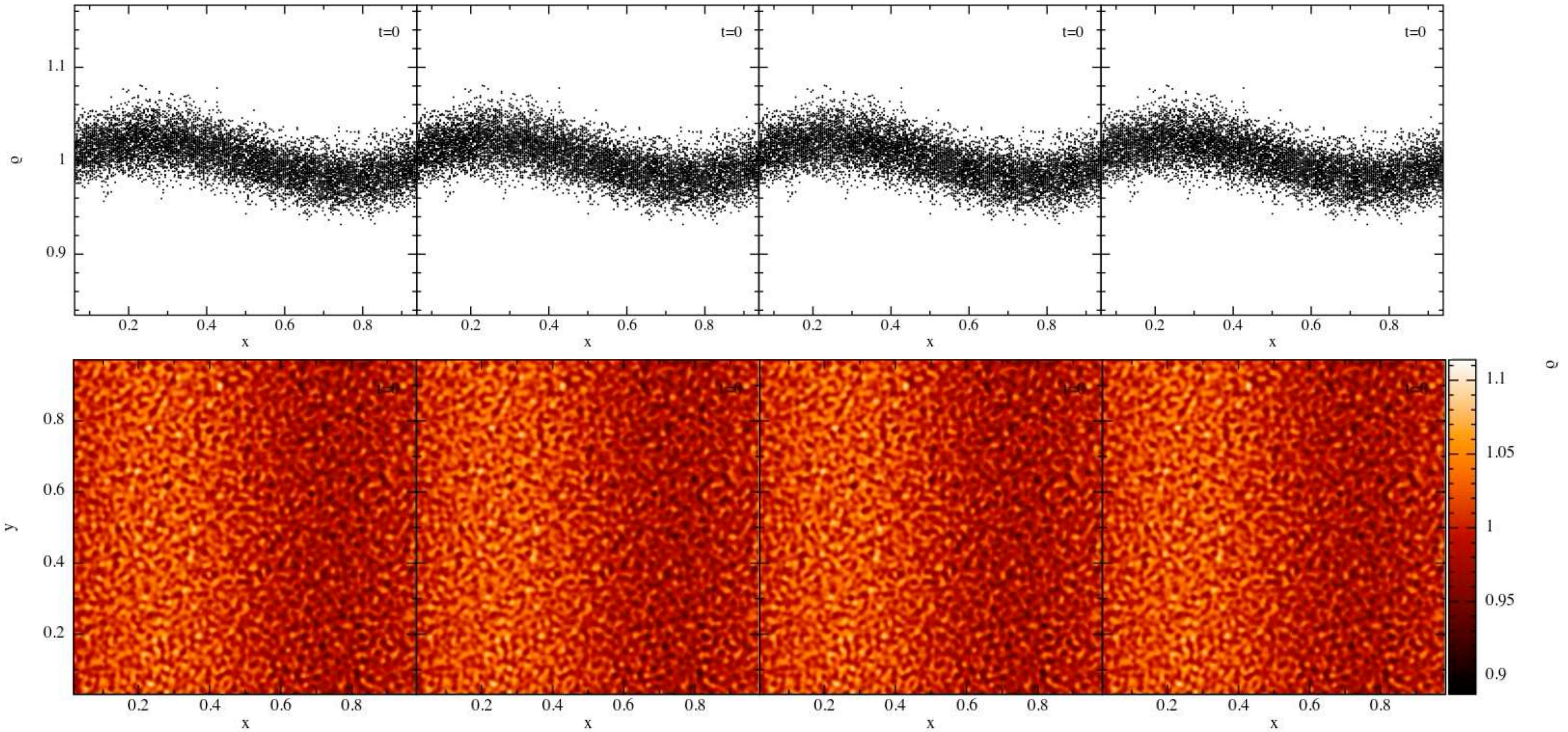
Wave in a box: splitting conditions

+relaxing, -directional

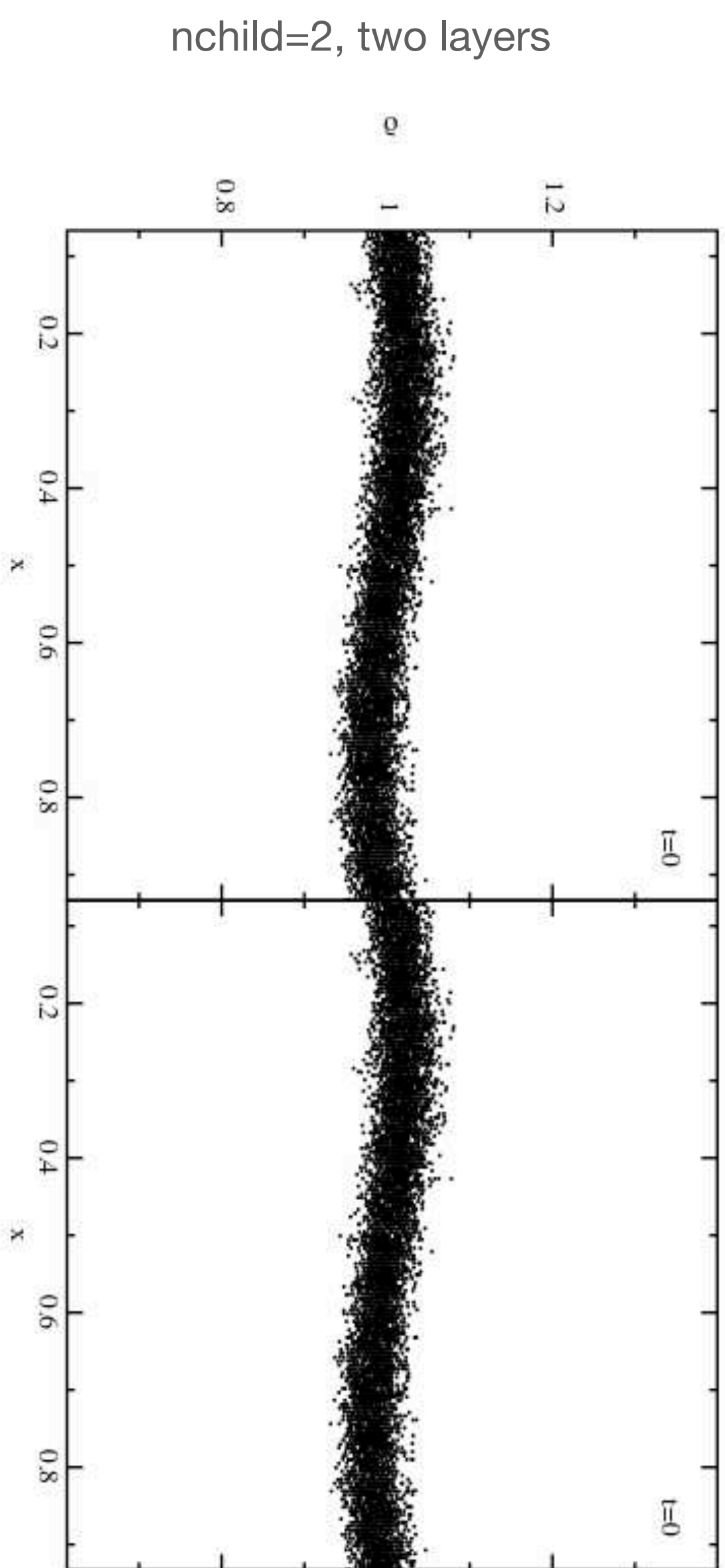
-relaxing, -directional

-relaxing, +directional

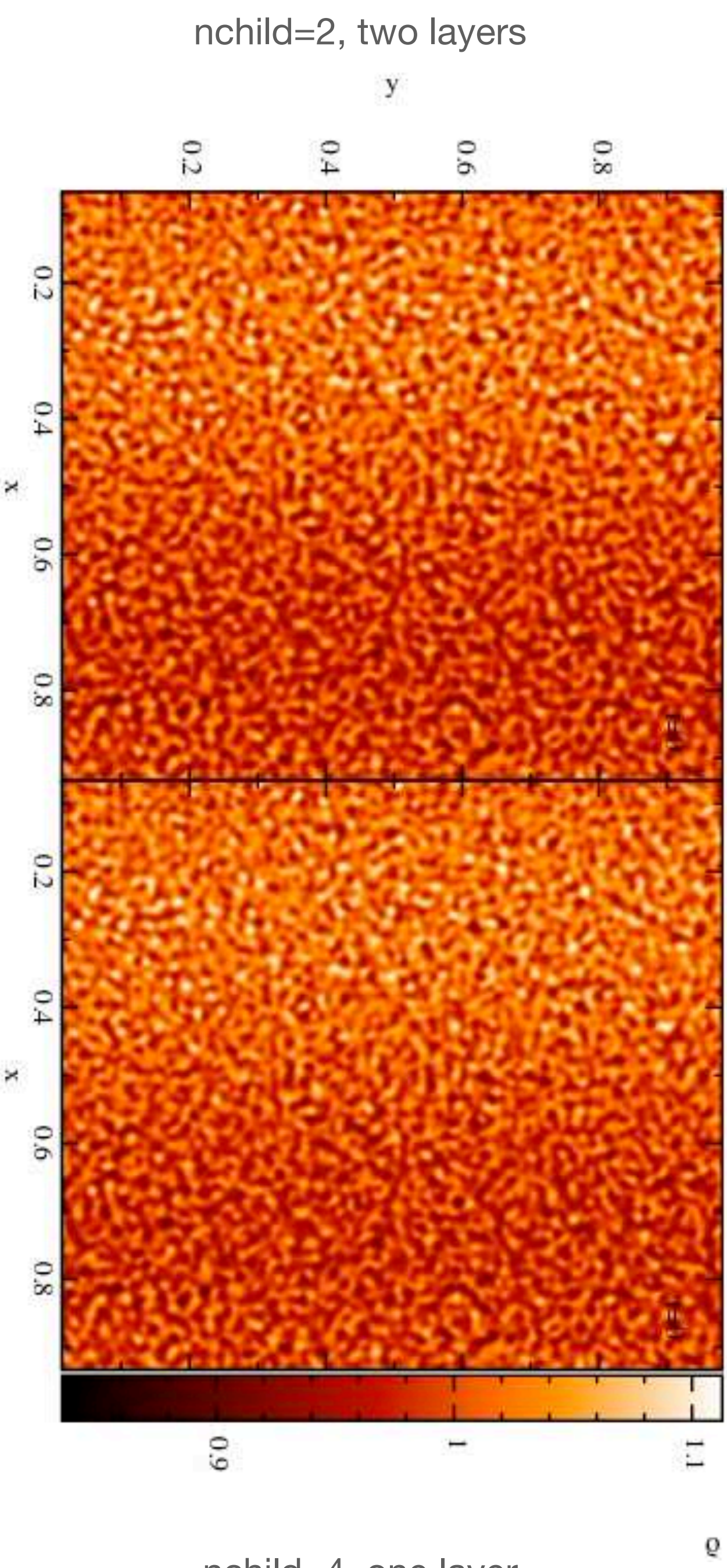
+relaxing, +directional



Wave in a box: how many children



nchild=4, one layer



The circumprimary disc in HD 142527

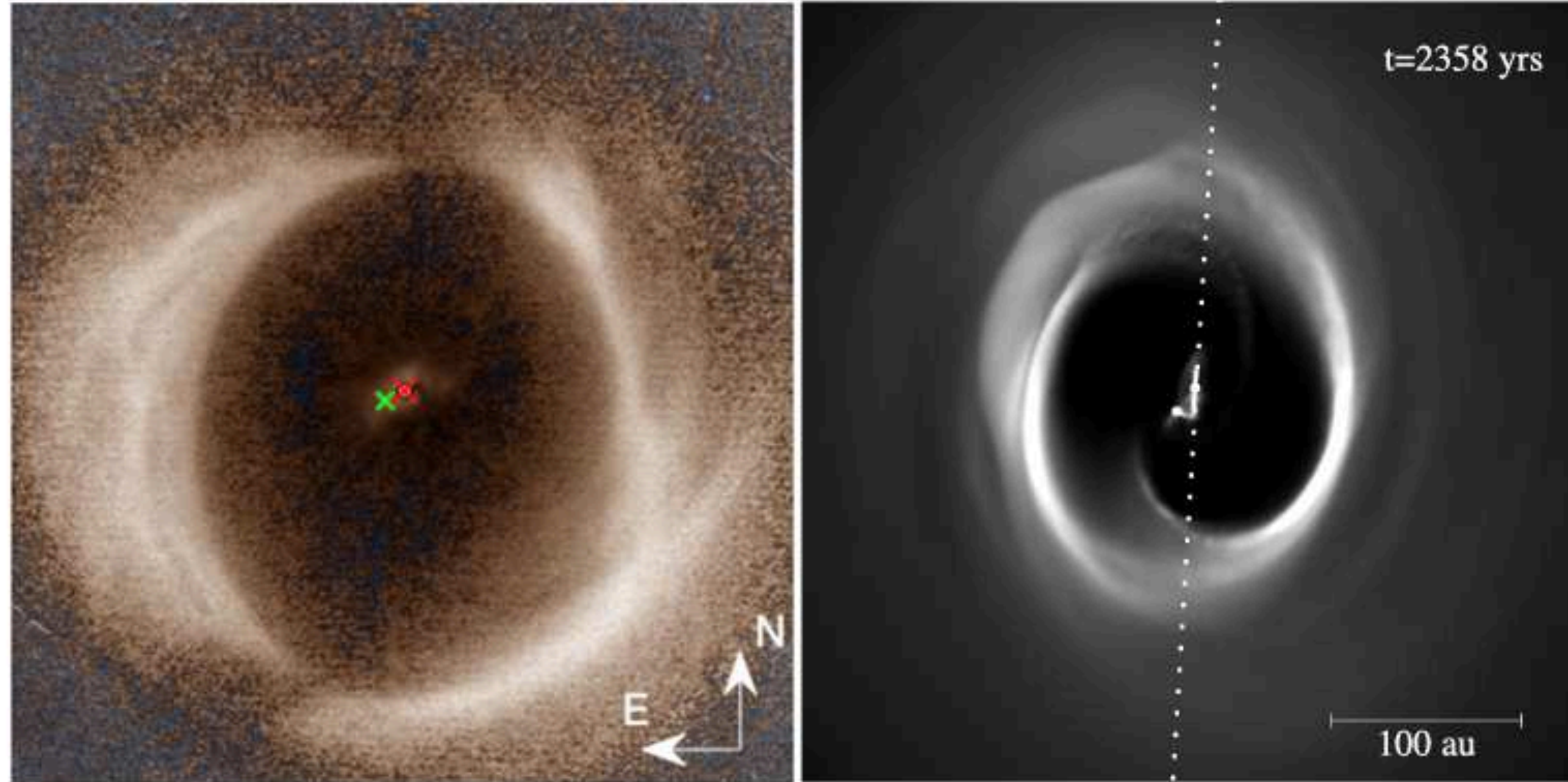
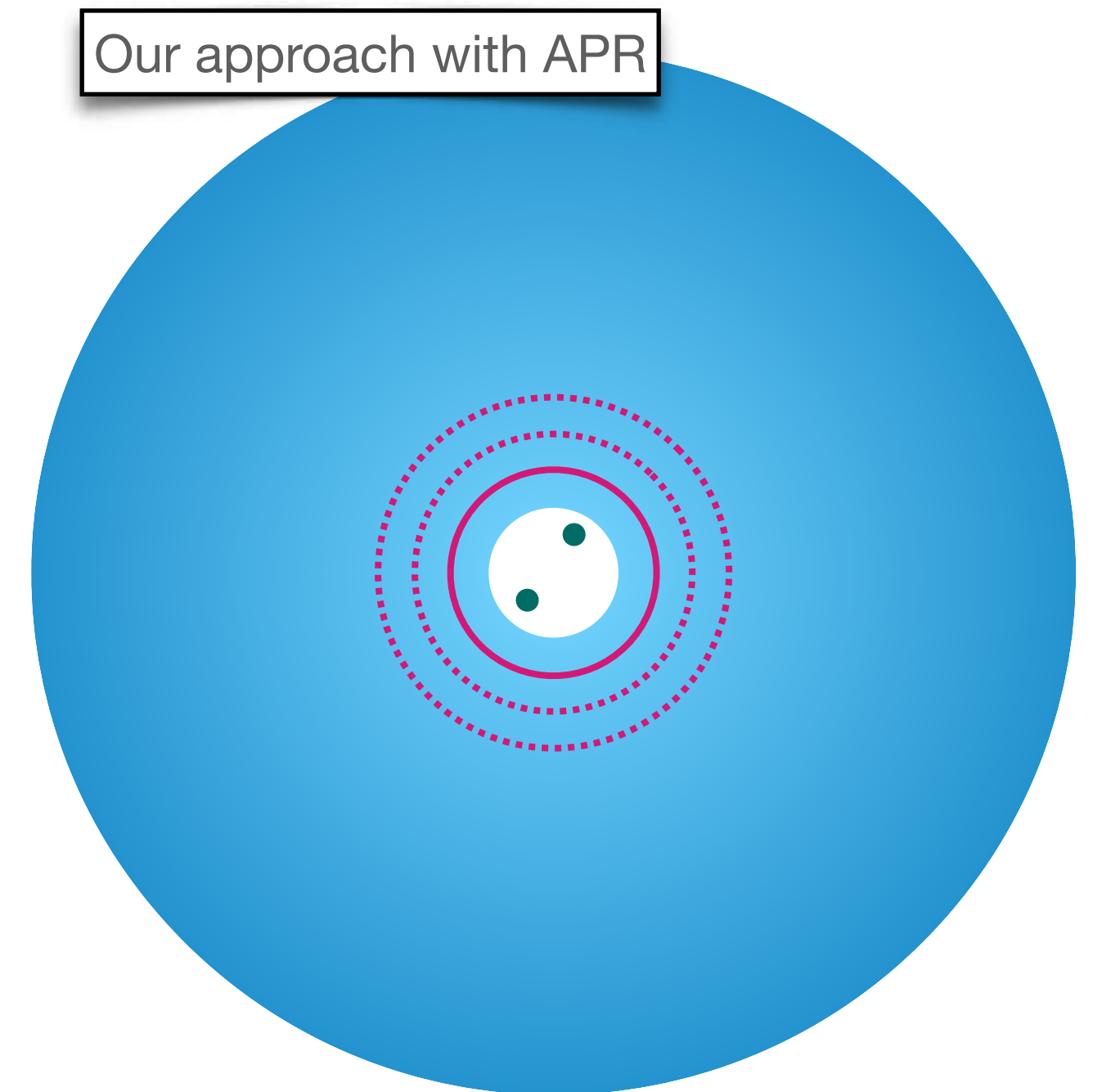
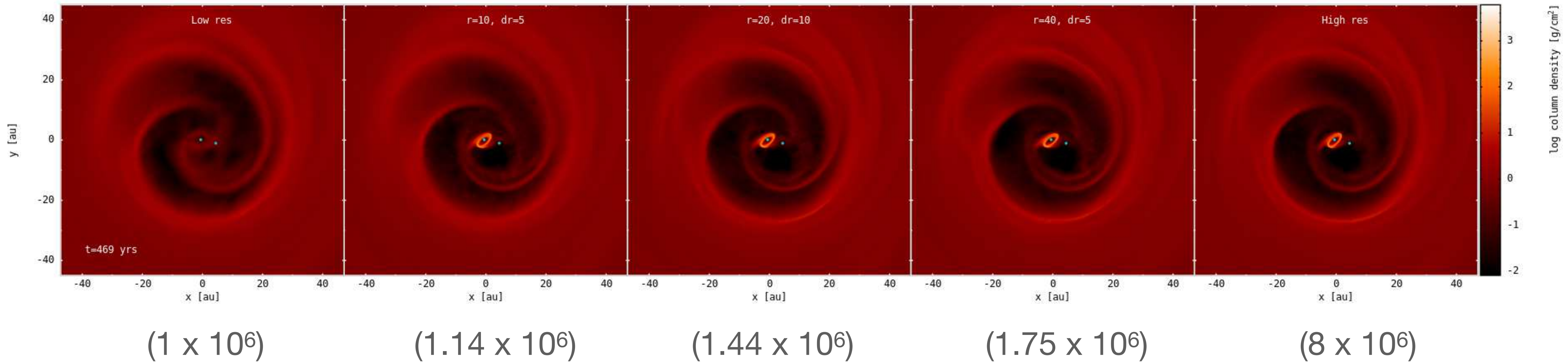


Figure 6. *Shadows.* Column density in the R1 orbit simulated with initial $R_{in} = 50$ au after 20 orbits at the observed orbital phase (right), showing the orientation of the (transient) circumprimary disc, compared to the scattered light (600–900 nm) the Zurich Imaging Polarimeter (ZIMPOL) polarization image (left; taken from fig. 1 of Avenhaus et al. 2017 ©AAS, reproduced with permission). Dotted line indicates the expected shadow from our simulated inner disc (right), which lies close to the orientation of the observed shadows (left).



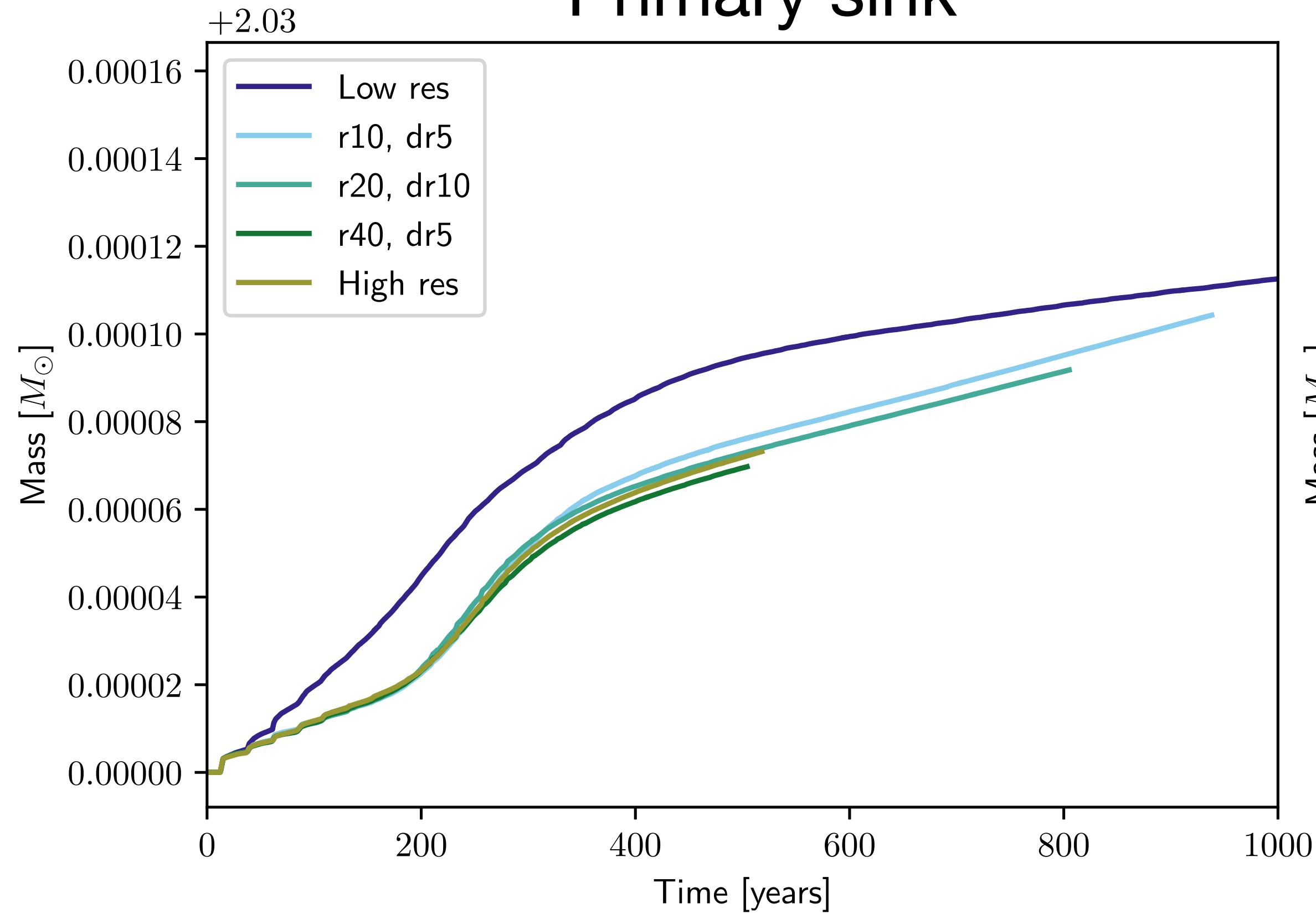
The circumprimary disc in HD 142527



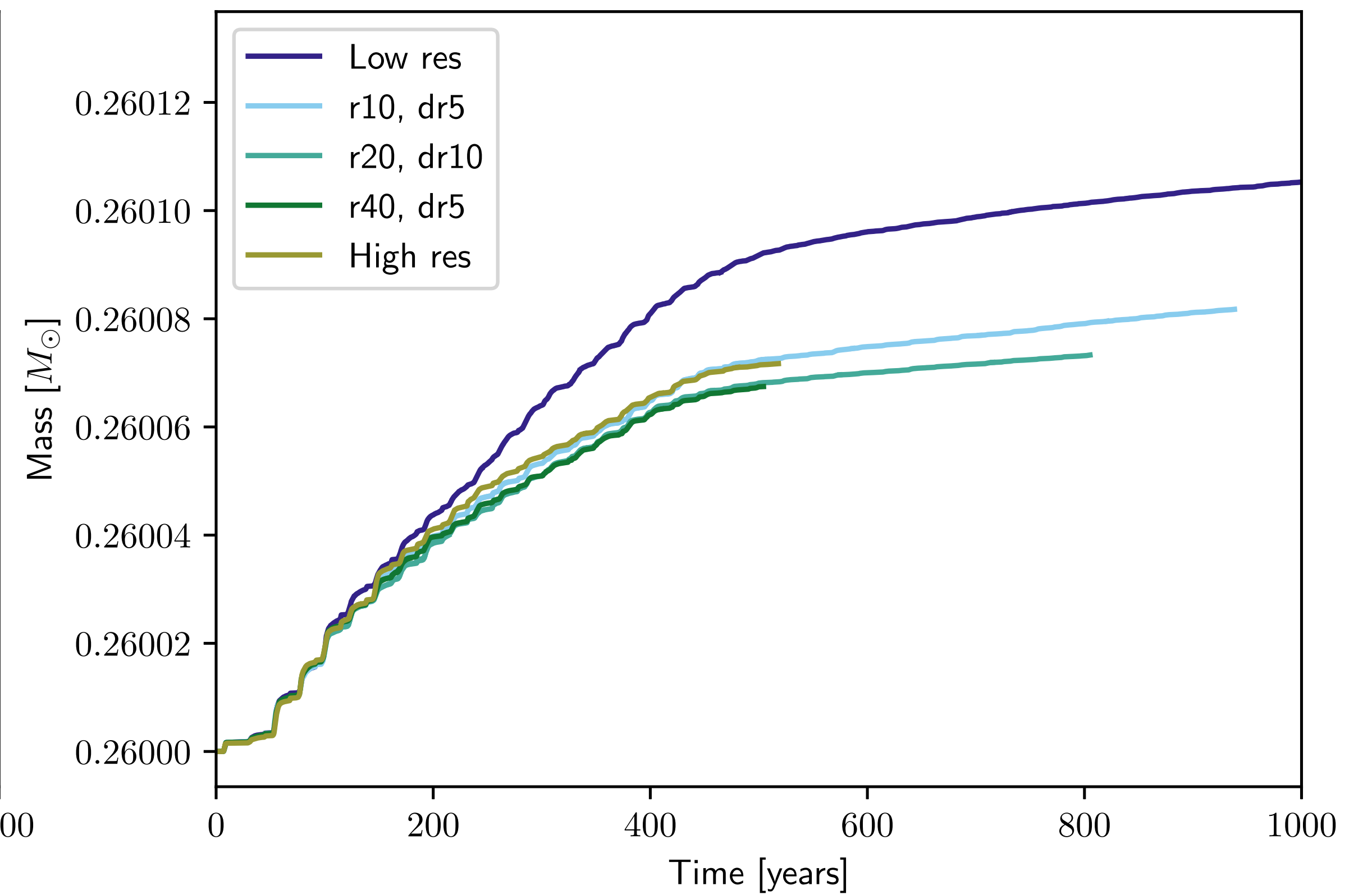
The circumprimary disc in HD 142527

Accuracy	Speed up	File size
0.002%	1.07-1.96x	22%

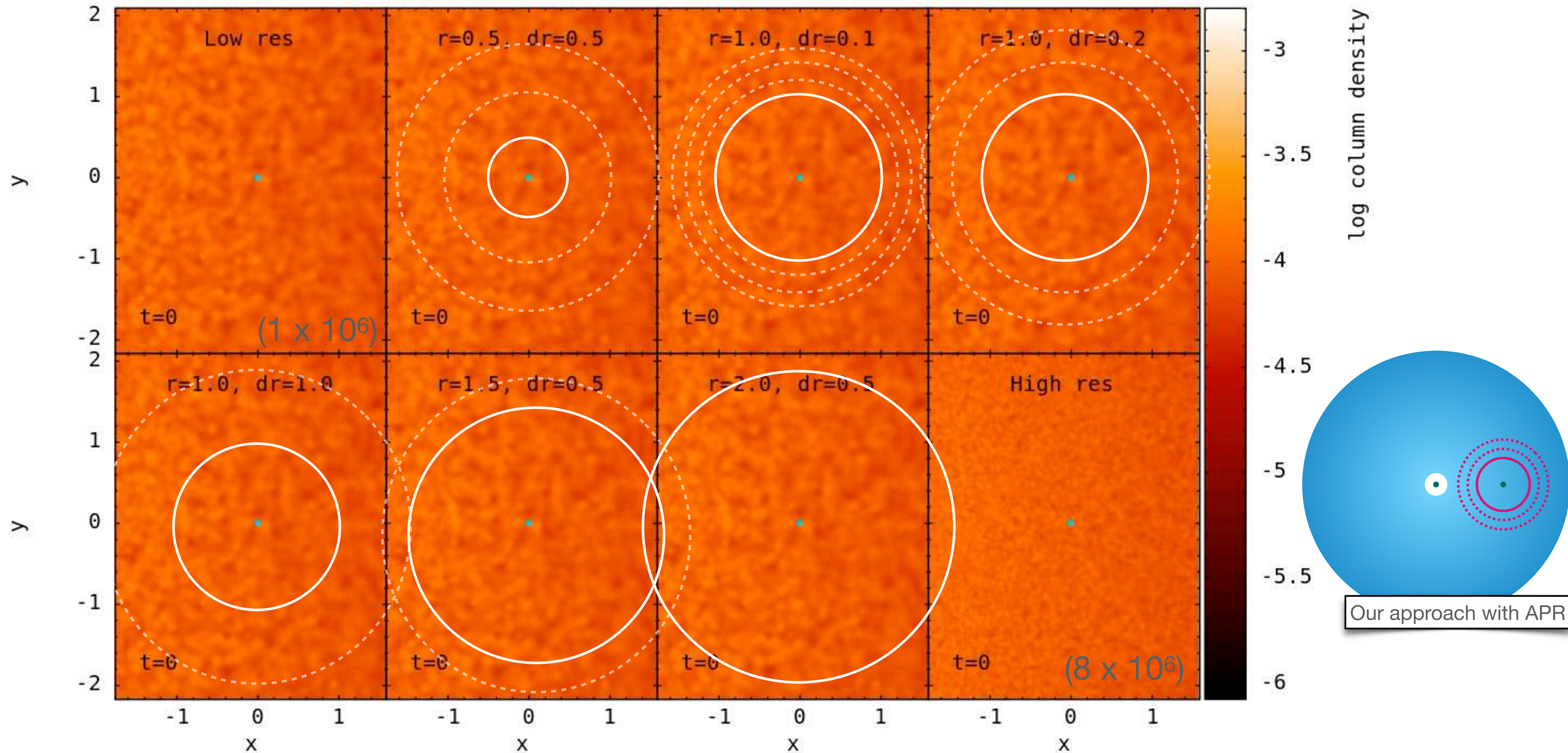
Primary sink



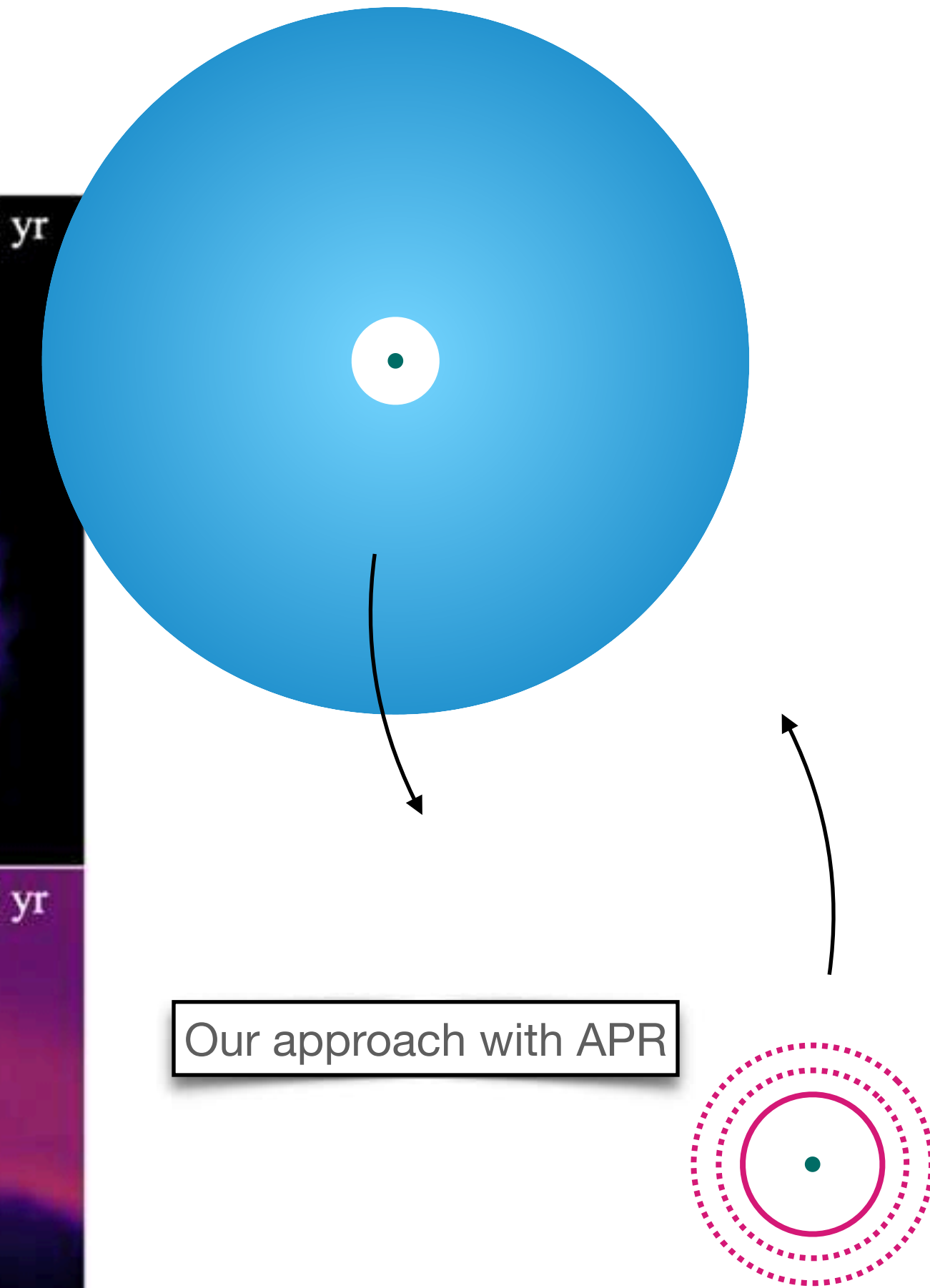
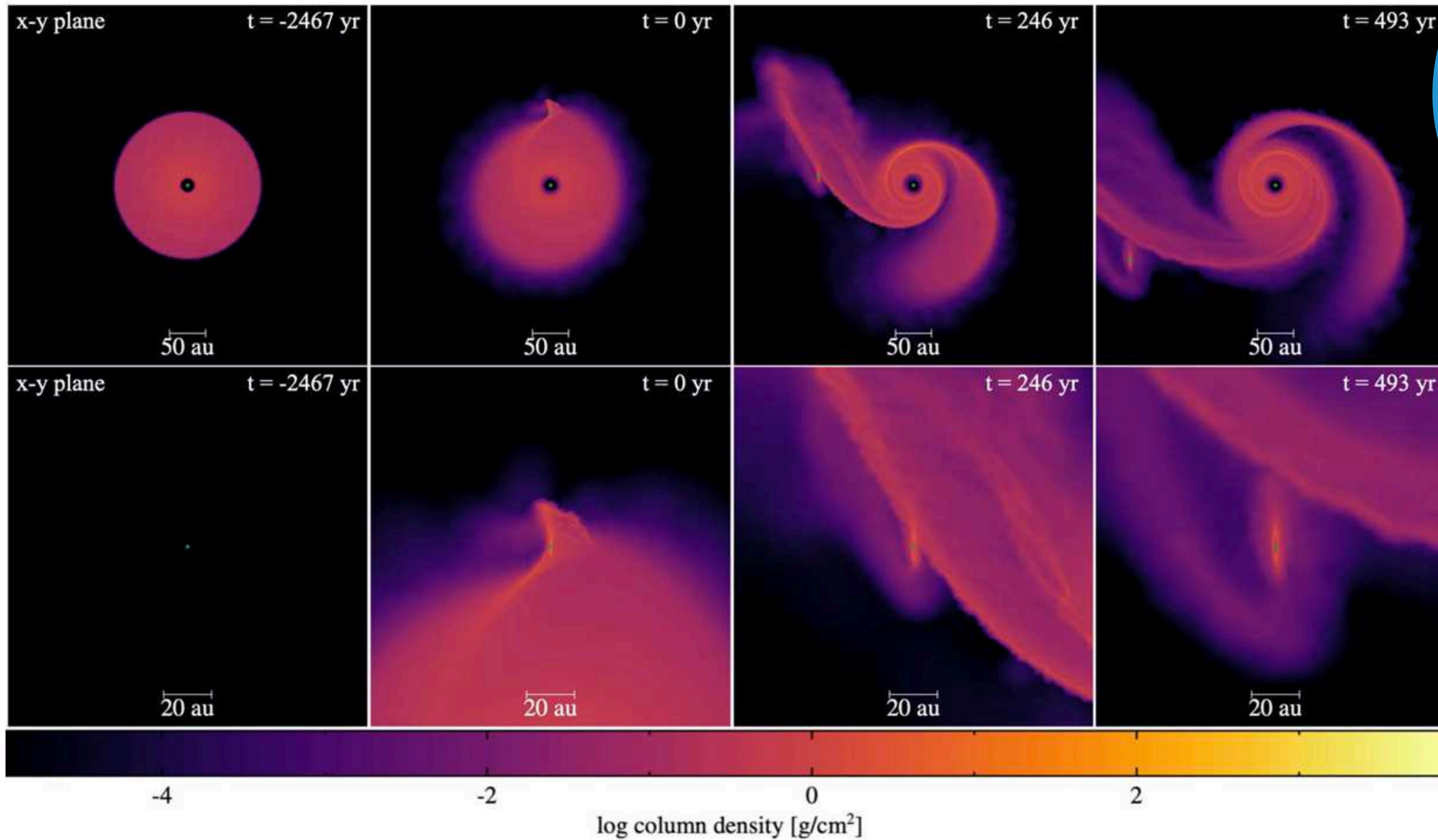
Secondary sink



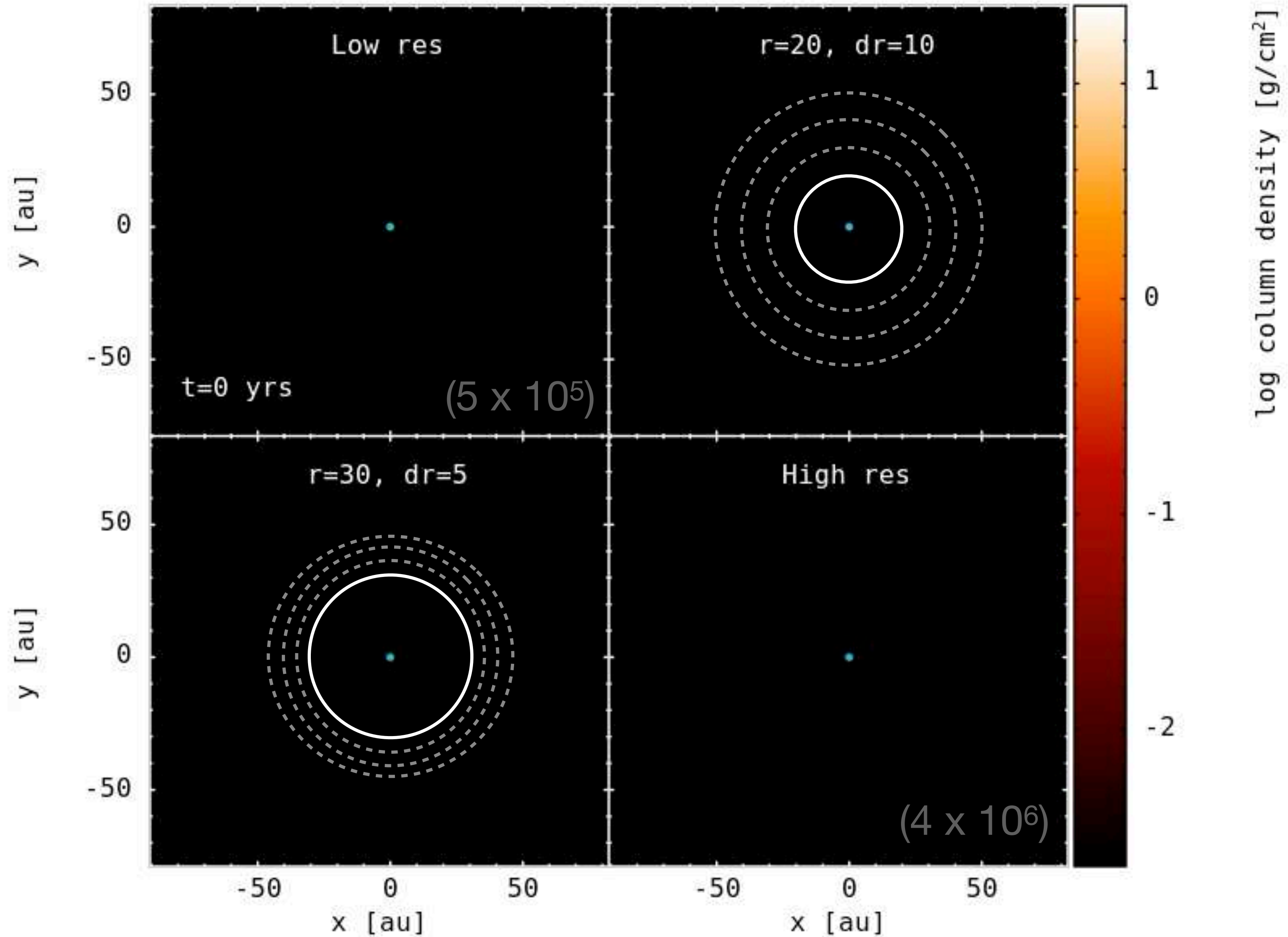
A circumplanetary disc



Material captured in a flyby



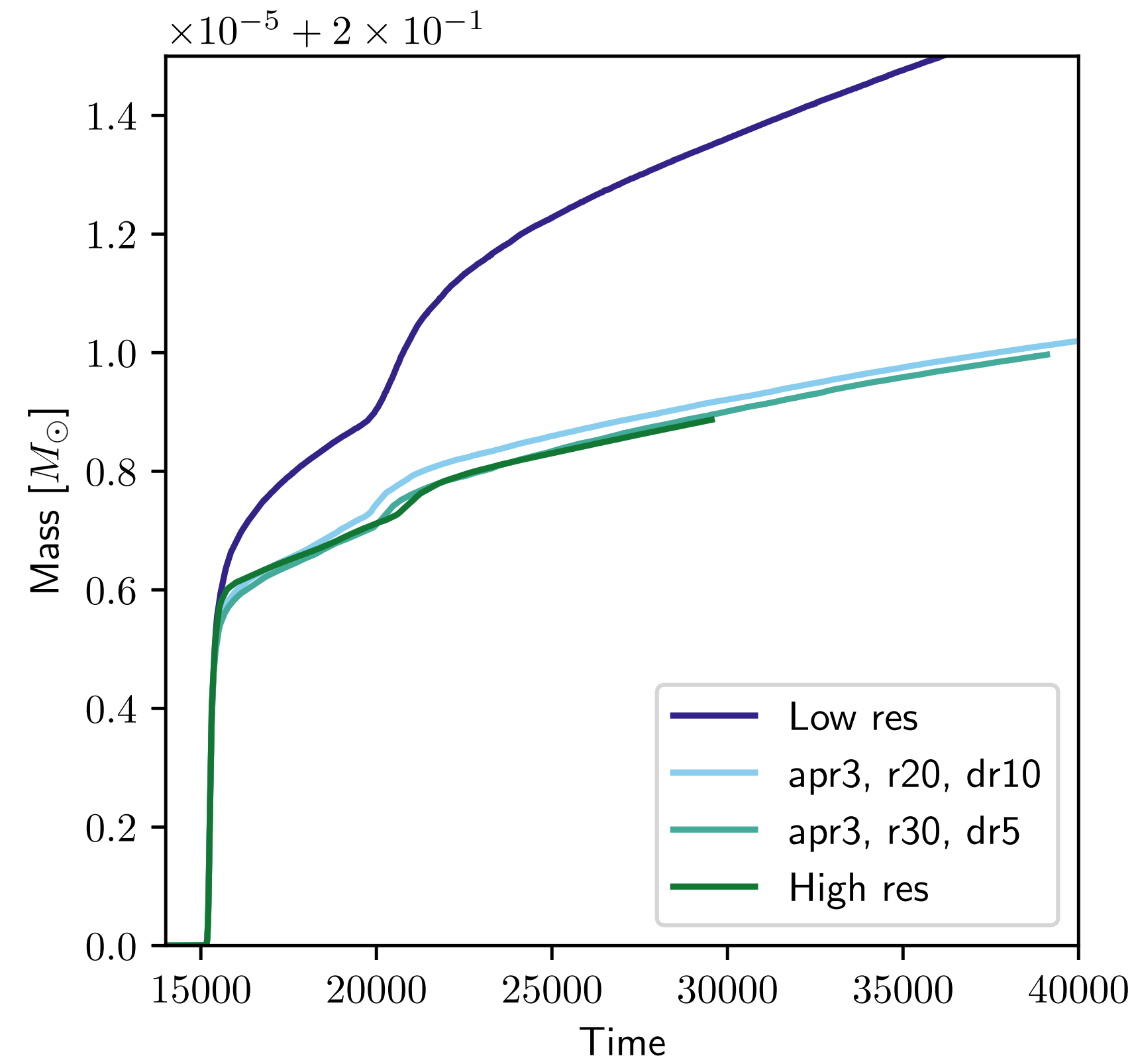
Material captured in a flyby



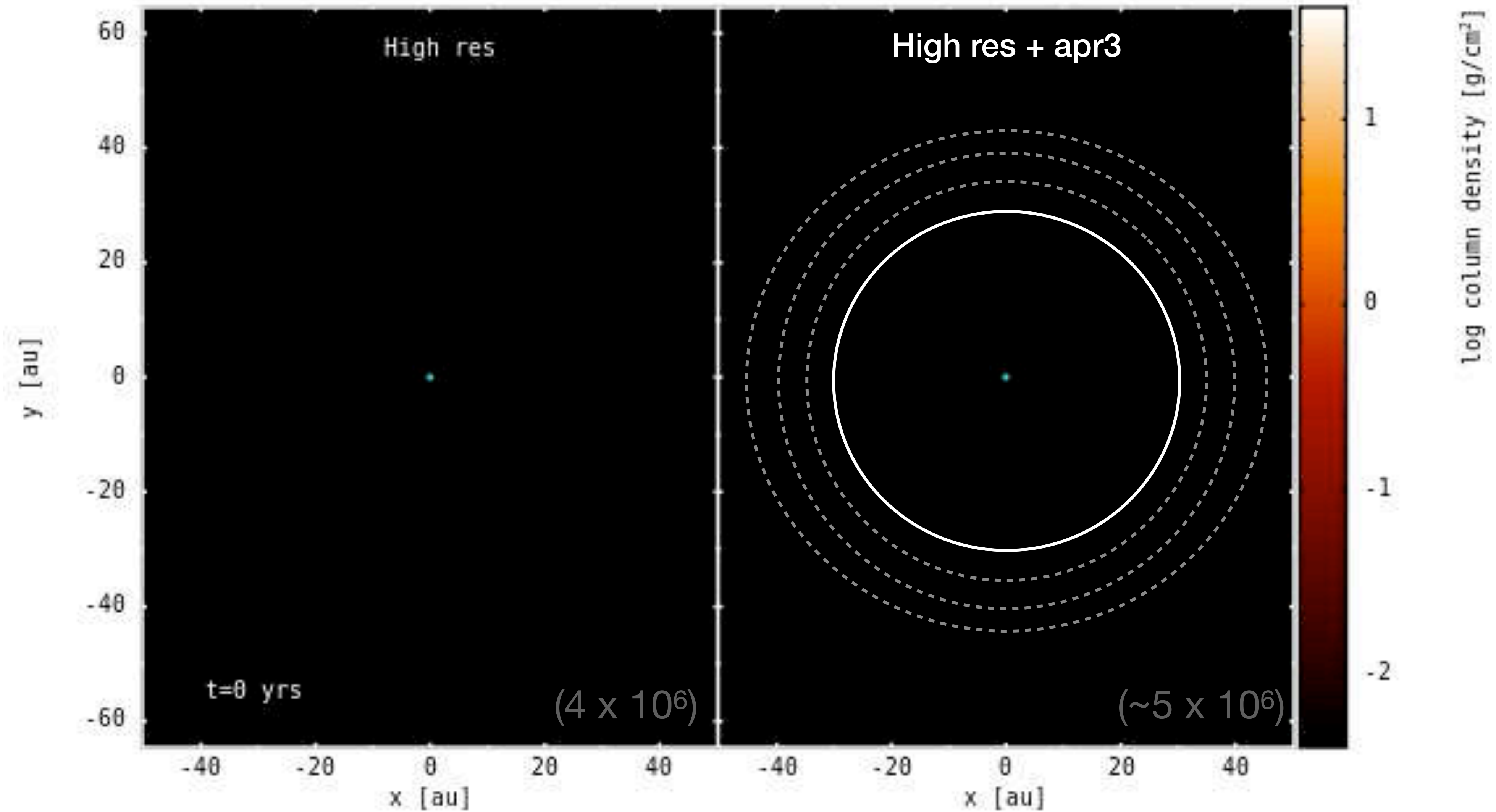
Material captured in a flyby

Accuracy	Speed up	File size
To <0.1%	~6.4x	17%

Perturber mass

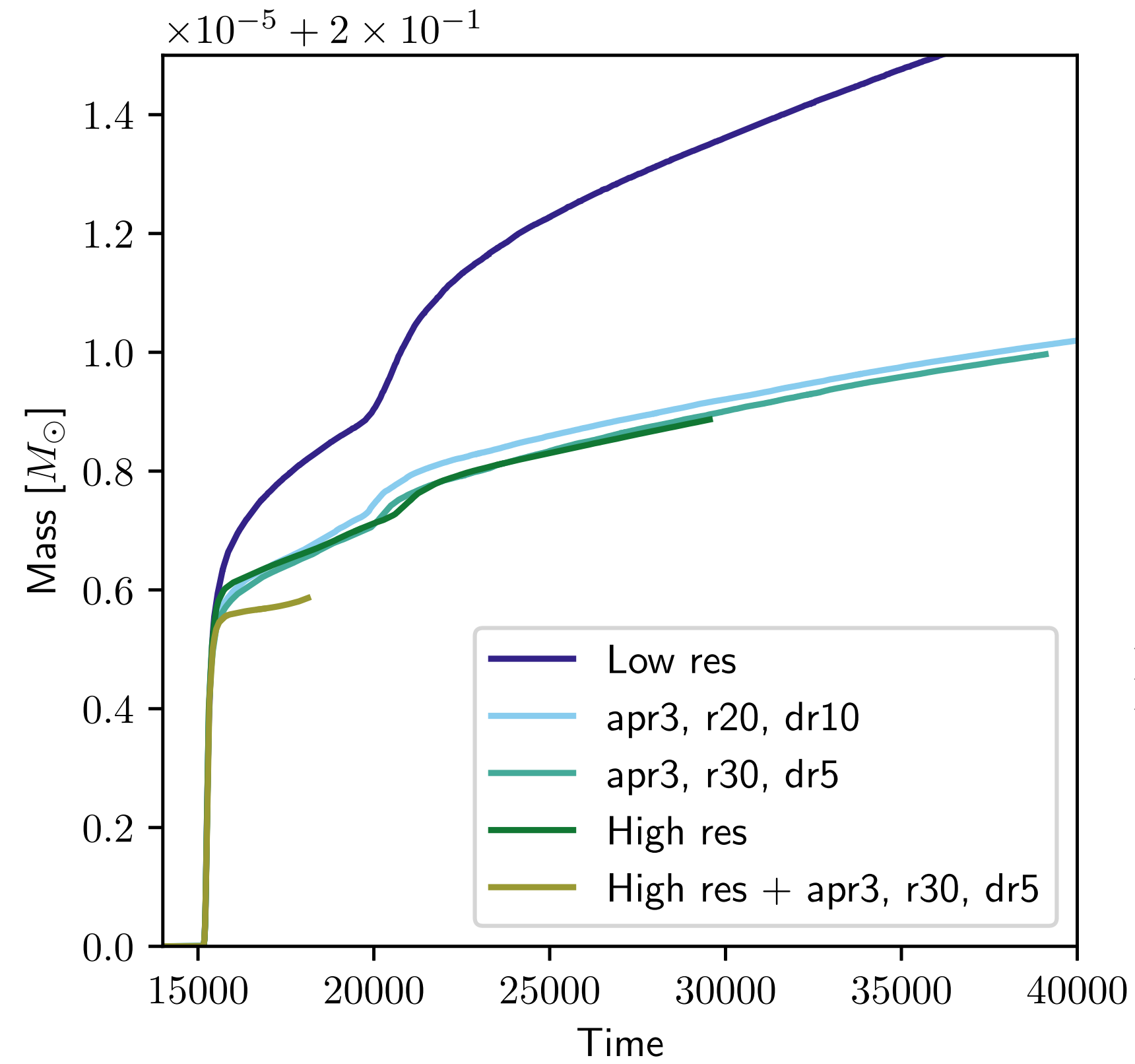


Material captured in a flyby

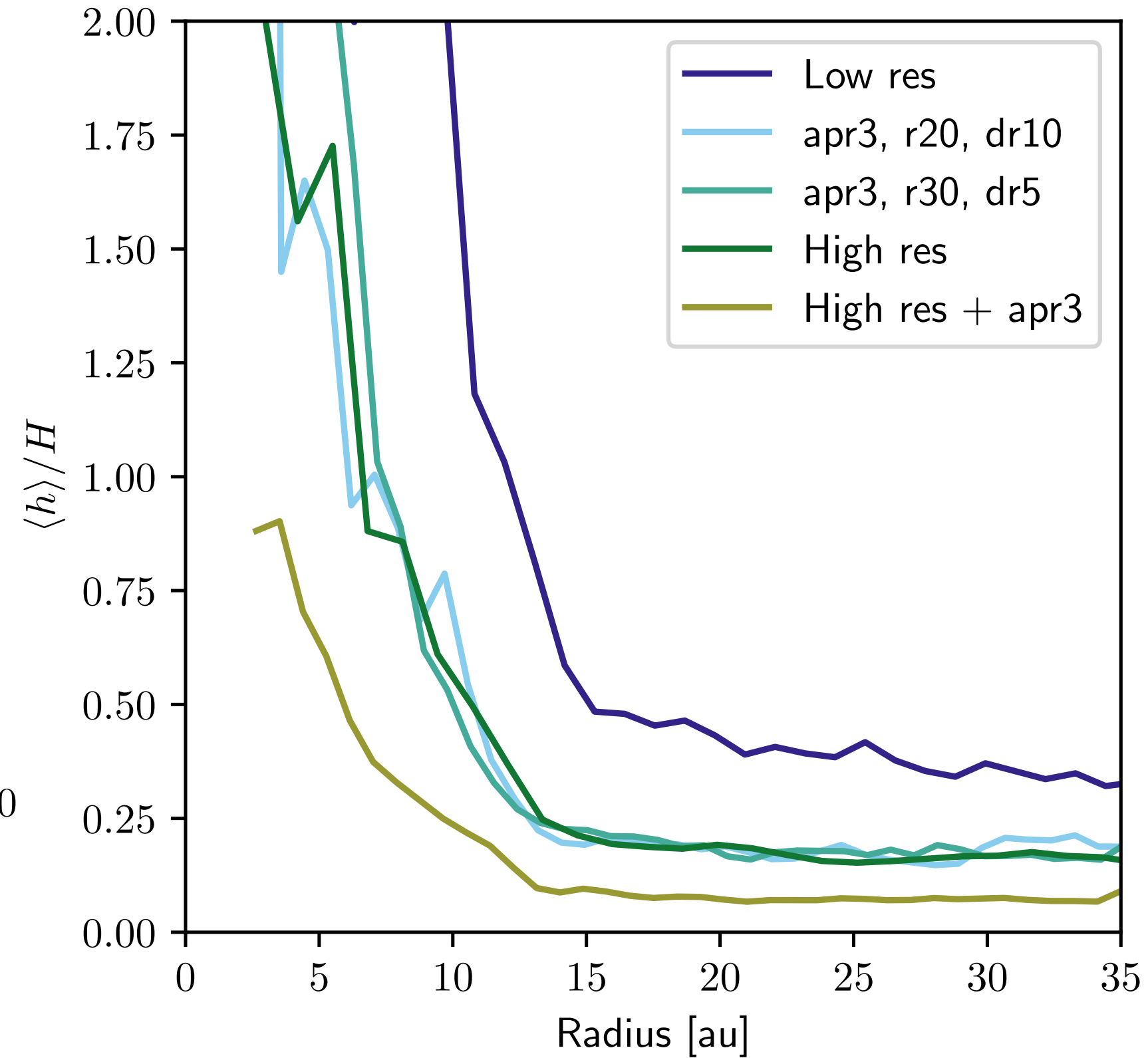


Material captured in a flyby

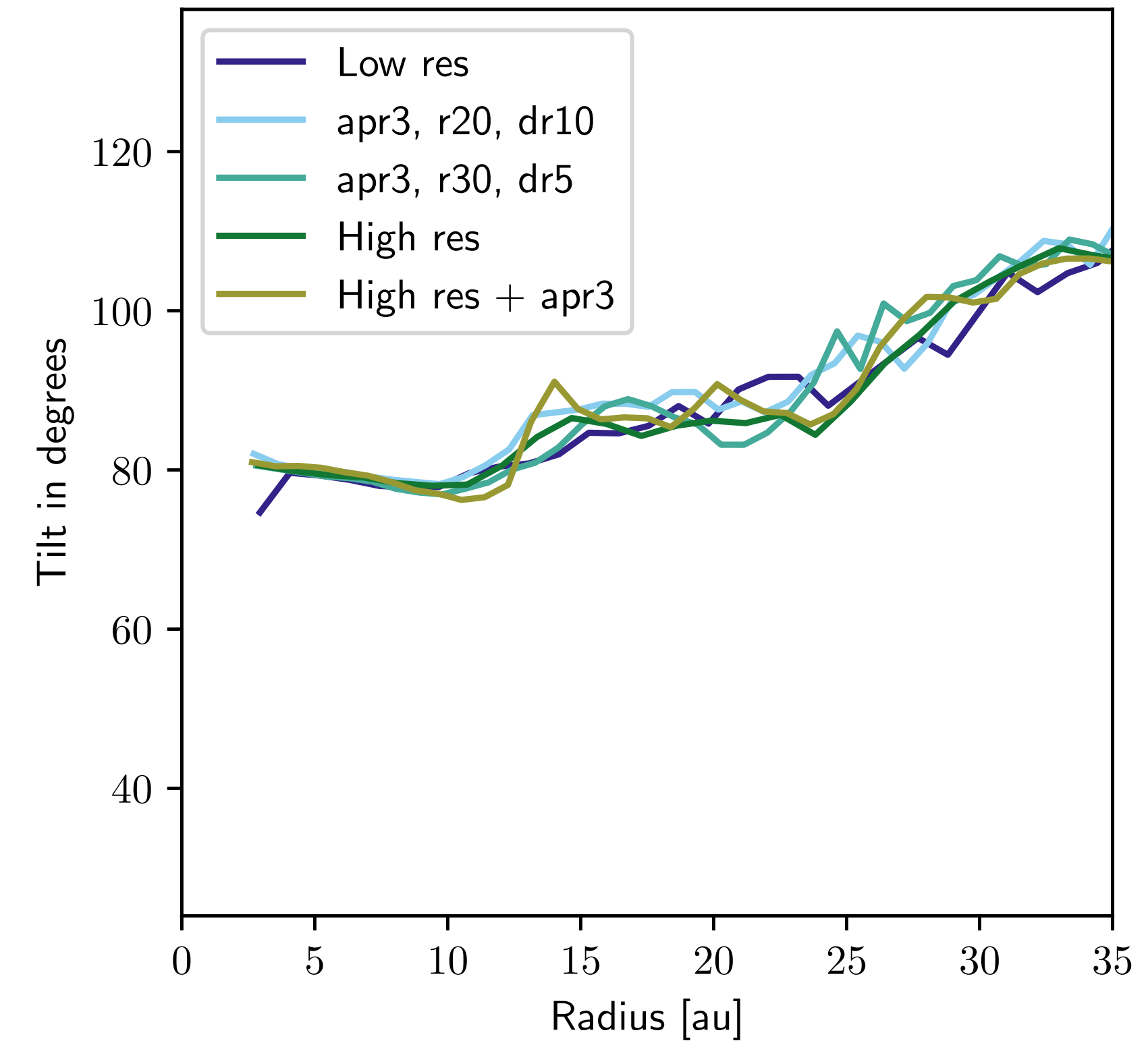
Perturber mass



Perturber disc resolution



Disc inclination



How do I use it?

1. Compile with APR=yes
2. Setup your problem like normal
3. Check the apr_region.f90 file to find your preferred region or create a new one
4. Set the apr parameters in the *.in file
5. Run

```
!-----  
!+  
! Setting/updating the centre of the apr region (as it may move)  
!+  
!-----  
  
subroutine set_apr_centre(apr_type, apr_centre)  
  use part, only: xyzmh_ptmass  
  integer, intent(in) :: apr_type  
  real,    intent(out) :: apr_centre(3)  
  
  select case (apr_type)  
  
    case(1) ! a static circle  
      dynamic_apr = .false.  
      apr_centre(1) = 0.0  
      apr_centre(2) = 0.0  
      apr_centre(3) = 0.0  
  
    case(2) ! around sink particle 2 - e.g. a planet  
      dynamic_apr = .true.  
      apr_centre(1) = xyzmh_ptmass(1,2)  
      apr_centre(2) = xyzmh_ptmass(2,2)  
      apr_centre(3) = xyzmh_ptmass(3,2)  
  
    case default  
      dynamic_apr = .false.  
      apr_centre(:) = 0.  
  
  end select  
  
end subroutine set_apr_centre
```

APR in Phantom is ...

Fast: around 1.07 -> 6.4x faster than globally high resolution (but problem dependent).

Accurate: all tests to within <1.5%, most much better than this.

Adaptable: allows for multiple regions, derefinement and setting the size of regions dynamically.

(It will be) **compatible:** currently only compatible with individual time steps, but plans for dust, MCFOST and self-gravity are on their way.

