

1.5M WITH DIFFUSION

This test is to show the capability of MESA to allow diffusion during stellar evolution. It evolves a $1.5 M_{\odot}$ star through the main sequence. Therefore, this test should be cut off when the mass fraction for center hydrogen drops below 0.01 (`xa_central_lower_limit_species(1) = 'h1'` ; `xa_central_lower_limit(1) = 0.01`).

There are many variables to control diffusion, and they are all listed in `mesa/star/public/star_defaults.dek`. To allow diffusion, the inlist for this test case sets `do_element_diffusion = .true.`. It also sets a range on temperatures in which diffusion is allowed: `diffusion_T_full_on = 1d3` ; `diffusion_T_full_off = 1d3`. This means that diffusion is turned fully on for temperatures above 1000 K, which in this case is the whole star. Diffusion-allowed regions can also be set by X, Y, and gamma. There are also diffusion controls for tolerance (`diffusion_atol = 1d-4` ; `diffusion_rtol = 1d-3`), timesteps (`diffusion_dt_limit = 7d11`), and ionization (`diffusion_calculates_ionization = .true.`).

Because diffusion calculation for each individual species would be computationally intensive, MESA groups species into classes for diffusion computation. Each class is given a ‘representative’ and an ‘A_max’. This test case has five classes, with ‘representative’ and ‘A_max’ listed for each respectively: ‘h1’, 2 ; ‘he3’, 3 ; ‘he4’, 4 ; ‘o16’, 16 ; ‘fe56’, 10000. Each species is placed in the first class, in ascending order, that has ‘A_max’ greater than, or equal to, the species’ atomic mass number. Therefore, hydrogen and deuterium would go in ‘h1’, carbon, nitrogen, and oxygen would go in ‘o16’, and anything heavier would go in ‘fe56’.

This test case loads a ZAMS model and evolves it through the main sequence, as shown in the HR-Diagram (figure 1). To the right is an abundance profile taken at the start of the run (figure 2), with the log mass fraction plotted against q, where q is the fraction of star mass interior to outer boundary of each zone, moving outwards from the core.

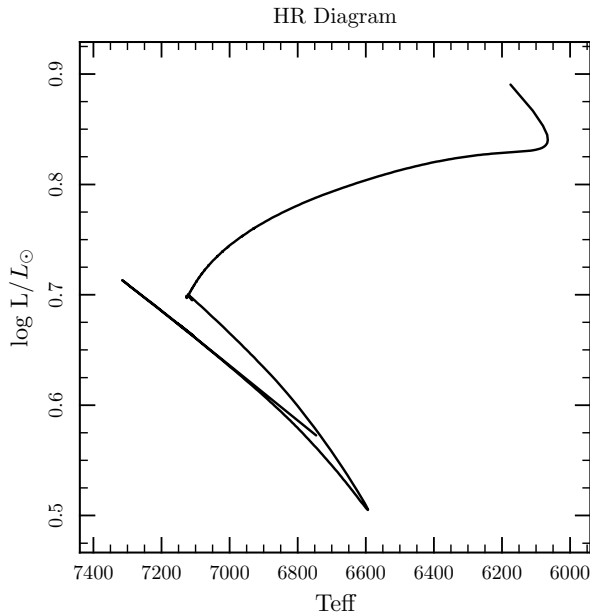


Figure 1: HR-diagram, main sequence track

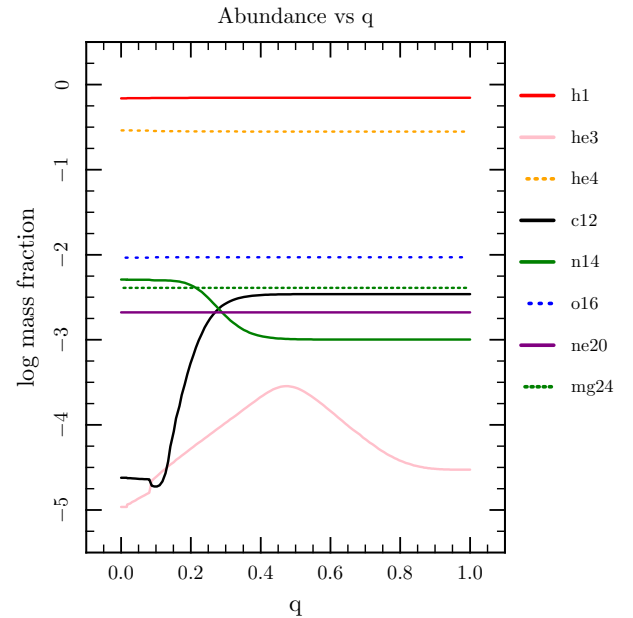


Figure 2: Abundance profile from start of run

The effects of diffusion in this test case are most readily apparent in the envelope of the star. To the left is an abundance profile from the end of the run (figure 3), with mass fraction plotted against $\log x_q = \log(1-q)$. The red dots mark the bottom of a convection zone. To the right is the same plot, but taken from a run in which diffusion is turned off (figure 4).

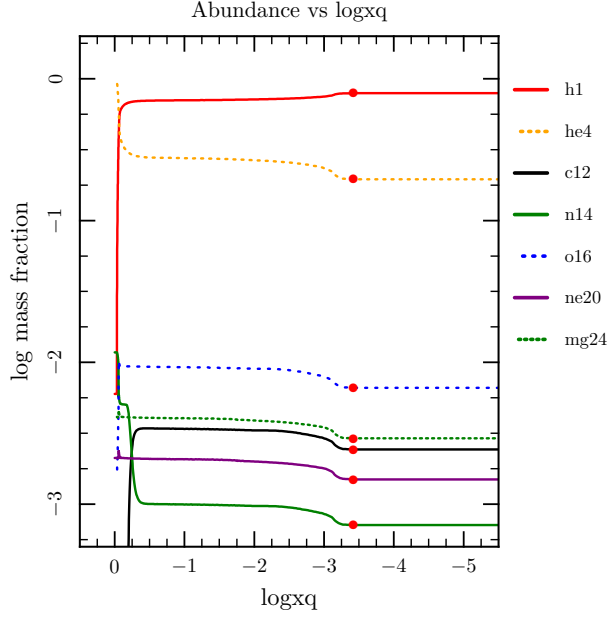


Figure 3: Abundance profile WITH diffusion

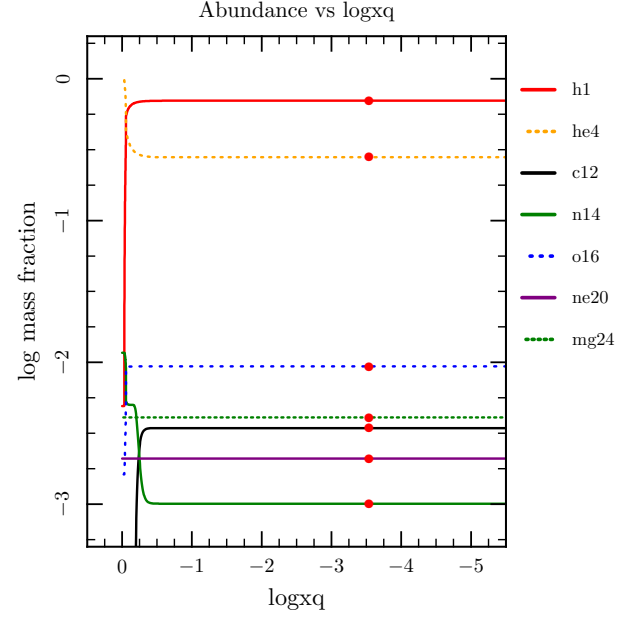


Figure 4: Abundance profile WITHOUT diffusion

This final plot (figure 5) is meant to show a few internal MESA variables, such as the size of the time-step, the number of zones, and the number of retries against the model number in order to give some understanding of how hard MESA is working throughout the run and where some areas of problems/interest might be.

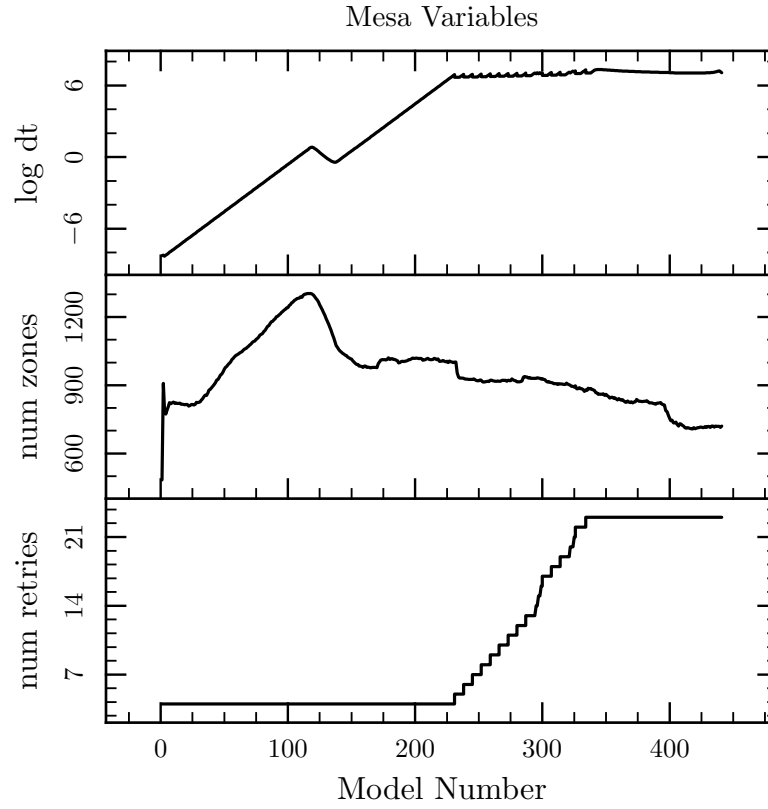


Figure 5: MESA variables plotted against model number show how hard MESA is working