## List of parametrs used in Mcluster

- Initial number of objects for each sub-population  $n_1$ ,  $n_2$ , ... with  $n_i = n_{singles} + n_{binaries}$ , where  $n_i$  is the total number of stars in the simulation
- Primoridal binary fraction  $fb_1$ ,  $fb_2$ , ... with  $n_{binaries} = fb_i \cdot n_i$
- Initial density distribution (could be different for sub-populations) initial Model
  - 0 Homogeneous sphere
  - 1 Plummer
  - 2 **King**
  - 3 Subr
- King model parameter (could be different for sub-populations)  $w_0$  for  $w_0$  in range of (1.0 12.0) DEFAULT  $w_0 = 5.0$
- Mass segregation parameter S in range of (0.0-1.0)  $S=0.0 \rightarrow$  unsegregated,  $S=1.0 \rightarrow$  completely segregated For King model take S=0.99 maximally - DEFAULT S=0.0
- Fractal dimensions fractal (2<sup>D</sup> children per parent) (could be different for sub-populations) DEFAULT fractal = 3.0 (unfractal)
- Virial ratio qvir,  $qvir > 0.5 \rightarrow$  expanding,  $qvir > 0.5 \rightarrow$  equilibrium,  $qvir > 0.5 \rightarrow$  collapsing DEFAULT q = 0.5
- Stellar mass function mfunc
  - 0 equal masses equivalent to a set to parameter single mass
    - A DEFAULT single\_mass= 1.0
  - 1 [Kroupa (2001)] IMF DEFAULT model
    - A lower mass limit default mlow m\_low = 0.08
    - B upper mass limit default mup m\_up = 100.00
  - 2 multi-power law (Subr)
    - A alpha slopes DEFAULT alpha\_ $\inf = [1.35, 2.35, 2.7, 0.0, 0.0]$
    - B mass limits DEFAULT mlim\_imf = [0.08, 0.5, 4.0, 100, 0.0, 0.0]
  - 4 L3 IMF [Maschberger (2012)]
    - A lower mass limit default mlow  $m_{low} = 0.08$
    - B upper mass limit default mup  $m_{-}up = 100.00$
    - C  $\alpha-$  slope for mass function default alpha\_L3 = 2.3
    - D  $\beta$ -slope for mass function default beta-L3 = 1.4
    - E  $\mu$ -parameter default mu\_L3 = 0.2
- Pairing of binary components pairing
  - 0 random pairing
  - 1 ordered pairing for components with masses  $M>5M_{\odot}$
  - 2 random but separate pairing for components with masses  $M>5M_{\odot}$
  - 3 uniform distribution of mass ratio (0.1 < q < 1.0) for  $M > 5M_{\odot}$  and random pairing for remaining [Kiminki & Kobulnicky (2012); Sana et al., (2012); Kobulnicky et al., (2014)] DEFAULT

- Semi-major axis distribution adis
  - 0 uniform distribution in log(a), between amin and amax
  - 1 lognormal distribution distribution for a
  - 2 based on [Kroupa (1995)] period distribution
  - 3 based on [Kroupa (1995)] period distribution for  $M < 5M_{\odot}$ ; based on [Sana et al.(2012); Oh, S., Kroupa, P., & Pflamm-Altenburg, J. (2015)] period distribution for  $M > 5M_{\odot}$  DE-FAULT distribution
  - 4 flat uniform distribution in a ranging from amin to amax
  - 5 based on [Duquennoy & Mayor (1991)] period distribution
  - 6 uniform distribution in log(a), between amin and amax for  $M < 5M_{\odot}$ ; Sana et al. (2012) period distribution for  $M > 5M_{\odot}$  ALERT: this will generate uniform distribution of mass ratio (0.1 < q < 1.0) for  $M > 5M_{\odot}$  and also for  $M < 5M_{\odot}$  indipendently from pairing!
- Eigenevolution eigen
  - 0 Off DEFAULT
  - $1\,$  [Kroupa (1995)] eigenevolution for pre-main sequence short-period binaries and feeding algorithm

ALERT: This will set adis = 2 and pairing = 1!

 $2\,$  - New eigenevolution and feeding algorithm [Kroupa (2013), rewieved in Belloni et al. (2017)]

ALERT: This will set adis = 3 and pairing = 3!

- Minimum binary semi-major axis amin defined in Solar radii  $[R_{\odot}]$ :
  - A  $amin > 0 \rightarrow amin = amin$
  - B  $amin < 0 \rightarrow amin = -amin \cdot R_{least}$ , where  $R_{least}$  is the stellar radius of the least massive star in the system
  - C DEFAULT amin = -1.0
- Maximum binary semi-major axis amax defined in Solar radii  $[R_{\odot}]$ :
  - A  $amax > 0 \rightarrow amax = amax$
  - B  $amax < 0 \rightarrow amax = -amax \cdot 2.5 \cdot R_h/N$ , where  $R_h$  is the total half-mass radius
  - C DEFAULT amax = 50 [a.u.] = 10747.0
- Tidal field tf
  - 0 no tidal field
  - 1 point mass galaxy DEFAULT tidal field
- **Tidal radius** rbar defined in parsec [pc] DEFAULT rbar = 35.8
- Half mass radius [pc] (for the whole system) rh\_mcl
  - A if  $rh\_mcl>1.d9$  the model is not underfilled (standard King model, for Plummer model it will set  $rh\_mcl=0.1\cdot rbar$ )
  - B if  $rh\_mcl < 1.d9$  the model is underfilled by a rplum factor, defined as  $rplum = rbar/rh\_mcl$
  - C DEFAULT  $rh_{-}mcl = 1.0$

- Concentration radius parameter  $conc\_pop$  defined as  $Rh_i/Rh_1$ , the ratio between the half-mass radii of the i-th and the first generation (it will be skipped for single stellar population)
  - the first value is  $Rh_2/Rh_1$  (the ratio between the half-mass radii of the second and the first generation)
  - the second value would be  $Rh_3/Rh_1$  (the ratio between the half-mass radii of the third and the first generation)
  - DEFAULT conc\_pop= 0.5
- Potential energy evaluation potential\_energy
  - 0 potential energy evaluated as sum of gravitational potential for every object  $(N^2)$
  - 1 potential energy evaluated in spherical symmetry (N ) DE-FAULT energy evaluation
- Age of population [Myr] DEFAULT epoch = 0.0 Myr
- Initial metallicity DEFAULT zini = 0.001
- Initial integer number to start random number generator for Mcluster initial conditions DEFAULT seedmc = 10
- Output format
  - 0 single nbody.dat and binary nbody.dat files are generated. The structure of those files are:
    - \* single.dat mass  $[M_{\odot}]$ , x, y, z, Vx, Vy, Vz [N-body units], age, metallicty, index of the population
    - \* binary.dat e, a [log10(Ro)], m1 [ $M_{\odot}$ ], m2 [ $M_{\odot}$ ], x, y, z, Vx, Vy, Vz [binary center of mass, N-body units], age, metallicity, index of the population
  - 1 standard dat.10 file is generated. The structure of the file is: binaries at the beginning of the file (i.e.  $2 \cdot NBIN$  lines with the binary individual masses, positions and velocities in the cluster frame) and remaining single star lines (with mass, positions and velocities in the cluster frame)
  - DEFAULT outputf = 0
- Make energy check at end of Mclusters
  - $0 \mathbf{off}$
  - 1 **on**
  - DEFAULT check\_en = 1