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^D children per parent) (could be different for sub-populations)
 - A fractal > 0: boxy distribution (Goodwin & Whitworth 2004)
 - B fractal < 0: spherical distribution (Alex Livernois 2021)
 - C DEFAULT fractal = 3.0 (unfractal)
- Virial ratio qvir, $qvir>0.5\to \text{expanding}$, $qvir>0.5\to \text{equilibrium}$, $qvir>0.5\to \text{collapsing}$ 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_imf = [-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 α -slope for mass function default alpha_L3 = 2.3
 - D β -slope for mass function default beta L3 = 1.4
 - E μ -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 for MOCCA simulations 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 for NBODY simulations 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)
 - 2 initial files for MOCCA & NBODY simulations will be generated at the same time.
 - DEFAULT outputf = 0
- Make energy check at end of Mclusters
 - 0 off
 - 1 **on**
 - DEFAULT check_en = 1
- Activate SSE/BSE for stellar/binary evolution

0 **- off**

1 **- on**

ALERT: this will not be activated if output f = 0 or output f = 2

- DEFAULT BSE = 0