rdc_SeBa
This program reduces the output file from SeBa. You can find it in the directory: src/amuse/community/seba/src/rdc where src can be found in the main directory of AMUSE. One of the big advantages of using rdc_SeBa is that it picks out only those binary systems that you're interested in, and reduces the output to a regular number of lines, which makes the data handeling easier.

To run:
less SeBa.data | ./rdc_SeBa -f -p white_dwarf -s white_dwarf

For a population of double white dwarfs on my laptop:
less SeBa.data | / /Users/silviato/Development/amuse/src/amuse/community/seba/src/rdc/rdc_SeBa -f -p white_dwarf -s white_dwarf > SeBa_wdwd.data

optional parameters:
-f first occasion - for a given binary system, the first occasion that fits the parameters. In case of double white dwarfs, this will be the formation of the double white dwarf system, and later stages of the double white dwarf system will not be shown.
-R full evolution - for a given binary that fulfills the criteria, every line in SeBa.data is printed.

-p primary type
-s secondary type
options for this are:
any, proto_star, planet, brown_dwarf, main_sequence, hertzsprung_gap, sub_giant, horizontal_branch, super_giant, helium_star, helium_giant, white_dwarf, neutron_star, black_hole
ps, pl, bd, ms, hg, gs, hb, sg, he, gh, hd, cd, od (last three are types of white dwarfs), ns, bh

-B binary_type
default: Detached
options for this are:
detached, semi_detached, contact, common_envelope, double_spiral_in, merged, disrupted, spiral_in

semi_detached means stable mass transfer
common_envelope means gamma common envelope
spiral_in means alpha common envelope

* Never used by me*
constraints on the binary parameters
-a -A min/max separation
-m -M min/max primary mass
-n -N min/max secondary mass

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-q -Q min/max mass ratio
-e -E min/max eccentricity
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