

# User Guide for falcON

version of August 6, 2006

**Summary.** `falcON` is the “Force Algorithm with Complexity  $\mathcal{O}(N)$ ” which is described by Dehnen (2000, 2002). With this package, you can use `falcON` in subroutine form as Poisson solver for particle based simulations. The package also has a full  $N$ -body code, based on `falcON`, called `gyrfalcON` (“Galaxy simulator using `falcON`”), which employs the  $N$ -body tool box `NEMO`. This code features individual adaptive time steps employing a block-step scheme, but can also be used in single-time-step mode (in which case momentum is exactly conserved). Additionally, there are several other programs and facilities that may prove useful for setting-up, running, and analyzing  $N$ -body simulations.

## 1 Guarantee

This package comes with absolutely no guarantee whatsoever! The unpacking, installation, and usage of the code is entirely at the risk of the user alone.

## 2 Credit

Any scientific publication or presentation which has benefited from using `falcON` in subroutine form or from using any of the programs `gyrfalcON`, `getgravity`, or `addgravity` should quote the papers

Dehnen, W., 2000, ApJ, 536, L39

Dehnen, W., 2002, JCP, 179, 27.

(please find the .pdf file of the latter paper in the subdirectory `falcON/doc.`) Papers that did not use these but other parts of this packages should acknowledge that whereby explicitly mentioning me (Walter Dehnen) as author of the code.

## 3 What is new?

This section has been added to the user guide in 2004; earlier changes are not all reflected here.

**August 2006** The public version of `falcON` has been put under CVS control under the `NEMO` package. This should significantly simplify installation, updating and downloading.

Some changes in the directory structure and filenames (`FALCON`→`forces`).

**July 2006** In order to allow their usage at the GH2006 summer school, several parts of the code have been migrated from the proprietary section into the public part. Of particular interest are extensions to the manipulators and support for communication between manipulators, as well as `bodyfunc.h`, which supports simple functions of a body (and time + parameters) to be generated on the fly given a user-provided string in some simple syntax (see man pages `1bodyfunc` and `5bodyfunc`); this is very similar to, but more powerful than, `NEMO`’s `bodytrans`). Parts of the code have been documented using `doxygen`, see `falcON/dox/html/index.html` for details (partly due to my inexperience with `doxygen` this documentation is very preliminary and incomplete, but should still be useful for anybody using the `falcON` library or using manipulators).

**April 2006** Some pieces of code which are not `falcON` specific have been taken out and put into a `utils` package, which resides in directory `utils` parallel to directory `falcON`, but there are some dynamic links. The `utils` package uses namespace `WDutils` and provides some generally useful code. It must be compiled **before** `falcON`.

**September 2005** A lot of changes have been introduced with this release, some of them affecting the users, for instance the change of the namespace's name from `nbdy` to `falcon`. Several files have been re-named to better describe their contents.

The body data layout has been changed so that adding and removing bodies becomes possible (the files `body.h` & `body.cc` and `io.h` & `io.cc` (previously `nmio.h` & `nmio.cc`) have been completely re-written). In this process, two new routines `get_data_blocked()` and `put_data_blocked()` have been added to NEMO.

When a `falcon` executable, like `gyrfalcon`, is run without any command-line arguments, the `help=h` argument is assumed. Output file names may be appended with an `!` or `?` to indicate that existing files shall be overwritten or appended to, respectively.

To startup `falcon`, the shell-script file `falcon.start` should be sourced, which also tries to start NEMO. While the `falcon` library is still dynamically linked, there is no need anymore to set the `LD_LIBRARY_PATH` environment variable (the executables know where to link to).

For FORTRAN and C users, the ordering of vector-typed arrays has been changed: where formerly three arrays of size  $N$  for the  $x$ ,  $y$ , and  $z$  components were required, we now expect one array of size  $3N$  with the order  $x_0, y_0, z_0; x_1, y_1, z_1 \dots$ .

**September 2004** The time integrator has been completely re-written (used to be in `inc/nbdy.h`; now in `inc/public/nbody.h`). Tests indicate that it behaves as the old one (but is easier to maintain and extend). `gyrfalcon` allows now for *run-time manipulators*, see §12 below and also the man page for `gyrfalcon`. For them to work, you need the environment variable `FALCON` to be defined, see §??.

**1<sup>st</sup> July 2004** The `gyrfalcon` options `potname`, `potpars` and `potfile` have been replaced by `accname`, `accpars` and `accfile`, respectively. This reflects the change in using an external acceleration field rather than the old-style NEMO potential.

**19<sup>th</sup> May 2004** All NEMO programs in this packages come with man pages, which replace the detailed documentation in this file.

**14<sup>th</sup> May 2004** The NEMO programs `mkdehnen`, `mkking`, and `mkplum` have been added to the public version of this package, see §11.2 for details.

**April 2004** We now use a dynamic library `libfalcon.so` instead of `libfalcon.a`, so that you must put the directory it resides in into the `LD_LIBRARY_PATH` environment variable, otherwise, the code will not work; see also §4.

**September 2003** Individual, but fixed, softening lengths have been added to the public version. See §5 below.

## 4 Installation

Since August 2006, (the public version of) `falcon` is under CVS control within the NEMO package and you are strongly advised to install and initialize `falcon` using NEMO.

If you are interested in using `falcon` standalone, i.e. only use it as a library for your force computation or SPH neighbour search, then you may still obtain `falcon` from NEMO, but must compile it without the NEMO environment variable set. In this case, only two executables will be made: `TestGrav` and `TestPair`, the first allows testing of the gravity approximation, the second the search for SPH interaction partners.

## Compiler Issues

You need to make the library `libfalcon.so` and, possibly, the executables you want to use. The code is written entirely in C++ and it is strongly recommended to use a compiler that understands standard C++<sup>1</sup>, I recommend GNU's `gcc` versions 3.4 or Intel's `icc` version 8.0 or higher. By default, we use `gcc`, if you want to use another compiler, edit the file `makedefs` and change the entry for `COMPILER`.

You may also edit the optimization flags in file `makedefs`. This applies particularly to Intel's `icc` compiler, which allows processor specific switches.

## 5 Individual Softening Lengths

Individual softening lengths are enabled, but not obligatory (in fact default is always to have a globally constant  $\epsilon$ ), if line 21 of the `Makefile`

```
DSOFT                                := -Dfalcon_INDI
```

is not commented out (by a `#` in the first column).

The softening length  $\epsilon_{ij}$  used in the interaction of nodes with individual softening lengths  $\epsilon_i$  and  $\epsilon_j$  is simply the arithmetic mean of the two. The softening length  $\epsilon_i$  of a cell is the arithmetic mean of the softening lengths of all its bodies.

## 6 Testing falcon

Please run `TestGrav` in order to get some rough check on the validity of your library. Issuing the command

```
TestGrav 2 1 1000000 901 0.01 1
```

shall generate a Hernquist sphere with  $N = 10^6$  particles, build the tree (twice: once from scratch and once again) and compute the forces using a softening length of  $\epsilon = 0.01$  scale radii with the  $P_1$  kernel (see §7). The output of this command may look like<sup>2</sup>

```
time needed for set up of X_i:           0.64
time needed for FALCON::grow():          1.21
time needed for FALCON::grow():          0.59
time needed for FALCON::approximate_gravity(): 4.77

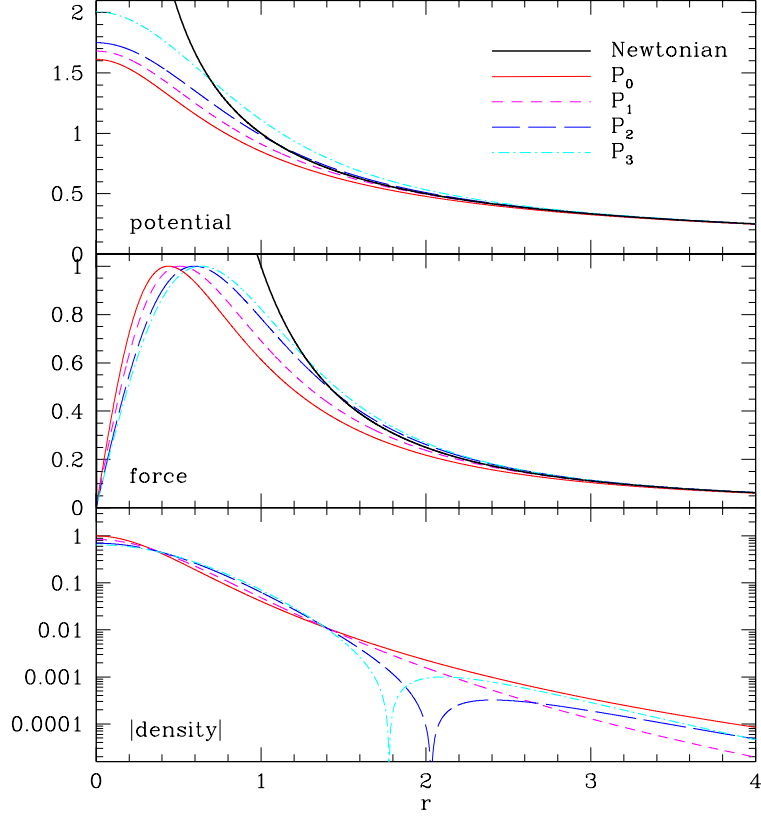
state:                                tree re-grown
root center:                          0 0 0
root radius:                           1024
bodies loaded:                         1000000
total mass:                             1
N_crit:                                 6
cells used:                             353665
of which were active                    353665
maximum depth:                          21
current theta:                          0.6
current MAC:                            theta(M)
softening length:                       0.01
softening kernel:                       P1
Taylor coeffs used:                     83880 in 4 chunks of 22108
interaction statistics:
  type      approx    direct    total
# body-body :      -         0         0 =      0%
# cell-body :  2138354  484564  2622918 =  18.427%
# cell-cell : 11302423 254979 11557402 =  81.194%
# cell-self :      -    53928    53928 =   0.379%
# total      : 13440777 793471 14234248 = 100.000%

ASE(F) / <F^2>      = 0.001392818172
```

---

<sup>1</sup>If you use a compiler version different (usually newer) than those against which this package was tested, you may get warnings or even error messages. These do not point to genuine errors in the code but rather reflect the fact that C++ compilers do not fully implement the standard but converge there with every new version. I would appreciate if you, in such a case, could email me the error messages together with details of the compiler and system used.

<sup>2</sup> Code compiled with `gcc` version 3.3.4, run on an AMD Opteron (tm) with 2190Mhz and 1024Kb cache size.



**Figure 1:** Potential, force, and density for the softening kernels of the table, including the standard Plummer softening ( $P_0$ ). The softening lengths  $\epsilon$  are scaled such that the maximum force equals unity. The kernels  $P_{>0}$  approach Newtonian forces more quickly at larger  $r$  than does  $P_0$ . The kernels  $P_2$  and  $P_3$  have slightly super-Newtonian forces (and negative densities) in their outer parts, which compensate for the sub-Newtonian forces at small  $r$ .

```
max (dF)^2      = 0.8913656473
Sum m_i acc_i   = 3.240235305e-10 1.787507139e-09 2.572656954e-09
```

Note that the second tree-build is much faster than the initial one. Note also the the total-momentum change (last line) vanishes within floating point accuracy – that’s a generic feature of `falcon`.

## 7 Choice of the Softening Kernel and Length

The code allows for various forms of the softening kernel, i.e. the function by which Newton’s  $1/r$  is replaced in order to avoid diverging near-neighbour forces. The following kernel functions are available ( $x := r/\epsilon$ )

name	density (is proportional to)	$a_0$	$a_2$	$f$
$P_0$	$(1 + x^2)^{-5/2}$	$\infty$	$\infty$	1
$P_1$	$(1 + x^2)^{-7/2}$	$\pi$	$\infty$	1.43892
$P_2$	$7(1 + x^2)^{-9/2} - 2(1 + x^2)^{-7/2}$	0	$\infty$	2.07244
$P_3$	$9(1 + x^2)^{-11/2} - 4(1 + x^2)^{-9/2}$	0	$-\pi/40$	2.56197

Note, that  $P_0$  is the standard Plummer softening, however, **recommended** is the use of  $P_1$  or  $P_2$ . There are several important issues one needs to know about these various kernels.

First, the softening length  $\epsilon$  is just a parameter and using the same numerical value for it but different kernels corresponds in effect to different amounts of softening. Actually, this softening is strongest for the Plummer sphere: at fixed  $\epsilon$ , the maximal force is smallest. In order to obtain comparable amounts of softening, larger  $\epsilon$

are needed with all the other kernels. An idea of the factor by which  $\epsilon$  has to be enlarged can be obtained by setting  $\epsilon$  such that the maximum possible force between any two bodies are equal for various kernels. The last column in the previous table gives these factors. Note, that using a larger  $\epsilon$  with other than the  $P_0$  kernel does **not** mean that your resolution goes down, it in fact increases, see Dehnen (2001), but the Poisson noise is more suppressed with larger  $\epsilon$ . It is recommended not to use Plummer softening, unless (i) you want  $\epsilon \equiv 0$ , (ii) in 2D simulations, as here  $\epsilon$  is the average scale-height of the disk, and, perhaps, (iii) in simulations made to compare with others that use Plummer softening (for historical reasons).

Second, as shown in Dehnen (2001), Plummer softening results in a strong force bias, due to its slow convergence to the Newtonian force at  $r \gg \epsilon$ . This is quantified by the measure  $a_0$ , which for  $P_0$  is infinite. In Dehnen (2001), I considered therefore other kernels (not mentioned above), which have finite support, ie. the density is exactly zero for  $r \geq \epsilon$ . This discontinuity makes them less useful for the tree code (which is based on a Taylor expansion of the kernel). In order to overcome this difficulty, the kernels  $P_1$  to  $P_3$ , which are continuous in all derivatives, have been designed as extensions to the Plummer softening, but with finite  $a_0$  ( $P_1$ ), zero  $a_0$  but infinite  $a_2$  ( $P_2$ ), or even zero  $a_0$  and finite  $a_2$  ( $P_3$ ).

## 8 Choice of the Tolerance Parameter

The code `falcON` approximates an interaction between two nodes, if their critical spheres don't overlap. The critical spheres are centered on the nodes' centers of mass and have radii

$$r_{\text{crit}} = r_{\text{max}}/\theta \quad (1)$$

where  $r_{\text{max}}$  is the radius of a sphere that is guaranteed to contain all bodies of the node (bodies have  $r_{\text{max}} = 0$ ), while  $\theta$  is the tolerance parameter. The default is to use a mass-dependent  $\theta = \theta(M)$  with  $\theta_0 \equiv \theta(M_{\text{tot}})$  being the parameter, see Dehnen (2002). For near-spherical systems or groups of such systems,  $\theta_0$  of 0.6 gives relative force errors of the order of 0.001, which is generally believed to be acceptable. However, the force error might often be dominated by discreteness noise, in which case a larger value does no harm. For disk systems, however, a smaller tolerance parameter, e.g.  $\theta_0 = 0.5$ , might be a better choice.

The recommendation is to either stick to  $\theta_0$  no larger than about 0.6, or perform some experiments with varying  $\theta_0$  (values larger than 0.8, however, make no sense, as there is hardly any speed-up).

## 9 Use of `falcON` as Poisson Solver in Your Code

You may use `falcON` like a subroutine in your existing code to serve as a Poisson solver for a particle distribution.

### 9.1 With C++

In order to make use of the code, you need to insert the C macro

```
#include <falcON.h>
```

somewhere at the beginning of your C++ source code. Make sure that the compiler finds the file `falcON.h` by including `-I $FALCON/inc` among your compiler options. The usage of the code in your application is explained in gory detail in the file `FALCON.h` (don't forget that `class FALCON` lives in namespace `falcON`). In order to make an executable, add the linker options `-L $FALCONLIB/lib -lfalcON -lm` so that the library will be loaded at runtime.

For examples of code using `FALCON.h`, see the file `TestGrav.cc` in subdirectory `src/mains/`, which may be compiled by typing `make TestGrav` and produce a short summary of their usage when run without arguments.

### 9.2 With C

In order to make use of the code, you need to insert the C macro

```
#include <falcON_C.h>
```

somewhere at the beginning of your C source code. Make sure that the compiler finds the file `falcON_C.h`

by including `-I falCON/inc` among your compiler options. The usage of the code in your application is explained in gory detail in the file `FALCON.C.h`. In order to make an executable, add the linker options `-L $FALCONLIB/lib -lfalCON -lstdc++ -lm` so that the library will be loaded at runtime.

For examples of code using `FALCON.C.h`, see the file `TestGravC.cc` in subdirectory `src/mains/`, which may be compiled by typing `make TestGravC` and produce a short summary of their usage when run without arguments.

### 9.3 With FORTRAN

In order to make use of the code, you need to insert

```
INCLUDE 'FALCON.f'
```

somewhere at the beginning of your FORTRAN program. Make sure that the compiler finds the file `FALCON.f` by including `-I $FALCON/inc` among your compiler options. The usage of the code in your application is explained in gory detail in the file `FALCON.f`. In order to make an executable, add the linker options `-L $FALCONLIB/lib -lfalCON -lstdc++ -lm` so that the library will be loaded at runtime.

For examples of code using `falCON.f`, see the files `TestGravF.F` and `TestPairF.F` in subdirectory `src/mains/`, which may be compiled by typing `make TestGravF` and `make TestPairF`. Just run these programs, they are self-explanatory and provide some statistics output. You may also use the input files given and run them as `TestGravF < treeF.in` and `TestPairF < pairF.in`.

## 10 The *N*-Body Code `gyrfalCON`

The package also contains a full *N*-body code, called “`gyrfalCON`” (Galaxy simulator using `falCON`)<sup>3</sup>. If you want to use this code, you need first to install and invoke the *N*-body tool box NEMO, version 3.0.13 or higher<sup>4</sup>, see <http://www.astro.umd.edu/nemo>. It is recommended to configure NEMO with `configure --enable-single --enable-lfs`. `gyrfalCON` comes with the usual NEMO help utility: calling `gyrfalCON` without arguments or with the argument `help=h` produces the following overview over the options.

`gyrfalCON -- a superb N-body code`

option summary:

<code>in</code>	: input file	[???
<code>out</code>	: file for primary output; required, unless <code>resume=t</code>	[ ]
<code>tstop</code>	: final integration time [default: never]	[ ]
<code>step</code>	: time between primary outputs; 0 -> every step	[1]
<code>logfile</code>	: file for log output	[ - ]
<code>stopfile</code>	: stop simulation as soon as file exists	[ ]
<code>logstep</code>	: # blocksteps between log outputs	[1]
<code>out2</code>	: file for secondary output stream	[ ]
<code>step2</code>	: time between secondary outputs; 0 -> every step	[0]
<code>theta</code>	: tolerance parameter at <code>M=M_tot</code>	[0.64]
<code>hgrow</code>	: grow fresh tree every <code>2^hgrow</code> smallest steps	[0]
<code>Ncrit</code>	: max # bodies in un-split cells	[16]
<code>eps</code>	: softening length	[0.05]
<code>kernel</code>	: softening kernel of family <code>P_n</code> ( <code>P_0=Plummer</code> )	[1]
<code>hmin</code>	: <code>tau_min = (1/2)^hmin</code>	[6]
<code>Nlev</code>	: # time-step levels	[1]
<code>fac</code>	: <code>tau = fac / acc</code> \ If more than one of	[ ]
<code>fph</code>	: <code>tau = fph / pot</code>   these is non-zero,	[ ]
<code>fpa</code>	: <code>tau = fpa * sqrt(pot)/acc</code>   we use the minimum	[ ]
<code>fea</code>	: <code>tau = fea * sqrt(eps/acc) / tau.</code>	[ ]
<code>time</code>	: time of input snapshot (default: first)	[ ]
<code>resume</code>	: resume old simulation? that implies:	

<sup>3</sup>Called “YancNemo” in former versions of this package (before December 2002).

<sup>4</sup>Older versions of this package contained a non-NEMO code, called “YANC”. This code was never properly tested and has hence been deprecated.

```

- read last snapshot from input file
- append primary output to input (unless out given) [f]
give          : list of output specifications.          [mxv]
give2         : list of specifications for secondary output [mxv]
Grav          : Newton's constant of gravity (0-> no self-gravity) [1]
root_center   : if given (3 numbers), forces tree-root centering []
accname       : name of external acceleration field      []
accpars       : parameters of external acceleration field []
accfile       : file required by external acceleration field []
manipname     : name of run-time manipulator             []
manippars     : parameters for manipulator               []
manipfile     : data file required by manipulator        []
manippath     : path to search for manipulator           []
manipinit     : manipulate initial snapshot?             [f]
startout      : primary output for t=tstart?             [t]
lastout       : primary output for t=tstop?              [t]
VERSION       : 22-mar-2006 Walter Dehnen                [3.0.5PSI]
COMPILED      : Apr  6 2006, 13:46:07, with gcc-3.3.5    []
STATUS        : proprietary version; usage restricted    []

```

The last column indicates the default value, with ‘[???’ indicating that the value for the keyword must be given, while ‘[]’ means that the corresponding feature is not used by default. In order to get a detailed explanation of the various options, see the manpage of `gyrfalCON`.

Traditionally on linux systems, there is a limit of 2Gb on the size of files. This will cause trouble with NEMO snapshot files, since the snapshots of all output times are written to one file. To overcome this, you must (i) configure NEMO appropriately (use `configure --enable-lfs` when installing) and (ii) ensure that your file systems supports large files – consult your system administrator.

## 10.1 An Example

In order to (1) create a Hernquist model with  $N = 10^6$  particles that are initially symmetric w.r.t. origin, and (2) integrate it for 10 time units (using units that imply  $G = 1$ ,  $r_s = 1$ , and  $M = 1$ ) using global softening length of  $\epsilon = 0.01$  and adaptive time steps with  $\tau_{\min} = 1/128$  and  $\tau = 0.01 \min\{|\mathbf{a}|^{-1}, |\Phi|^{-1}\}$ , you may issue the commands

```
mkdehnen out=- nbody=500000 gamma=1 seed=1 q-ran=t | \
symmetrize in=- out=- use=1 copy=1 | \
gyrfalcon in=- out=D.snp tstop=10 eps=0.01 \
hmin=7 Nlev=5 fac=0.01 fph=0.01 logfile=D.log
```

gyrfalcon creates an output file ‘D.snp’, containing output every full time unit until time  $t = 10$ , and a logfile ‘D.log’ which looks like this <sup>5</sup>.

```
# -----
# "gyrfalcon in=- out=DS.snp tstop=10 eps=0.01 hmin=7 Nlev=5 fac=0.01 fph=0.01 logfile=DS.log VERSION=2.4Igcc-3.4"
#
# run at Wed Sep 22 13:28:00
# by "wdll"
# on "virgo"
# pid 11564
#
# time E=T+V T V_in W -2T/W |L| |v_cm| 1/8 1/16 1/32 1/64 2^-7 tree grav step accumulated
# -----
0.0000 -0.08322965 0.083410 -0.16664 -0.16663 1.0012 0.0012842 0.0 213490 187896 298948 290762 8904 0.99 8.37 9.58 0:00:09.58
0.12500 -0.08323056 0.083422 -0.16665 -0.16664 1.0012 0.0012843 2.2e-09 218720 182980 299486 287664 11150 11.19 47.19 60.15 0:01:09.74
0.25000 -0.08323026 0.083425 -0.16666 -0.16664 1.0013 0.0012842 1.8e-09 213636 188360 299961 284743 13300 11.16 48.29 61.11 0:02:10.86
0.37500 -0.08323025 0.083422 -0.16665 -0.16664 1.0012 0.0012841 6.6e-10 218578 183742 300587 282059 15034 11.17 48.82 61.67 0:03:12.54
.
.
9.6250 -0.08322973 0.083188 -0.16642 -0.16640 0.99985 0.0012829 7.8e-08 215630 189874 297455 273872 23169 11.32 50.93 63.98 1:21:47.22
9.7500 -0.08323000 0.083185 -0.16642 -0.16640 0.99981 0.0012828 7.9e-08 216330 189142 297484 273889 23155 11.37 50.92 63.97 1:22:51.20
9.8750 -0.08322990 0.083187 -0.16642 -0.16640 0.99983 0.0012827 8.2e-08 215680 189697 297464 274026 23133 11.36 50.84 63.91 1:23:55.12
10.000 -0.08322997 0.083183 -0.16641 -0.16640 0.99981 0.0012825 8.0e-08 216340 188937 297452 274266 23005 11.34 50.85 63.90 1:24:59.03
```

The first eight columns give the simulation time, total energy (which changed only by 0.002%), kinetic energy, internal gravitational energy  $V_{\text{in}} \equiv (\sum_i m_i \Phi_i)/2$ , and  $W \equiv (\sum_i m_i \mathbf{x}_i \cdot \mathbf{a}_i)/2$ , virial ratio, absolute total angular momentum, and absolute center-of-mass motion. The latter hardly changes due to the momentum-conserving nature of `falcon` (when integrating with a single time step, the center of mass will not move within floating point precision). The next five columns give the number of bodies that move with the given time step. Usually, these numbers adjust from the initial assignment within a few blocksteps. The last four columns contain the CPU time in seconds spent on the tree building, force computation, and full time step, as well as the accumulated time (in h:min:sec format).

**Note** that in absence of external gravitational forces, both  $V_{\text{in}}$  and  $W$  measure the gravitational potential energy, but in two different ways. Only if gravity is exactly Newtonian (no softening), do they agree. Thus, the difference between the two is indicative of the bias in the estimated gravity. This true for all types of  $N$ -body codes, not just `gyrfalcon`.

The CPU time consumption in the above example corresponds to about 4sec per shortest time step for  $N = 10^6$ .

<sup>5</sup>Code compiled with gcc version 3.4, run on a laptop with Pentium-M 735 with 1.7Ghz, 64kb cache size, and 1Gb RAM.



## 11 Additional NEMO-type Programs in `falCON`

Note that all NEMO-type programs have a help utility: when calling them without argument or with the option `help=h`, a listing of their options is printed. If a name for an I/O file is given as `-`, the program will instead read from `stdin` or write to `stdout`, which allows piping into another program. When an output file name reads `.`, it is interpreted as `sink`, i.e. no output is ever made. If an output file name is appended with a `!` or `?` any existing file of the same name (without this appendix) is overwritten or appended to, respectively.

Below, we give a short summary of the programs. For more details, see the relevant man page(s).

### 11.1 Computing Gravity

The program `addgravity` adds gravitational potential and acceleration to existing snapshot(s). `getgravity` computes the gravity generated by one set of particles (source) at the positions of another (usually smaller) set (sinks). This is useful, for instance, for computing the rotation curves of  $N$ -body galaxies.

### 11.2 Creating Initial Conditions

#### 11.2.1 `mkdehnen`

This program creates initial conditions from an isotropic spherical Dehnen (1993) model, which has density

$$\rho(r) = \frac{3 - \gamma}{4\pi} \frac{M r_s}{r^\gamma (r + r_s)^{4-\gamma}}. \quad (2)$$

#### 11.2.2 `mkking`

This program creates initial conditions from a spherical King model of single-mass stars.

#### 11.2.3 `mkplum`

This program creates initial conditions from a spherical Plummer model with isotropic velocities.

### 11.3 Manipulating Snapshots

These programs read a stream of NEMO snapshots, manipulate each of them, and write out another stream of NEMO snapshots. Both in and output may be either file or pipe. All of these programs have the following keywords in common. `in` and `out` specify the in and output streams, `times` (defaulting to `times=all`) specifies the times of the snapshots to be read, manipulated, and written out.

It is recommended to manipulate snapshots on- and off-line using manipulators (see section 12).

#### 11.3.1 `manipulate`

This program (public since May 2005) initiates an off-line analysis via manipulators (see section 12).

#### 11.3.2 `symmetrize`

(public since May 2004) This simple program may be used to symmetrize a snapshot with respect to the origin ( $x = v = 0$ , and, possibly, the equator ( $z = 0$  plane)).

Note that this program is useful for isolated galaxies only.

### 11.4 Analyzing Snapshots On or Off Line

These programs read in a stream of snapshots, analyze each of them, and write diagnostics output. Optionally, they also write the snapshots out. This option allows to have several analysis tools piped one after the other (the user has to take care that each receives the proper type of body data).

It is recommended to analyse snapshots on- and off-line using manipulators (see section 12).

#### 11.4.1 `lagrange_radii`

(public since May 2004, previously proprietary as `'lagrange_rad'`) Given a set of fractions  $\in (0, 1)$ , the radii (w.r.t. the origin) containing corresponding fraction of the total mass are computed and written in ASCII format to a file. In order to center the snapshot, use `density_centre` before. This program is much faster than a global sort on the radii.

Note that this program is useful for isolated galaxies only.

Note that the manipulator `lagrange` does exactly the same job and is more flexible in that the subset of bodies which are used can be defined more generally.

## 12 Run-Time Manipulators

Run-time manipulators have been added in September 2004. They are functions (in fact C++ classes) that operate on the snapshot data and are called in `gyrfalcON` (for on-line analysis or manipulation) after every complete blockstep or in `manipulate` (for off-line analysis or manipulation) for every snapshot stored in file. Run-time manipulators are loaded at run-time, according to the keywords `manipname`, `manippars`, `manipfile`, and `manippath`, and hence no recompilation of the code is required. Up to 100 Manipulators can be concatenated, i.e. one called after the other, by using `manipname=name1+name2` etc., `manippars="pars1 ; pars2` etc., and `manipfile="file1 ; file2"`<sup>6</sup>. Alternatively, if only a `manipfile` (but no `manipname`) is given, that file is interpreted to contain the name, parameters and filenames of manipulators. Such a file may look like this:

```
#
# manipulators for simulation
#
name1    file1    # manipulator name1 takes no parameter, but needs file

name2    0,1,5    # manipulator name2 requires 3 parameters.
#
```

Lines whose first non-space character is ‘#’ are ignored and anything following a free (i.e. preceeded by space) ‘#’ is also ignored (can be used to put comments into the file).

The potential use of run-time manipulators is almost unlimited (one may use them for on-line analysis as well), but currently only four instances are contained in the package.

From July 2006 manipulators can communicate data via a pointer bank supported by class `snapshot`. Supopse you want to compute the lagrange radii of a bound ( $E < 0$ ) stars (particles with  $i < N_*$ ) w.r.t. the position of their maximum density. While it is possible to write a single manipulator for this job, it is much more convenient to use three existing manipulators which communicate their data; the input file may look like this:

```
#
# 1 pick subset: all bound with i<10000
set_subset 10000 (i<#0)&&(E<0)
# 2 find density centre of subset
dens_centre 500
# 3 compute lagrange radii of subset w.r.t. density centre
lagrange    0.01,0.03,0.05,0.1,0.3,0.5,0.7,0.9,0.95 simul.rad
#
```

A detailed *doxygen* documentation for the manipulators listed below can be found at `falcON/dox/html/namespa`

### 12.1 set\_subset

This manipulator creates a filter from a boolean `bodyfunc` expression, see man pages (5bodyfunc), given in `manipfile`, with parameters from `manippars` (an empty expression makes the open filter: all bodies are accepted). At each manipulation, bodies not passing the filter are flagged to be ignored, while those passing the filter will be flagged not to be ignored. This is equivalent to the sequence of manipulators `set_filter` and `use_filter`.

A simple usage is to restrict the range of bodies. For instance the `bodyfunc` expression `"#0<=i&&i<#1"` filters bodies with index between parameters `#0` and `#1` (note that the the indices of bodies may not be preserved; in this case use the key instead, that is ‘k’ instead of ‘i’ in the expression).

### 12.2 set\_filter

This manipulator creates a filter from a boolean `bodyfunc` expression, see man pages (5bodyfunc), given in `manipfile`, with parameters from `manippars` (an empty expression makes the open filter: all bodies are accepted). The (pointer to the) filter is then registered under the key ‘filter’ with the pointer bank.

---

<sup>6</sup>In previous (pre July 2006) versions, the character ‘#’ was allowed as a separator of file names or parameters. This is no longer supported, but instead of the semicolon, you can also use a space. In either case, the whole list of parameters or file names must be given in quotes.

### 12.3 use\_filter

This manipulator uses a filter, registered under the key ‘filter’ to flag bodies not passing the filter to be ignored.

### 12.4 dens\_centre

This manipulator iteratively finds the position of the (global) density maximum of the defined subset (only bodies not flagged to be ignored, default: all). More specifically, it finds the position  $\mathbf{x}_c$  where

$$\rho_h(\mathbf{x}_c) \equiv h^{-3} \sum_i m_i W \left[ \frac{|\mathbf{x}_c - \mathbf{x}_i|}{h} \right] \quad (3)$$

has a global maximum. Here, the smoothing kernel is a Ferrers  $n = 3$  sphere:  $W(r) \propto (1 - r^2)^3$  for  $r < 1$  and  $W = 0$  otherwise. The position  $\mathbf{x}_c$  and the corresponding velocity  $\mathbf{v}_c$  are then registered under the keys ‘xcen’ and ‘vcen’, respectively.

### 12.5 set\_centre

This manipulator set ‘xcen’ to the position  $(p_0, p_1, p_2)$  and ‘vcen’ to  $(p_3, p_4, p_5)$ . If no parameters are given, ‘xcen’ and ‘vcen’ are deleted, implying using the origin instead for most other manipulators.

### 12.6 lagrange

This manipulator computes the Lagrange radii at masses given by total mass times the parameters and writes them to the file. Only bodies in the defined subset (those not flagged to be ignored, default: all) are used. The centre is taken to be that found under the key ‘xcen’ (default: origin).

### 12.7 sphereprof

This manipulator estimates the radial profiles of density, velocity, velocity dispersion, axis ratios, and orientations from spherical binning of all bodies in the defined subset (those not flagged to be ignored, default: all) w.r.t. position and velocity ‘xcen’ and ‘vcen’ (defaults: origin). This is similar to, but more powerful than, the NEMO program `radprof`.

### 12.8 projprof

This manipulator estimates the projected radial profiles of surface density; mean, rotational, and dispersion of the line-of-sight velocity; the axis ratio; position and rotation angle for all bodies in the defined subset (those not flagged to be ignored, default: all) w.r.t. position and velocity ‘xcen’ and ‘vcen’ (defaults: origin).

### 12.9 symmetrize\_pairs

Assuming the initial conditions were forced to be reflection symmetric w.r.t. the origin (using `symmetrize`), there is no guarantee that this symmetry will be preserved during a simulation, since truncation errors eventually break the symmetry. To avoid this, you may want to enforce symmetry by keeping pairs of particles symmetric w.r.t. the origin. Exactly this is done by `symmetrize_pairs` for body pairs with the first body being in the subset (those not flagged to be ignored, default: all).

### 12.10 randomize\_azimuth

Suppose you want to suppress any non-axisymmetric perturbations, such as a bar mode or spiral waves. One way to do this is to randomize the disk bodies’ azimuths every blockstep. Exactly this is done by `randomize_azimuth` for bodies in the subset (those not flagged to be ignored, default: all) using a random seed given by  $p_0$  (if  $p_0 = 0$ , a random seed is generated from the current time).

### 12.11 add\_plummer

You may add new bodies to the simulation. `add_plummer` is a very simple manipulator that at each time step adds one new body, drawn from a Plummer sphere, to the simulation. If you fancy to design similar manipulators, you are recommended to model them on `add_plummer`.

## 13 Bugs and Features

### 13.1 Test-Particles

`falcON` does not support the notion of a test particle, i.e. a body with zero mass. Such bodies will never get any acceleration (that is because the code first computes the force, which is symmetric and hence better suited for mutual computations, and then divides by the mass to obtain the acceleration). To overcome this, you may use tiny masses, but note that the forces created by such light bodies will be computed, even if they are tiny, and contribute to the computational load. Actually, this is exactly what we do in `getgravity`.

### 13.2 Bodies at Identical Positions

The code cannot cope with more than `Ncrit` bodies at an identical position (within floating point accuracy). Such a situation would result in an infinitely deep tree; the code aborts with an error message. Note then when this has occurred in the past, it was often because the body positions were faulty, either all zero, `nan`, or `inf`.

### 13.3 Unknown Bugs

A bug that lead `falcON` or `gyrfalcON` to occasionally crash with ‘Segmentation fault’ I have recently tracked down and debugged (as of 3rd April 2003). However, there may perhaps still to be similar bugs around, which are not reproducible and hence hard to track down and weed out. Measures have been taken to solve such problems eventually. If you ever encounter a problem that you think might be a bug and which is not mentioned in this documentation, please report it to me (`walter.dehnen@astro.le.ac.uk`). Thanks.

## References

- Dehnen, W., 1993, MNRAS, 265, 250
- Dehnen, W., 2000, ApJ, 536, L39
- Dehnen, W., 2001, MNRAS, 324, 273
- Dehnen, W., 2002, JCP, 179, 27