

A brief introduction to GENE

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WARNING

This tutorial aims at providing the basics for installing and running GENE. Please check

- the website `http://genecode.org`
- the documentation

for more recent or more detailed information regarding required libraries, input parameters, file formats etc.!

Outline

- 1 What is GENE?
- 2 How to get and install the code
- 3 Setting up a simulation
- 4 Analyzing and post-processing
- 5 The Diagnostics Tool

What is GENE ?

GENE = Gyrokinetic Electromagnetic Numerical Experiment

- designed for numerical investigations of plasma microturbulence
- solving the δf -splitted gyrokinetic system of equations using a Eulerian approach (fixed grid) in 5D phase space
- initial value or eigenvalue computations
- radially local^a (flux tube) or global (up to full torus) simulation domain
- various interfaces to MHD equilibrium codes and transport solvers
- massively parallelized using (mainly) MPI and OpenMP

^aaddressed in this tutorial

Gyrokinetic system of equations I

Gyrokinetic Vlasov equation per species σ with collisions

$$\frac{\partial f_\sigma}{\partial t} + \dot{\mathbf{X}} \cdot \nabla f_\sigma + \dot{v}_\parallel \frac{\partial f_\sigma}{\partial v_\parallel} + \dot{\mu} \frac{\partial f_\sigma}{\partial \mu} = C(f_\sigma, f_{\sigma'}) \quad (1)$$

gyrocenter position \mathbf{X}

$$\dot{\mathbf{X}} = v_\parallel \mathbf{b}_0 + \frac{B_0}{B_{0\parallel}^*} \mathbf{v}_\perp$$

with the combined drift velocities

$$\begin{aligned} \mathbf{v}_\perp \equiv & \frac{c}{B_0^2} \bar{\chi}_1 \times \mathbf{B}_0 + \frac{\mu}{m_\sigma \Omega_\sigma} \mathbf{b}_0 \times \nabla B_0 \\ & + \frac{v_\parallel^2}{\Omega_\sigma} (\nabla \times \mathbf{b})_\perp \end{aligned}$$

and the generalized potential

$$\bar{\chi} = \bar{\phi}_1 - \frac{v_\parallel}{c} \bar{A}_{1\parallel} + \frac{\mu}{q_\sigma} \bar{B}_{1\parallel}$$

parallel velocity v_\parallel

$$\dot{v}_\parallel = \frac{\dot{\mathbf{X}}}{m_\sigma v_\parallel} \cdot (q_\sigma \bar{\mathbf{E}}_1 - \mu \nabla (B_0 + \bar{B}_{1\parallel}))$$

with the electric field

$$\bar{\mathbf{E}}_1 = -\nabla \phi_1 - \frac{\mathbf{b}_0}{c} \frac{\partial}{\partial t} A_{1\parallel}$$

magnetic moment μ

$$\dot{\mu} = 0$$

... which is δf -splitted in GENE

Gyrokinetic system of equations II

Gyrokinetic field equations

Poisson equation

$$\nabla_{\perp}^2 \phi_1 = -4\pi \sum_{\sigma} q_{\sigma} n_{1\sigma}$$

Ampère's law

$$\nabla_{\perp}^2 A_{1\parallel} = -\frac{4\pi}{c} \sum_{\sigma} j_{1\parallel\sigma}$$
$$B_{1\parallel} = -4\pi \sum_{\sigma} \frac{p_{1\perp,\sigma}}{B_0}$$

... all in all a nonlinear, 5D partial integro-differential system of equations

Relevant moments (in local approx./Fourier space)

$$n_{1\sigma,\mathbf{k}} = \frac{2\pi B_0}{m_{\sigma}} \int d v_{\parallel} d\mu \left[J_0 h_{1\sigma,\mathbf{k}} - q_{\sigma} \phi_{1,\mathbf{k}} \frac{F_{0\sigma}}{T_{0\sigma}} \right]$$

$$j_{1\parallel\sigma,\mathbf{k}} = q_{\sigma} \frac{2\pi B_0}{m_{\sigma}} \int d v_{\parallel} d\mu v_{\parallel} \left[J_0 h_{1\sigma,\mathbf{k}} - q_{\sigma} \phi_{1,\mathbf{k}} \frac{F_{0\sigma}}{T_{0\sigma}} \right]$$

$$p_{1\perp\sigma,\mathbf{k}} \equiv \frac{2\pi B_0}{m_{\sigma}} \int d v_{\parallel} d\mu \mu B_0 I_1 h_{1\sigma,\mathbf{k}}$$

with the nonadiabatic part of f_1

$$h_{1\sigma} \equiv f_{1\sigma} + \left[q_{\sigma} J_0 \phi_1 + \mu I_1 B_{1\parallel} \right] \frac{F_{0\sigma}}{T_{0\sigma}}$$

and the Bessel functions

$$J_0 = J_0(k_{\perp}\rho)$$

$$I_1 = I_1(k_{\perp}\rho) = 2J_1(k_{\perp}\rho)/(k_{\perp}\rho)$$

How to get and install GENE

How to get and compile the code

1 visit `http://genecode.org`,
fill and submit the short form in “Get GENE”

2 download the code as indicated via email

```
git clone https://<USER>@gitlab.mpcdf.mpg.de/GENE/gene.git -b release-<X.Y> <genedir>
```

3 change to the `<genedir>` directory

4 call `make doc` or `gmake doc` to create the documentation to be found in
`<genedir>/doc/gene.pdf`

5 call `make mach_wrapper` and check resulting string `<mach>`

- ▶ if `<mach>` is other than `new_machine` and clearly related to your machine, **check the header of makefiles/`<mach>`/`<mach>.mk` for modules to be loaded – on some machines you may also run `make get_required_modules` (skip the next slide)**
- ▶ otherwise, you need to set up the machine dependent part of the makefile (see next slide)

6 finally, type `make` (or `make -j` for parallel compilation); the resulting binary can be found in `<genedir>/bin/gene_<mach>`

Setting up the makefile for an unknown machine

- define a meaningful name for your machine (<mach> in the following)
 - ▶ either by adding an appropriate identification in <genedir>/makefiles/machine.def (preferred; *one time change only*)
 - ▶ or by *permanently* setting the environment variable MACHINE
- copy and rename the makefile template from <genedir>/makefiles/new_machine/new_machine.mk to <genedir>/makefiles/<mach>/<mach>.mk
- open <genedir>/makefiles/<mach>/<mach>.mk, search for and fill at least the following tokens (check the documentation for details)
 - ▶ the Fortran compiler COMPILER (e.g., intel, gnu, cray, pgi, etc.)
 - ▶ FFTLIB (fftw, mkl or essl) and the corresponding block
 - ▶ the compiler flag for double precision (search for DOUBLE_PREC)
 - ▶ the **complex** versions of PETSC and SLEPC via PETSC_DIR, SLEPC_DIR, PETSC_ARCH; set SLEPC = yes
- compile, run the *test suite* and optionally send modifications to support@genecode.org

note: changes to makefiles/<mach>/<mach.mk> require gmake distclean

Setting up a simulation

Running GENE

Example

This would be the way how to call GENE in a shell or batch script with 8 MPI processes

```
mpiexec -n 8 ./gene_<mach>
```

where `mpiexec -n` might need to be substituted by *mpirun*, *aprun*, *poe*, ...

The input file

The simulation parameters are set in the `parameters` input file which ***must be located in the same directory*** & will be ***read upon simulation start***

Remarks

- a strategy to organize your simulations is to create individual `prob` (~ problem) directories containing `parameters`, a link to the executable, batch scripts, etc. for each of them
- the command `./newprob in <genedir>` will automatically perform those steps

The `parameters` input file

Setting up the `parameters` input file is the crucial part when attempting to run a simulation. As this file uses formatted data and Fortran namelists, it can either be modified with

(a) the *text editor* of your choice

or

(b) the *graphical launcher*

... which furthermore tries to automatically resolve inconsistencies and assist with job submission

The parameters file - parallelization namelist

```
&parallelization
n_procs_s = 1 !divisor of n_spec
n_procs_v = 1 !divisor of nv0 (max: 0.5*nv0)
n_procs_w = 8 !divisor of nw0
n_procs_y = 1 !divisor of nky0 (keep low)
n_procs_z = 1 !divisor of nz0 (maximum: 0.5*nz0)
/
```

- This namelist sets the number of **MPI** processes in each dimension.
- Set to ≤ 0 if the appropriate value is unknown and should be detected by GENE (will increase the initialization time); Lower (upper) bounds for the automatic parallelization tests can be specified by `min_npA` (`max_npA`) where `A=s, v, w, y` or `z`.

The parameters file - box namelist I

Perpendicular box sizes

```
&box
kymin      = 0.05 ! min. binormal Fourier mode
adapt_lx   = .t. ! adapt lx to ky mode (in linear sim's)
lx         = 128. ! radial box width (determines  $\Delta k_x$ )
```

- typical ky_{min} value $\lesssim 0.1$ ($ly \gtrsim 60 \rho_{ref}$) for nonlinear sim's
- $adapt_lx = .t.$ **replaces** lx by $1/(ky \cdot \text{shat})$ to maximize number of poloidal connections n_{exc} in **linear** sim's
- lx should be $\gtrsim 60 \rho_{ref}$ and will be adjusted to $ky_{min} \cdot \text{shat} \cdot lx \in \mathbb{N}$;
alternatively, the number of poloidal connections n_{exc} can be specified

```
kx_center = 0.0 ! kx center value for linear studies
```

- typically, linear investigations are considering the dominant nonlinear mode which is typically $k_x = 0$ (+connections); however, particularly in strongly shaped geometries other k_x values might be interesting, as well.

The parameters file - box namelist II

Perpendicular grid points

```
nx0 = 128    !number of grid points in x direction
nky0 = 16    !number of Fourier modes in y direction
```

guideline for perpendicular grid points:

- linearly:
 - ▶ at least $nx0 \gtrsim 4$ (if `adapt_lx` is true)
 - ▶ $nky0 = 1$ - individual simulations per k_y are recommended!
 - ▶ $k_y = k_{ymin}$ (and multiples if $nky0 > 1$)
- nonlinearly:
 - ▶ radial resolution $lx/nx0 < 1$ (down to $\mathcal{O}(0.1)$);
 - ▶ number of Fourier modes in binormal (y) direction should be $k_{ymin} \cdot nky0 \gtrsim 1.0$ (check for vanishing growth rate with linear sim's);
powers of low prime numbers are recommended (better FFT performance)
 - ▶ $k_y = 0, k_{ymin}, \dots, k_{ymin} \cdot (nky0 - 1)$

remark: number of y grid points in real space $ny0 = 2 \cdot nky0$

The parameters file - box namelist III

Velocity space grid

```
lv = 3.0 ! box size in  $v_{\parallel}$  direction  
lw = 9.0 ! upper simulation box end in  $\mu$  direction
```

- lv should be ≥ 3.0 (in units of $v_{T\sigma} = (2T_{\sigma 0}/m_{\sigma})^{1/2}$, σ : species index)
- the parallel velocity points span the range from $-v_{T\sigma}$ to $v_{T\sigma}$
- lw should be ≥ 9.0 (in units of $T_{\sigma 0}/B_{\text{ref}}$)

```
nv0 = 32 !  $v_{\parallel}$  grid points (usually 32, 64)  
nw0 = 8 !  $\mu$  grid points (typically 8, 16)
```

- equidistant grid in v_{\parallel} , Gauss-Laguerre knots for μ grid

The parameters file - box namelist IV

```
nz0 = 16 !grid points in z(||) direction
```

- simple circular geometries: 16 or 24 parallel grid points sufficient
- realistic MHD-equilibria: up to 100 grid points needed

```
n_spec = 1 !number of particle species
```

- $n_spec = 1$: oppositely charged species is assumed to be adiabatic!

```
x0 = 0.5 !macroscopic radial position of box center in  $L_{ref}$ 
```

- req'd only if some parameters are set by MHD or profiles interfaces;
often given as normalized ρ_{tor}

The parameters file - in_out namelist

Usually, no changes are needed in this namelist except for the following parameters:

```
&in_out  
diagdir = '/ptmp/exampledir' ! output file dir  
read_checkpoint = .f.
```

- output files (e.g. nrg, mom, field) are written to `diagdir`;
make sure to use a high performance I/O file system
- to continue an old simulation set `read_checkpoint` to `.t.` to read an existing checkpoint file from `chptdir` (=diagdir by default) when starting the next simulation

The parameters file - general namelist I

```
&general nonlinear = .t.      !switch on/off nonlinear terms  
comp_type = 'IV'      !initial (IV) or eigenvalue (EV) comput.
```

```
comp_type = 'IV'  
calc_dt = .t.      !switch on/off  
                !dt_max calculation  
dt_max = 0.0385 !maximum time step  
                !in  $L_{ref}/c_{ref}$ 
```

```
comp_type = 'EV' (lin. only)
```

```
n_ev = 1 !no. of EVs
```

- `calc_dt = .t.`
 - ▶ PETSc/SLEPc linked → exact determination of `dt_max`
 - ▶ not linked → approximated by CFL
- `calc_dt = .f.`
 - ▶ use `dt_max`

The parameters file - general namelist II

Termination conditions

```
ntimesteps = 100000 !maximum number of time steps
timelim    = 64500  !(system) time limit in sec
simtimelim = 5000   !simulation time limit
omega_prec = 1e-3   !convergence precision (absolute value)
```

- simulation will stop in a controlled way, if
 - ▶ number of time steps exceeds `ntimesteps`
 - ▶ simulation runs longer than `timelim` seconds; **set < wallclock limit!**
 - ▶ simulation time in $L_{\text{ref}}/c_{\text{ref}}$ reaches `simtimelim`
 - ▶ growth rates and real frequencies are converged up to a precision of `omega_prec` (only for linear simulations and `istep_omega > 0`).

The parameters file - general namelist III

Physics parameters

```
beta          = 0.71E-02  ! $\beta_{\text{ref}} \approx 403 \cdot 10^{-5} n_{e19} T_{\text{ref,keV}} / B_{\text{ref,T}}^2$ 
coll          = 0.68E-02  !normalized collision frequency
collision_op  = 'landau'   !'landau', 'sugama', or 'none'
debye2        = 0.0       !normalized  $\lambda_{\text{Debye}}^2 / \rho_{\text{ref}}^2$ 
```

Hyper diffusion

```
hyp_x = 0.0    !radial hyper diffusion (keep small)
GyroLES = T    !nl. sims only! adaptive perp. hyper diffusion
hyp_z = 2.0    !parallel hyper diffusion
hyp_v = 0.2    ! $v_{\parallel}$  hyper diffusion (collisionless sims only)
```

- If parallel profiles show *zig-zag* patterns and `nx0` and/or `nz0` cannot be increased try `hyp_z = -1` for automatic adjustment
- to avoid recurrence effects, we recommend to set `hyp_v` to a value $\sim 0.1 - 0.5$ in **collisionless** simulations and to 0 or small values else

The parameters file - geometry namelist

Geometry

```
&geometry  
magn_geometry = 's_alpha' !'slab','circular','miller'  
                !'chease','tracer_efit','gist'
```

analytic models: s_alpha, circular, miller, slab

```
q0           = 1.4    !safety factor q  
shat         = 0.796  !magnetic shear parameter  
amhd         = 0.0    ! $\alpha_{\text{MHD}} = -q^2 R (d\beta/dr)$  (-1 for automatic)  
trpeps       = 0.18   ! $r/R$  at flux tube position r  
major_R      = 1.0    !major radius with respect to  $L_{\text{ref}}$ 
```

interfaces: chease, tracer_efit, gist

minimum requirement:

```
geomfile     = 'examplefile' !declaration of interface file
```

Optional: enforce plasma current (Ip) / toroidal magnetic field (Bt) orientation (see documentation)

```
sign_Ip_CW   = -1    !counter-/clockwise (-1/1)  
sign_Bt_CW   = 1     !counter-/clockwise (-1/1)
```

The parameters file - species namelist(s)

Add a species namelist for each species:

```
&species
name = 'ions'      !species name string
omn  = 2.22        !density gradient  $\omega_n = -(L_{\text{ref}}/n) (dn/d\rho)$ 
omt  = 6.92        !temperature gradient  $\omega_t = -(L_{\text{ref}}/T) (dT/d\rho)$ 
mass = 1.0         !mass normalized to  $m_{\text{ref}}$ 
charge = 1         !charge norm. to elementary charge
temp = 1.0         !temperature normalized to  $T_{\text{ref}}$ 
dens = 1.0         !density normalized to  $n_{\text{ref}}$ 
/
```

- check documentation for interfaces to profile files (e.g., `prof_type`, `iterdb_file`, etc.)

The parameters file - units namelist

Optional(!) namelist for

- denormalisation in post-processing routines
- consistent and automatic calculation of physics parameters as, e.g., β

```
&units
Tref = 0.9688      !reference temperature in keV
nref = 4.081       !reference density in  $10^{19} \text{ m}^{-3}$ 
mref = 2.0         !reference mass in proton mass units
Lref = 0.6757      !reference length in m
Bref = 2.424       !reference magnetic field (typically on axis) in T
omegatorref = 6305 !reference toroidal angular velocity in rad/s
/
```

- check documentation for automatic calculation in profile file interface cases

The parameters file - automatic computations

Recommended/helpful settings if all ref. value are filled/requested(*) in units:

```
&box
n0_global = -1111 !find min. toroidal mode number closest
                  !to given kymin or force a given value
adapt_ly = T !adapt kymin to n0_global for given rhostar;
              !recommended for applications to expt.

&general
beta = -1      !beta consistently from ref. values
coll = -1      !coll consistently from ref. values
debye2 = -1    !debye2 consistently from ref. values
zeff = -1      !zeff from data base(*)

&geometry
amhd = -1      !amhd consistently from gradients and beta
rhostar = -1   !rhostar consistently from ref. values
dpdx_pm = -2   !pressure gradient from equilibrium (amhd)

&external_contr
ExBrate = -1111 !ext. shear flow rate from data base(*)
pfssrate = -1111 !parallel flow shear rate from data base(*)
```

(*) requires active data base interface (see documentation/prof_type)

The parameters file

Some remarks

- Information on further parameters, e.g. concerning the initial condition, numerical schemes, frequency of data output, etc. can be found in the GENE documentation located in the `/doc/` subdirectory of your GENE installation.

Convergence

- In principle, each simulation has to be carefully checked for convergence with regard to numerical parameters that is e.g. doubling box sizes and/or grid resolution for testing purposes.

Setting parameters with the launcher

The screenshot shows the GENE Launcher GUI with the following sections:

- Jobs =>**: A row of five tabs labeled 1, 2, 3, 4, and 5.
- Left sidebar**: A vertical list of buttons: Operation, Input/Output, Domain, General, Collisions, Geometry, Species, Nonlocal, Ref. Values, Development, and Clear form.
- Operation mode**:
 - ☒ Nonlinear ☐ Nonlocal (x)
 - ☐ Parameter scan
 - ☒ Initial value solver
 - ☐ Eigenvalue solver
 - ☐ Neoclassical equilibrium solve
- Parallelization (MPI)**:
 - ☒ Species: 0
 - ☒ Par. velocity (v_{par}): 0
 - ☒ Perp. velocity (mu): 0
 - ☒ Radial (x): 0
 - ☒ Binormal (y): 0
 - ☒ Parallel (z): 0
 - ☐ # par. simulations: 1
 - Total:** 8
- Numerical options**:
 - Par. hyperdiffusion: 2.0 Order: 4
 - Radial hyperdiffusion: 0.0 Order: 4
 - Binormal hyperdiffusion: 0.0 Order: 4
 - V-space hyperdiffusion: 0.2
 - ☒ Parallel Arakawa discretization
- Right sidebar**: Buttons for Read parameters, New 'prob' dir., Write parameters, Save as..., Check, Submit (in red), and Quit. At the bottom is an ☐ Advanced options.

- start python based GUI by calling `./GENE-GUI.py` in `<genedir>`
- click on `Default values` to fill with Cyclone-like parameters
- set a least the number of total MPI processes and check all parallelization choices if not sure what to do here
- click on `New 'prob' dir.` for creating a new problem directory
- ...and finally save your parameters here

Setting parameters with the launcher II

The screenshot shows the GENE Launcher application window. The title bar reads "GENE Launcher". Below the title bar, there's a tabbed interface with tabs labeled "1", "2", "3", "4", and "5". The "1" tab is selected. On the left side, there's a vertical menu with buttons: "Jobs =>", "Operation", "Input/Output", "Domain", "General", "Collisions", "Geometry", "Species", "Nonlocal", "Ref. Values", "Development", "Clear form", "Default values", "Quick Intro", and a question mark icon. The main area is divided into sections. The "Input/Output parameters" section includes fields for "Output directory:" (with a text input containing "<Please enter output directory>"), "Checkpoint directory:" (with a text input), and checkboxes for "Read checkpoint", "Write checkpoint", "Write Standard output", "Write HDF5 output", and "HDF5 checkpoint". The "Output intervals" section includes a table with parameters and values: Avg. moments (nrg): 10, Fields: 100, Moments: 100, Energy: 0, Energy (3D): 0, Profiles: 100, V-space: 500, NC fluxes: 0, and Secure checkpoint: 5000. On the right side, there are buttons: "Read parameters", "New 'prob' dir.", "Write parameters", "Save as...", "Check", "Submit", "Quit", and a checkbox for "Advanced options". At the bottom right, there's a "Check scan status" button and a "Current path:" label. At the bottom left, there's a "Messages" section with a text area showing "New lx: 125.628140704" and "Hints: Many labels and buttons show tooltips when the mouse pointer hovers over them. The names of".

- fill at least the Output directory

Setting parameters with the launcher III

The screenshot shows the GENE Launcher application window. The title bar says "GENE Launcher". Below the title bar, there's a section labeled "GENE Launcher" with five tabs labeled 1, 2, 3, 4, and 5. Tab 1 is selected. On the left side, there's a vertical menu with buttons: "Jobs =>", "Operation", "Input/Output", "Domain", "General", "Collisions", "Geometry", "Species", "Nonlocal", "Ref. Values", "Development", "Clear form", and "Default values". The main area is divided into two sections: "Number of grid points" and "Box properties".

Number of grid points

Radial (x):	128
Binormal (y):	16
Parallel (z):	16
Par. velocity (v_par):	32
Perp. velocity (mu):	8

Box properties

Minimum ky:	0.05
Rad. box factor (nexc):	?
Radial extent (lx):	125.6281
Index of lowest ky:	0
kx_center:	0.0
<input type="checkbox"/> Adapt radial size	
v_par grid extent (lv):	3.0
mu grid extent (lw):	9.0

On the right side, there's a vertical stack of buttons: "Read parameters", "New 'prob' dir.", "Write parameters", "Save as...", "Check", "Submit", "Quit", and "Check scan status". There's also a checkbox labeled "Advanced options".

- fill proper grid numbers (rules of thumb in previous section)
- note that the number of poloidal connections (n_{exc}) can be entered directly and consistently with the radial box extension (l_x)

Many labels and buttons show tooltips when the mouse pointer hovers over them. The names of the actual parameters can also be found there.

Setting parameters with the launcher IV

The screenshot shows the GENE Launcher application window. The title bar reads "GENE Launcher". Below the title bar, there is a tabbed interface with tabs labeled "1", "2", "3", "4", and "5". The "1" tab is selected. On the left side, there is a vertical menu with buttons for "Operation", "Input/Output", "Domain", "General", "Collisions", "Geometry", "Species", "Nonlocal", "Ref. Values", and "Development". Below these buttons are "Clear form" and "Default values" buttons. The main area of the window is divided into several sections:

- Termination conditions:** Timesteps: 50000, Time limit [s]: 86000, Simul. time limit: (empty), Freq. precision: 0.001, Overflow limit: (empty), Underflow limit: 1e-15.
- Initial value solver:** Max. timestep: 0.0385 (with a checked "Auto" checkbox), Courant factor: 0.3, Initial condition: 'ppj', aux x: -100, aux y: -100, aux z: -100.
- Dimensionless parameters:** Beta: 0.001, Sq. Debye length: 0.0.
- Equilibrium flows:** ExB shear: 0.0, Parallel shear: 0.0, Start time: 0.0, kx index: 0, Amplitude: 0.0.
- Eigenvalue computations:** Number of EVs: 1, Max. iterations: 0.
- Neoclassics:** ☐ Use neoclassical term, ☐ Remove electrostatic potential.

On the right side, there are buttons for "Read parameters", "New 'prob' dir.", "Write parameters", "Save as...", "Check", "Submit", and "Quit". Below these buttons is a checkbox for "Advanced options" and a "Check scan status" button. At the bottom of the window, there is a "Hints" section that reads: "Hints: Many labels and buttons show tooltips when the mouse pointer hovers over them. The names of the actual parameters can also be found there."

- set time limit according to your batch system
- fill dimensionless physical parameters as needed

Setting parameters with the launcher V

The screenshot shows the GENE Launcher application window. The title bar reads "GENE Launcher". Below the title bar is a tabbed interface with five tabs labeled "1", "2", "3", "4", and "5". The "1" tab is selected. On the left side of the window is a vertical sidebar with buttons for "Jobs =>", "Operation", "Input/Output", "Domain", "General", "Collisions", "Geometry", "Species", "Nonlocal", "Ref. Values", "Development", "Clear form", "Default values", and "Quick Intro". The "Geometry" button is highlighted. The main area of the window is titled "GENE Launcher" and contains a "Geometry" section. This section has a label "Select geometry:" followed by a text box containing the word "circular". Below this are four input fields: "Major radius:" with the value "1", "Safety factor:" with the value "1.4", "Global shear (shat):" with the value "0.796", and "Inv. aspect ratio:" with the value "0.18". On the right side of the window is a vertical column of buttons: "Read parameters", "New 'prob' dir.", "Write parameters", "Save as...", "Check", "Submit" (in red), "Quit", and "Check scan status". At the bottom right of this column is a checkbox labeled "Advanced options" which is currently unchecked. At the bottom of the window is a "Hints" section with the text: "Hints: Many labels and buttons show tooltips when the mouse pointer hovers over them. The names of the actual parameters can also be found there."

- choose MHD equilibrium
- fill the requested fields

Setting parameters with the launcher VI

GENE Launcher

Jobs => 1 2 3 4 5

Operation
Input/Output
Domain
General
Collisions
Geometry
Species
Nonlocal
Ref. Values
Development
Clear form
Default values

Species information

Number of species: 2 New species

Profile type: 0

Current species: < 1 > < 2 >

Species name: 'Ions' 'Electrons'

Particle mass: 1. 2.725e-4

Charge: 1 -1

☐ Passive advection ☐ Passive advection

Delete Delete

Profile information

Temperature: 1. 1.

Temperature gradient: 6.92 6.92

Density: 1. 1.

Density gradient: 2.22 2.22

Read parameters
New 'prob' dir.
Write parameters
Save as...
Check
Submit
Quit

☐ Advanced options

Check scan status

- add and remove species using the 'New species' and 'Delete' buttons
- fill the corresponding list for each species
- to read numerical profiles select the appropriate profile type, and fill the requested fields

Setting parameters with the launcher VII

- optionally fill reference values for denormalization in the post-processing
- optionally set dependent dimensionless input parameters self-consistently by clicking the buttons

Many labels and buttons show tooltips when the mouse pointer hovers over them. The names of the actual parameters can also be found there.

Setting parameters with the launcher VIII

The GENE Launcher GUI is titled "GENE Launcher" and features a sidebar on the left with buttons for "Jobs =>", "Operation", "Input/Output", "Domain", "General", "Collisions", "Geometry", "Species", "Nonlocal", "Ref. Values", "Development", "Clear form", "Default values", and "Quick Intro". The main area is divided into several sections:

- Operation mode:** Includes checkboxes for "Nonlinear" (checked) and "Nonlocal (x)", a checkbox for "Parameter scan", and radio buttons for "Initial value solver" (selected), "Eigenvalue solver", and "Neoclassical equilibrium solve".
- Parallelization (MPI):** Includes checkboxes for "Species", "Par. velocity (v_{par})", "Perp. velocity (mu)", "Radial (x)", "Binormal (y)", and "Parallel (z)", all of which are checked. It also has a checkbox for "# par. simulations" (set to 1) and a "Total:" field (set to 8).
- Numerical options:** Includes input fields for "Par. hyperdiffusion" (2.0), "Radial hyperdiffusion" (0.0), "Binormal hyperdiffusion" (0.0), and "V-space hyperdiffusion" (0.2), each with an "Order:" field (all set to 4). It also has a checkbox for "Parallel Arakawa discretization" (checked).

On the right side, there are buttons for "Read parameters", "New 'prob' dir.", "Write parameters", "Save as...", "Check", "Submit" (in red), "Quit", and "Check scan status". A checkbox for "Advanced options" is also present.

- Check
- and Submit
(this requires a `launcher.cmd` batch script template in `makefiles/<mach>/`)

The scanscript

A well known problem ...

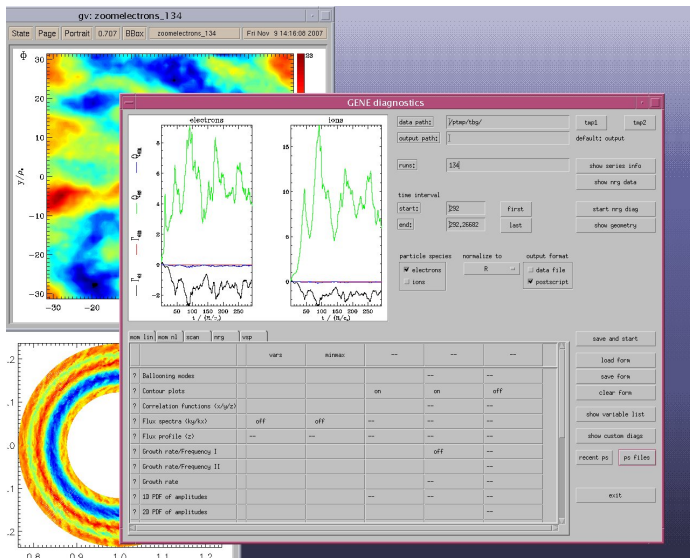
The need to scan over multiple parameter values, e.g., to determine a threshold

Solution

- add Fortran comments as follows to the desired parameters, e.g.,
omt = 6.9 !scanlist:0.0,3.0,4.0,5.0,6.9
...representing a scan over a list of temperature gradient values
This also works in the launcher tool!
- use the proper system call!
 - ▶ either just activate *parameter scan* in the launcher
 - ▶ or replace `mpiexec -n <NMPI> ./gene_<mach>` in your batch script by
`./scanscript -np <NMPI> -ppn <MINPROCS>`
<NMPI>: total number of mpi processes
<MINPROCS>: minimum number of processors per simulation (scanscript might run several simulations in parallel for optimum efficiency)
- (linear) scan results will be collected in `diagdir/scanfiles<ID>/scan.log` at the *end of the job*; call `./scanscript --mks` in the directory where the job has been launched for a manual update of `scan.log` at runtime
- check `./scanscript --help` and the documentation for further options and output file arrangement

Analyzing and post-processing

The Diagnostics Tool



The Diagnostics Tool I

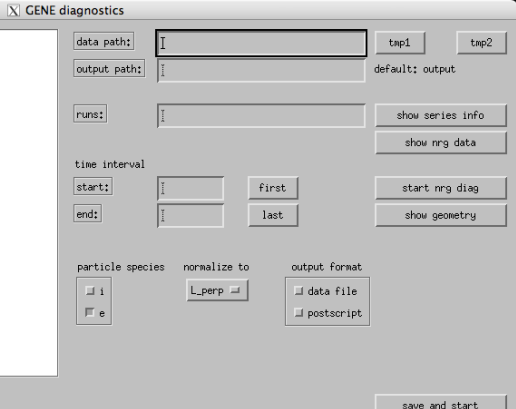
Starting

- regular IDL version (requires IDL licence):
full functionality, user can customize diagnostics
- IDL Virtual machine version:
no manipulation of source possible; IDL VM is free
- Both versions: platform-independent (Unix, Mac OS, Win32; for latter, see documentation)
- IDL: start `idl` in diagnostics directory, then run `@diag`
- IDL VM: start `idl -vm=vm_diag.sav`

Warning

The diagnostics tool needs to be run on a platform from which one's data is accessible via the file system!

The Diagnostics Tool II Graphical User Interface



- runs: e.g. 256,261-264,270+, [enter] rec'd
- series info: important parameters → window
- nrg data: nrg time traces → window
- nrg diag: growth rate and saturation analysis
- geometry: parallel variation → window

? Amplitude spectra (ky/kx)					
? Time trace					
? Toroidal slice					off
? Zonal flow diagnostic		off			
? Amplitude profiles (z)				off	

- `diag table:`
 - ▶ `tabs:` analyze mom/scan/vsp files
 - ▶ `?:` help text
 - ▶ activation status: if active, x
- save and start: selected mom/scan/vsp diags
- variable list: variable ↔ number for diag table par's
- recent ps: ps files in gv after save and start
- ps files: open dialog, output directory
- exit: close, GUI state not saved

mom scan vsp

	--	--	--	--	--
? Ballooning modes				--	--
? Contour plots			on	on	off
? Contour plots HQ	0		on	on	--
? Correlation functions (x/y)				--	--
? Flux spectra (ky/kx)	off	off	--	--	--
? Flux profile (z)	--	--	--	--	--
? Growth rate/Frequency				off	--
? 1D PDF of amplitudes			--	--	--
? 2D PDF of amplitudes					--
? Cross phases	off	off		--	--
? Amplitude spectra (ky/kx)			--	--	--
? Time trace					
? Toroidal slice					off
? Zonal flow diagnostic		off		--	--
? Amplitude profiles (z)				off	--

save and start
load form
save form
clear form
show variable list
show custom diags
recent ps ps files
exit

The Diagnostics Tool III

Using the Diagnostics Tool

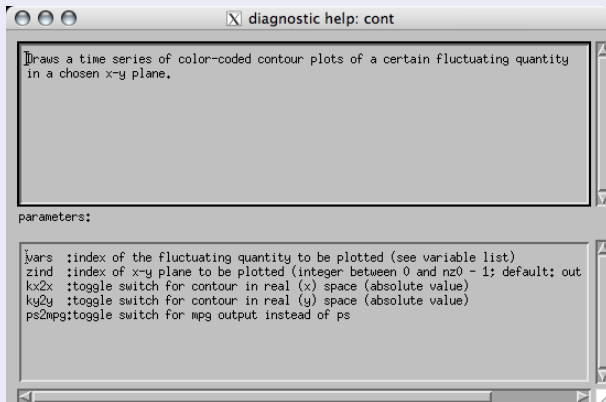
- **preliminaries** (to check run parameters and/or time evolution): run number, [enter], normalization, show series info/show nrg data
- **full nrg analysis**: time window, species, normalization, output format, start nrg diag, (hourglass cursor), recent ps
- **full mom/scan/vsp analysis**: time window, species, normalization, output format, **select diags in table** (check third column with x), fill in diag parameters, repeat this with other diags, save and start, wait for completion dialog, recent ps

mom		scan		vsp									
						vars		zind		kx2x		ky2y	
?	Ballooning modes										--		--
?	Contour plots		X		1:3,5					on		on	of

The Diagnostics Tool III

Using the Diagnostics Tool

- for help with specific diags, press ? next to diag name → general description, parameters info
- custom diags: can modify with Diagnostics Tool open, auto-recompiled on save and start (only with full IDL)



The Diagnostics Tool IV

Scans and Data Output

Scan analysis: `runs – ignored; sort method – 0`

Data output:

- (plain text) data files with predefined output
- for modification/specific info, change source: `prog/[diag].pro`
 - search for `dat=`
 - modify content (e.g., variables) to be written to file

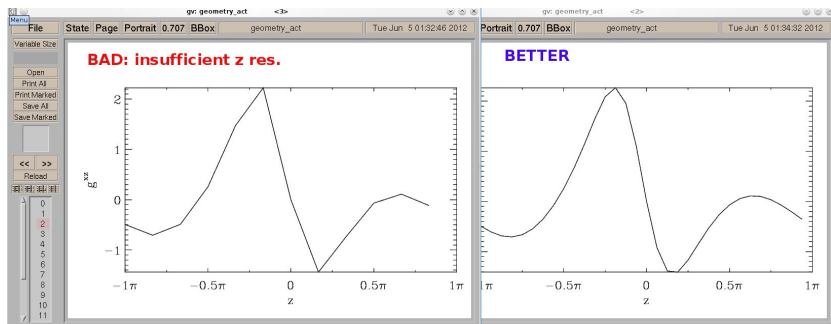
Reality Check: Which Diags Are Essential?

- **linear runs:** Growth rate/Frequency, Amplitude spectra, Amplitude profiles
- **nonlinear runs:** Contour plots, Flux spectra, Flux profile

Note: for eigenvalue analysis, enter `–[EV number]` as time window

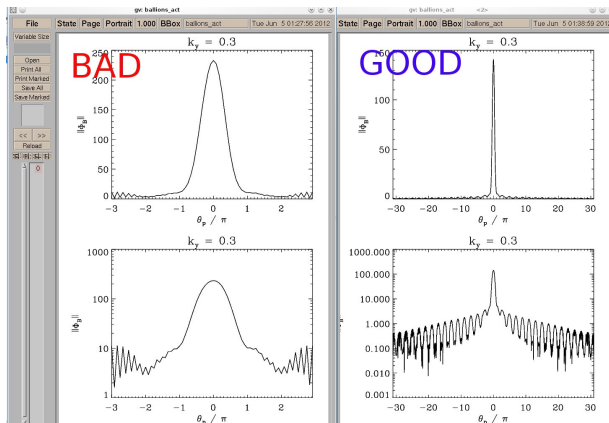
Some basic checks & examples

Check the metric coefficients for realistic geometries



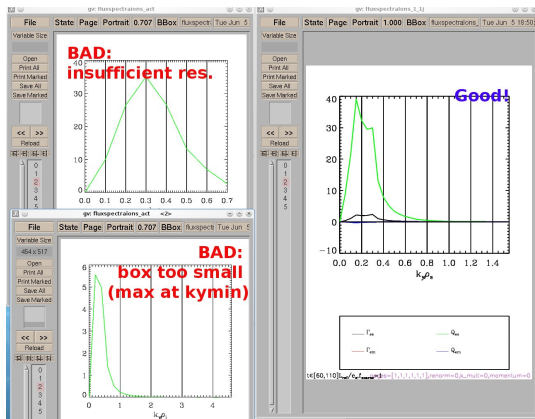
- click "show geometry"
- check *smoothness*
- if jagged, increase `nz0`

Linear: Check ballooning structure



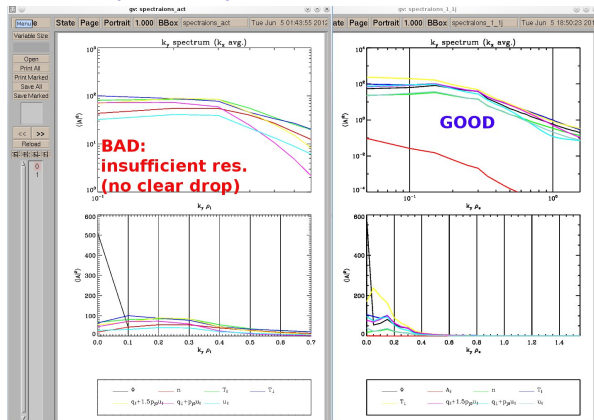
- select “Ballooning modes” for the last time steps
- mode structure should significantly fall off; if not increase n_{x0}
- if still jagged afterwards, increase n_{z0} or (carefully) apply hyp_z

Nonlinear: Check flux spectra



- select "Flux Spectra (k_y/k_x)"
- (!)use long time windows *beyond the overshoot* for nonlinear analysis(!)
- transport should be small at highest k_y, k_x , otherwise increase n_{x0}, n_{k_y0}
- transport should not peak at lowest k , increase box size l_x /decrease k_{ymin} else

Nonlinear: Check amplitude spectra



- select “Amplitude spectra (ky/kx)”
- (!)use long time windows *beyond the overshoot* for nonlinear analysis(!)
- observables should be small at highest k_y , k_x and a power law should typically develop
- otherwise increase $n \times 0$, $n_{ky} 0$

Happy computing!

Feel free to contact
support@genecode.org if you have
questions or comments

Appendix

The parallel boundary condition

Standard flux tube (flux bundle) parallel boundary condition

$$F(\rho, \nu, \chi + 2\pi) = F(\rho, \nu - 2\pi q, \chi)$$

with flux surface label ρ , field line label ν , and straight field line angle χ .

In GENE coordinates and Fourier transformed in 2nd dimension

$$F(x, k_y, z + L_z) = F(x, k_y, z) \exp(-2\pi i n q(x))$$

with toroidal mode number n , and radial/binormal/parallel coordinates $x/k_y/z$.

Local limit: Fourier transformed in 1st dimension and linearized safety factor

$$F(k_x, k_y, z + L_z) = F(k'_x, k_y, z) (-1)^{\mathcal{N}j} \text{ with } k'_x = k_x + k_x^{\min} \mathcal{N}j \text{ and } \mathcal{N} = \hat{s} k_y^{\min} L_x.$$

Here, \hat{s} corresponds to `shat`, \mathcal{N} to the optional input parameter `nexc` and j denotes the index in k_y .

Note that k_x wave numbers become coupled due to the parallel b.c.!
A mode might require several connections, see ballooning diagnostic!