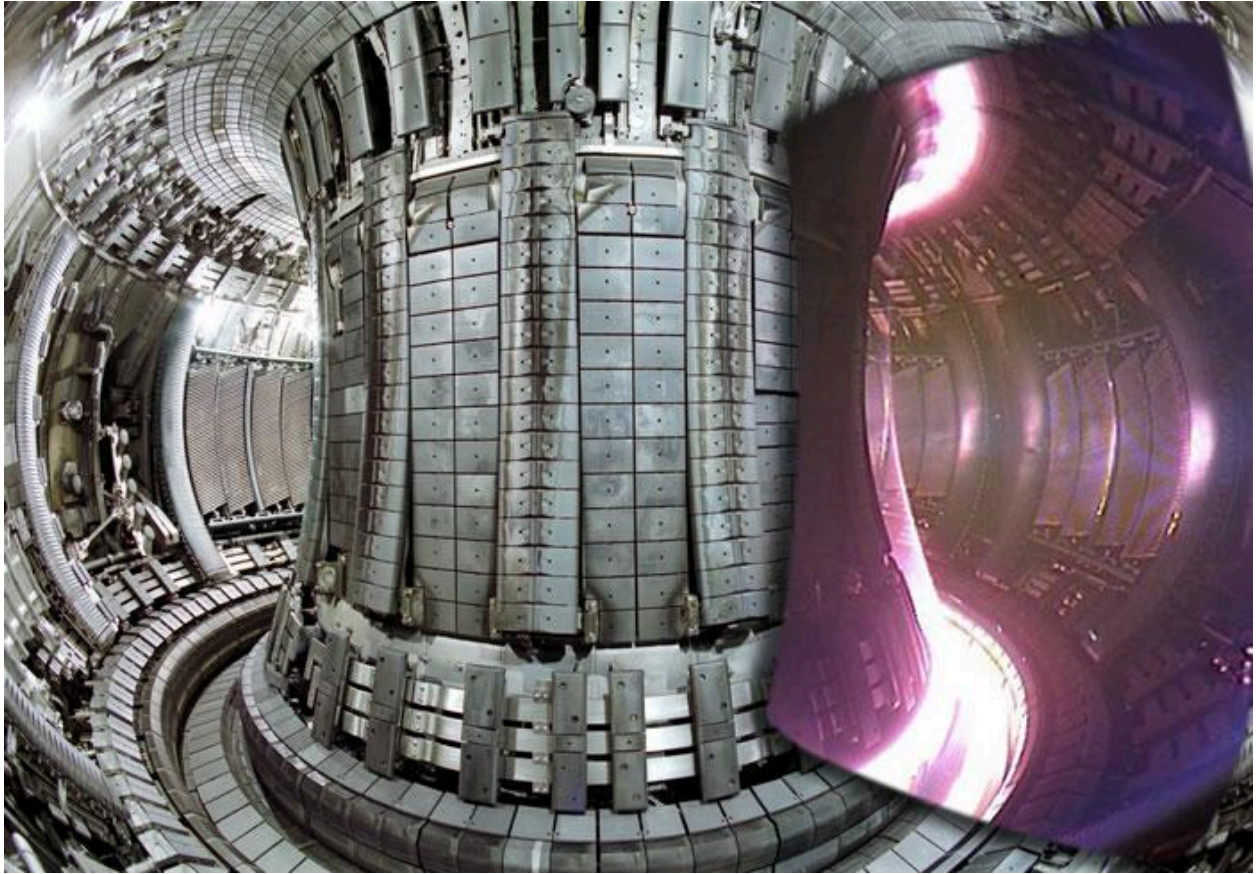


The OMFIT TRANSP Submission System For JET



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Preliminaries

Requesting access (1st time users)

In order to run TRANSP from off-site (not through direct PPPL log-in to portal) you need to set up an account through the Open Science Grid ([wiki](#), [OSG](#)) with an OSG Information Management (OIM) account. This is effectively an scp that allows remote users to send a data package from a remote server (GA, JET, ASDEX, etc...) into the secure PPPL computing cluster. This OSG is used by high energy (CERN) and other areas of physics and is commonly mentioned on the popular TV series “Big Bang Theory”.

Acquiring an OSG Certificate

To obtain a Grid Certificate please follow the directions on the PPPL website:

<https://w3.pppl.gov/transp/CILogon/Instructions.html>

Using CILogin requires an account with a valid identity provider. One could use a google account for this. If one does not have such an account or does not wish to use google then we recommend creating a Github account (<https://github.com/>) and using this instead. The advantage here is that the OMFIT source code is stored on Github, consequently if one has a github account one can submit issues and report problems directly to the OMFIT authors. To do this contact Orso Meneghini at GA and ask that your Github account be permitted access to the OMFIT source repository.

As well as a FusionGRID certificate one also needs a TRANSP-only account at PPPL and to be a member of the TRANSP users group at JET. For the former contact transp_support@pppl.gov, for the latter open a computing ticket at JET requesting membership of the group.

Introduction

In order to perform a TRANSP simulation two things are required: A TRANSP namelist, which contains a set of switches configuring how the simulation is to be run, and a dataset, typically containing information such as the electron density and temperature, ion

temperature and rotation profiles if available, Z effective and bolometry data etc. This dataset must be provided in a particular file format that TRANSP understands known as a *Ufile*.

The new TRANSP submission system for JET utilises the OMFIT scientific workflow system <http://gafusion.github.io/OMFIT-source/>. This provides a graphical user interface and tools which assist users in preparing both the TRANSP namelist and the required input data for a TRANSP simulation before submitting it. The GUI hides a lot of the complexity of understanding the meaning of the numerous namelist switches that can be used to configure a TRANSP run and OMFIT handles the conversion of input data to Ufiles behind the scenes. One need only specify which PPFs one wishes to use for the various required data items. Once the namelist has been configured and the required data has been read in, the run can be submitted to the FusionGRID at Princeton (PPPL <http://w3.pppl.gov/transp/>), monitored during execution and fetched on completion.

OMFIT

There are two versions of OMFIT installed on FREIA. The 'Master' version is updated every few months and should be quite stable. The 'unstable' (or development) version is less stable but will have more recent updates, bug fixes and features. It is recommended that users usually use the unstable version. The master version can be used as a fallback in the event that something is broken in the unstable version.

To start OMFIT first log into a machine on FREIA. Then to start the unstable version of OMFIT type:

```
/common/transp_shared/omfit/bin/omfit-dev
```

For the Master version type:

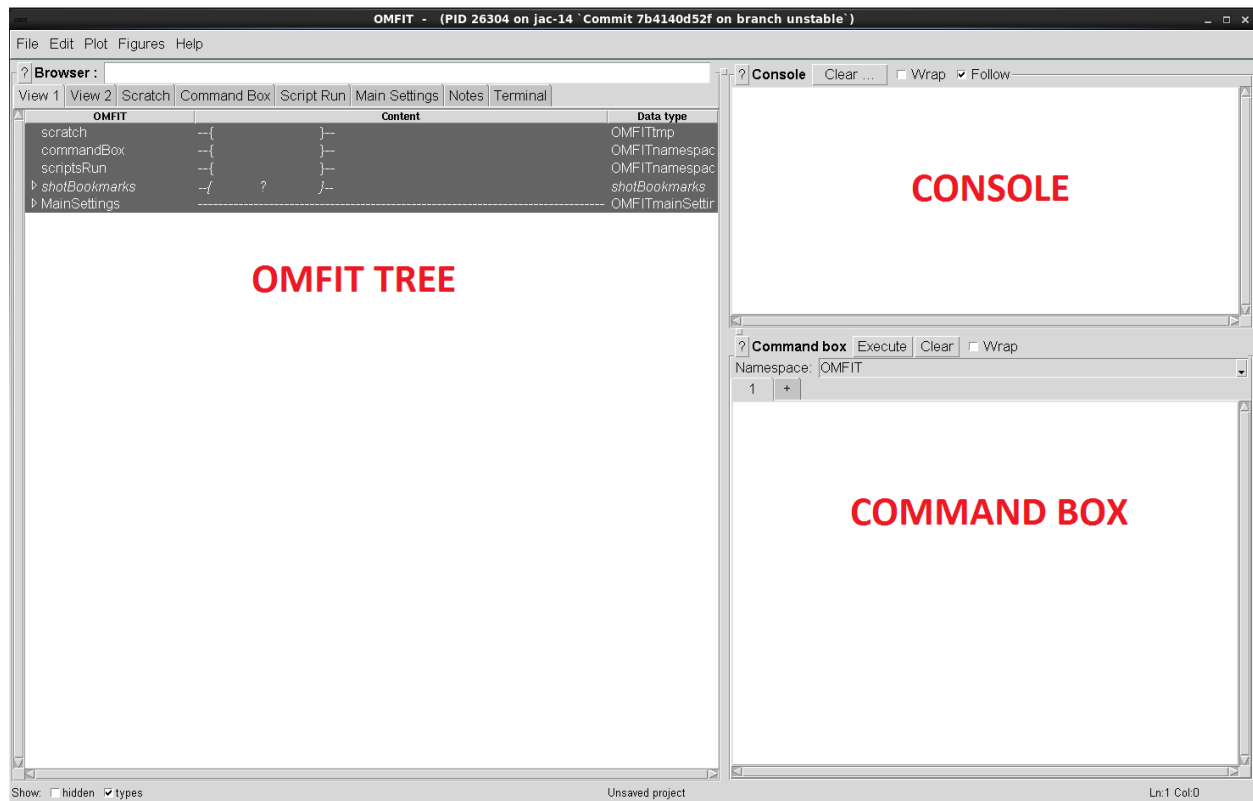
```
/common/transp_shared/omfit/bin/omfit
```

These commands will open the main OMFIT window shown below. On the introduction window click on 'Continue to OMFIT >>>' to proceed. If this is your first time using OMFIT see the [First Time Settings](#) section at the end of this document. Note the above commands can be aliased in your .bashrc script for ease of use. E.g.

```
alias omfit-dev="/common/transp_shared/omfit/bin/omfit-dev"
```

Then one can simply type omfit-dev to start OMFIT.

The main OMFIT window consists of three main parts, only two of which will be of interest to most users. In the top right of the window is the **console**. This is the area where OMFIT prints out any status information or error messages produced during the preparation of the TRANSP run. You should pay attention to what is printed here. In the lower right is the **command box**. This is a python interpreter and allows the user to execute python commands in OMFIT. This can be useful for directly modifying tree entries but will not be useful to most users and can usually be ignored unless doing development work. Lastly, on the left hand side is the **OMFIT tree**. This is a hierarchical data structure that contains all of the scripts, files and data items that are used or created during the submission process. Entries in the tree with little arrows next to them contain other sub-entries beneath them. Clicking on the little arrow shows what is contained. Only a few entries in the tree will be of interest to TRANSP users and will be described in this document. For the most part the users will be able to just use the GUI to do things and will not have to care much about the tree structure, however knowing a little about what things are stored and where can be beneficial.

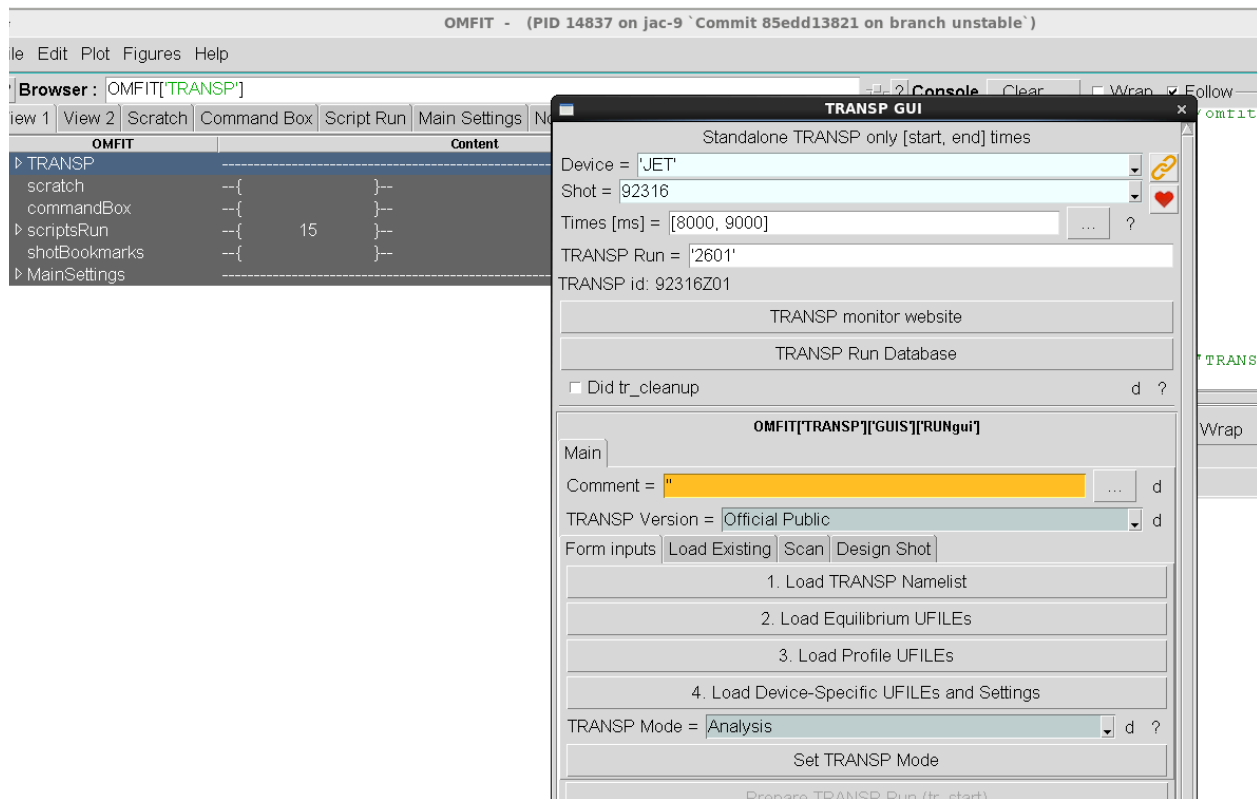


At present the OMFIT tree does not contain very much. As we are interested in doing a TRANSP run we must read in OMFIT's TRANSP module. This will populate the tree with the scripts needed to submit a TRANSP run. To do this use the file menu at the top left to do:

```
File->Import Module
```

Then on the dialogue box that appears scroll down and select the TRANSP module, then click on 'Load'. A TRANSP entry will now have appeared at the top left in the OMFIT tree. Clicking on it's little arrow shows you what's inside! There are now many things, but again note that only a few will be of interest. The **INPUTS** entry will contain input objects, most notably the TRANSP namelist itself once one has been read in. The **UFILE** entry is where all of our Ufile data items will be stored and **OUTPUTS** is where the output NetCDF file created by TRANSP as well as some other outputs will be put.

To start preparing a TRANSP run we need to load up the TRANSP GUI. To do this double click on the top level TRANSP entry in the tree. You should see the following window, which will be what you spend most of your time interacting with to prepare your TRANSP run.



The GUI has several sections. At the very top is an entry called '*Device*' which should be set to '*JET*'. This simply selects the tokamak you are performing a simulation for. Underneath this is an entry called '*shot*' where one enters the shot number of interest. Next is an entry called times where one should enter the desired start and end times of the run as a 2 element list, so [8000,9000] means start at 8s and finish at 9s (it's in ms). **WARNING:** Once a namelist has been read in, the default values are set and this entry no longer has any effect. If you want to change the simulation time later, don't use this, use the [TIME SETTINGS](#) section of the namelist GUI described below.

The last entry at the top is labeled '*TRANSP Run*'. This is where you set the sequence number for the TRANSP run. TRANSP runs are given a run identifier constructed from the shot number, a letter, usually associated with a particular user, and a two digit number. This entry specifies the letter and the two digit number (referred to as the *sequence number*). The letter is set as a two digit number itself so '0501' would represent 'E01'. The resulting run ID is shown underneath this entry in its alphanumeric form.

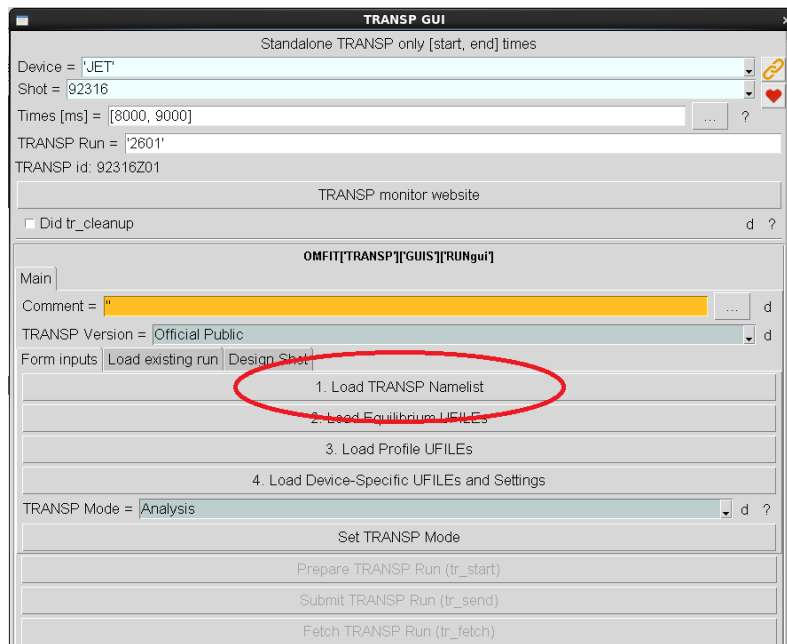
Beneath these entries is a button labelled **TRANSP monitor website**. This brings up the TRANSP monitor website at PPPL. It will be discussed later. There is also a button to bring up the JET TRANSP run database so you can make an entry for your run or check which runs already exist for this shot.

The large pane underneath these buttons is the main area where one spends most of their time. It has only one tab at present, named **main**, but will acquire more as a namelist and Ufiles are read in. The first entry in the main tab is called '*comment*'. This should be set to a string containing a useful comment about the particular run being prepared. Note that when entering a string in OMFIT you should include surrounding " marks. If you make a valid entry the box will turn **green**. You then need to **PRESS ENTER** to confirm the entry. This is always true in OMFIT, you must press enter in entries to set them. A common mistake is to write something in a box, not press enter and then not actually set a value.

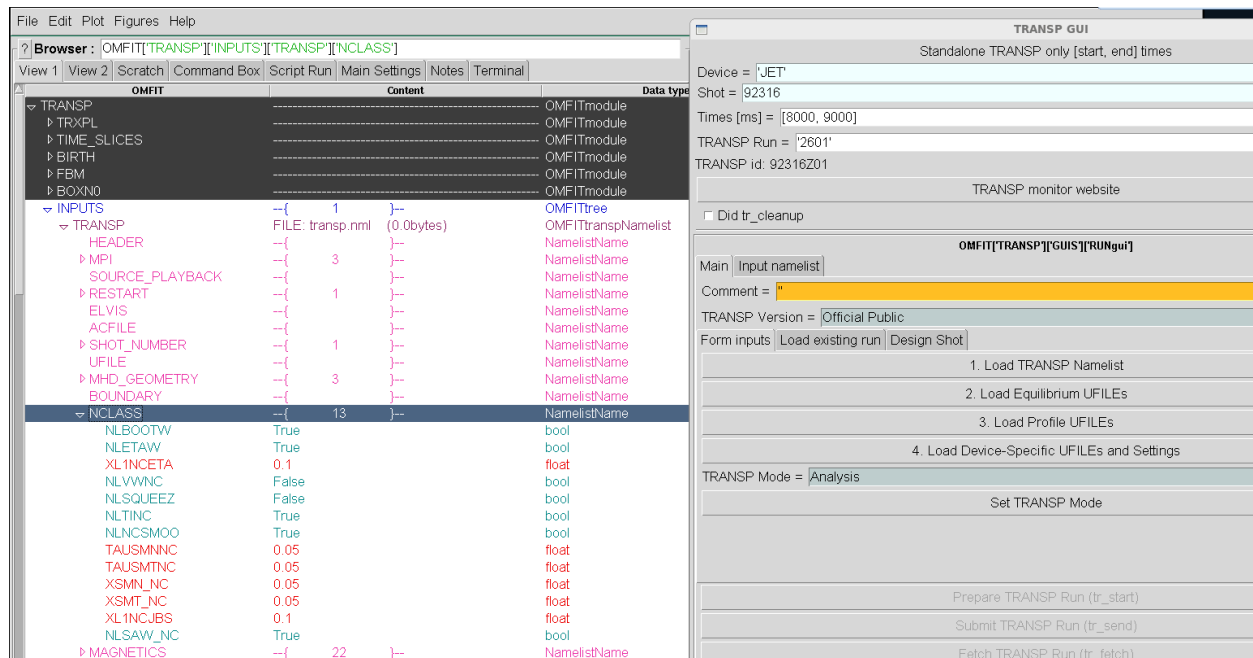
Beneath the comment box is a selection box allowing you to choose the version of TRANSP to run. Usually one will want the official public version but sometimes if one is working on a newer feature it may be required to use the development version.

Reading in a Namelist

Before doing anything else it is necessary to read in a TRANSP namelist. A template namelist with commonly used default settings can be read into OMFIT by pressing the button labelled **1) Load TRANSP Namelist** under the 'Form Inputs' tab.



Once the template has been read in, an entry named 'TRANSP' will appear under the **INPUTS** entry in the OMFIT tree. By clicking on it's arrow one can see the various sections in the namelist, and by further clicking on these one can see the default namelist settings.



A new tab will also have appeared next to the main tab named **Input namelist**. This tab contains many sub-tabs which correspond to the different subsections of the namelist and

allow the user to configure the run. These sections and their meanings are discussed in the following section.

Configuring the Namelist

The different tabs under the **Input Namelist** tab and the controls within them are described in the subsections below. **TIP: If you see a ? next to an entry, clicking on it will bring up context help for that entry. So if you aren't sure what something does, see if there's a ? tooltip!** Not everything in the GUI is described here as tooltips will tell you what the entries do.

Time settings

The main features of interest in this section are the entries for setting the start and end times of the simulation. They will have been defaulted to the values set in the *'Times'* entry at the top of the GUI window but if you want to change the simulation time window after reading in the namelist you need to use these entries.

This section also contains tabs allowing the user to set the time resolution of input and output data, the time steps used when solving the heat and particle balance equations, the time steps used by the TEQ equilibrium solver if it is being used and the timesteps used by the heating codes. Note that if both beams and ICRH are being used, the ICRH code inherits its timestep from the beam code and so the *'ICRH Heating Time Step'* entry is redundant. Note also that the neutral beam fidelity settings (discussed later in the [heating section](#)) will set a value for the beam time step.

Other than the simulation start and end times, these settings can usually be left as defaulted.

OMFIT[TRANSP][GUIS][RUNgui]

Main

Time
Radius
Equilibrium
Plasma
Heating
Diagnostics
ACFILE
Sawteeth
Pellets

OMFIT[TRANSP][GUIS][TIMEgui]

TRANSP Time Range

Start time (s) = ?

End time (s) = ?

Input
Output
Balance
Equilibrium
Heating

Input Time Resolution Settings

Scalar Time Resolution (s) = d ?

Profile Time Resolution (s) = d ?

Radius

These settings allow you to set the number of radial zones used by the main TRANSP code and for the neutral beam distribution function. They can usually be left as defaulted.

Equilibrium

OMFIT[TRANSP][GUIS][RUNgui]

Main

Time
Radius
Equilibrium
Plasma
Heating
Diagnostics
ACFILE
Sawteeth
Pellets

OMFIT[TRANSP][GUIS][EQUILIBRIUMgui]

Geometry
Magnetics

OMFIT[TRANSP][GUIS][MHD_GEOMETRYgui]

Equilibrium Source DDA = d ?

Equilibrium Solver = d ?

All equilibrium info taken from UFILES

Under the '*Geometry*' tab one can choose whether to read in a pre-existing full EFIT equilibrium or whether to use the TEQ inverse solver in TRANSP to solve for the equilibrium using the plasma boundary and q profile. In both cases the EFIT equilibrium still needs to be read in (see section [Reading an Equilibrium](#)) however in the latter case only the q profile and boundary information are used.

There are pros and cons to both cases. If one is using for instance HRTS data which needs to be mapped onto a flux coordinate prior to input (as it is not taken along the midplane), this mapping will usually be performed using the EFIT equilibrium so using a different equilibrium for the TRANSP run is not entirely consistent. However using TEQ allows the fast particle pressure from TRANSP to be included in the equilibrium calculation. It is for the user to decide which is best for their run.

Under the magnetics tab is a checkbox to use current diffusion. If this is selected TRANSP will solve the poloidal field diffusion equation to determine the evolution of the q profile. In this case it is necessary to select a resistivity model and a bootstrap model. At JET it is common to use NCLASS. This should only be selected when using TEQ, an input EFIT equilibrium will already have a consistent q profile.

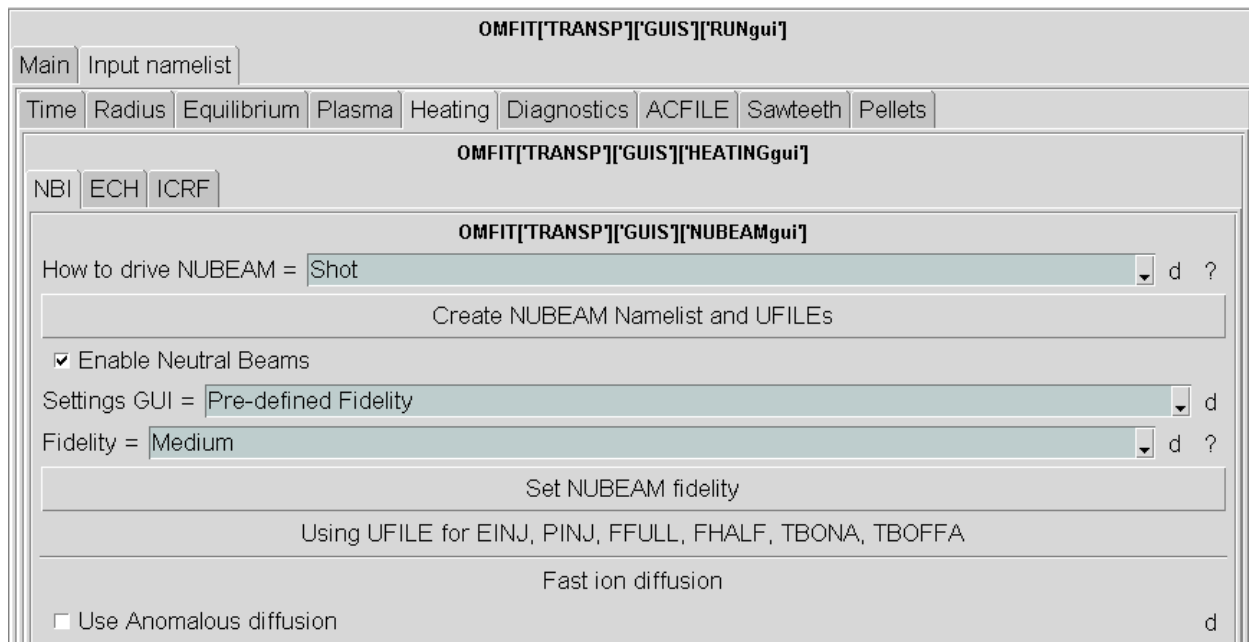
Plasma

This section allows the user to configure the composition of the plasma, the fusion product model settings and whether to take the ion temperature from data or set it as a given multiple of the electron temperature. The composition section allows the user to set the bulk plasma and impurity species as well as a value of Z effective to use if input data is not being used.

Heating

This section is the most complicated and is where the user sets up the beam information and ICRH information. In both cases the information on the beams or RF antennas must either be read from the PPF system or manually entered by the user. The process for doing this is similar for the two cases and is described below.

Neutral Beams



The neutral beam GUI is shown above. To turn on beams click on the '*Enable Neutral Beams*' checkbox. As stated above, information on the configuration of the beams (powers, energies, full and half energy fractions, geometry) needs to be provided and this can be done either by reading the required information from the PPF system or by manually entering it. This choice is made using the drop-down box labelled '*How to drive NUBEAM*'. This has two options: '*shot*' which indicates that the information will be read from the PPF system or '*Namelist Only*', which indicates that the information will be manually set. Once the desired option has been chosen pressing the button labelled **Create NUBEAM Namelist and UFILES** will either automatically read the information and create the required Ufiles in the former case (the created Ufile has extension .NB2) or bring up a GUI allowing the user to manually configure the beams in the latter case. This GUI is shown below:

DreamBeam

Octant 4 (P) Default Settings

☒ Turn on Octant 4

Species = D

Start Time = 4.0

End Time = 8.0

Voltage (kV) = 80.0

Octant 8 (Q) Default Settings

☒ Turn on Octant 8

Species = D

Start Time = 4.0

End Time = 8.0

Voltage (kV) = 80.0

Set Octant Defaults

Total Octant 4 Power = 0.000 MW

PINI P1 PINI P2 PINI P3 PINI P4 PINI P5 PINI P6 PINI P7 PINI P8

☒ PINI on

Species = D

Start Time = 0.0

End Time = 0.0

Voltage = 0.0

Power (MW) = 0.000 Current (A) = 0.000

Full Energy Fraction = 0.000 Half Energy Fraction = 0.000

Pervience (microP) = 0.000

Total Octant 8 Power = 0.000 MW

PINI Q1 PINI Q2 PINI Q3 PINI Q4 PINI Q5 PINI Q6 PINI Q7 PINI Q8

☒ PINI on

The top two sections allow default settings to be entered for the two beam octants (4 & 8). These include the beam injection voltages, start and end times and beam species. Once the defaults have been selected pressing the **Set Octant Defaults** button will set these values for all PINIs in the two octants. Beneath this button are individual tabs allowing configuration of individual PINIs as well as information about the total power of the two octants. Once all the PINIs are configured as desired press the **Update Namelist** button at the very bottom of the GUI to update the namelist with the new beam settings. **Warning:** Clicking on the Set Defaults button does not propagate changes to the namelist, only to the rest of this GUI. The namelist is only updated once the 'Update Namelist' button is pressed.

Once the beam information has been read in, information about the beams will be visible in the main GUI window and a **Plot NUBEAM** button will have appeared allowing the user to plot the beam power time traces.

The only other thing to be set here is the NUBEAM Fidelity. This sets several namelist switches which govern how accurate the beam simulation is. The options are as follows:

Low Fidelity

Intended for control room analysis for time to solution, and kineticEFITs

Monte-carlo particles `NPTCLS=2000`

Deposition tracks `NDEP0 = 500`

Beam timestep `DTBEAM = 0.25`

Numerical acceleration `GOOCON = 5.0`

No usage of MPI parallel processing because the overhead outweighs the benefits

Medium Fidelity

Intended for standard particle and power balance calculations and reasonable torque density

Monte-carlo particles `NPTCLS=32000`

Deposition tracks `NDEP0 = 5000`

Beam timestep `DTBEAM = 0.005`

Numerical acceleration `GOOCON = 10.0`

MPI - 8 cores for 4,000 particles / core

High Fidelity

Intended for detailed momentum transport and fast-ion distribution function evolution

Monte-carlo particles `NPTCLS=256000`

Deposition tracks `NDEP0 = 5000`

Beam timestep `DTBEAM = 0.001`

Numerical acceleration `GOOCON = 20.0`

MPI - 64 cores for 4,000 particles / core

The default is medium. If you are an expert you can select '*Expert User*' from the '*Settings GUI*' drop-down menu to configure these options yourself.

RF Heating

Main
Input namelist
View/Modify UFILES
UFILE options

Time
Radius
Equilibrium
Plasma
Heating
Diagnostics
ACFILE
Sawteeth
Pellets

OMFIT[TRANSP][GUIS][HEATINGgui]

NBI
ECH
ICRF

OMFIT[TRANSP][GUIS][TORICgui]

☒ Turn on ICRF Heating
d

Number of TORIC cores = 1
d
?

Antenna Power and Frequency Settings

How to drive ICRF code = Shot
d
?

Create ICRF Namelist and UFILES

Antenna Toroidal Power Spectra

There are currently 5 active ICRH antennae.

A2 A
A2 B
A2 C
A2 D
ILA

Please ensure the following two entries are of the same length and that the mode numbers are strictly increasing.

Toroidal Mode Numbers = [27]
d
?

Power Fractions = [1.0]
d
?

General Settings

ICRH Code = SPRUCE
d
?

Number of Radial Grid Points = 128
d
?

Number of Poloidal Grid Points = 128
d
?

Minority Species Settings

Total Minority Fraction = 0.0
d
?

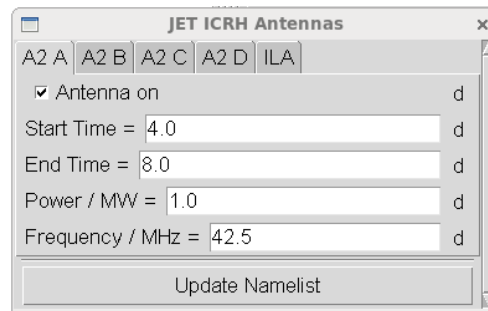
RF Current Drive Settings

☒ Turn on ICRF Current Drive
d
?

RF Driven Current Anomalous Multiplier = 1.0
d
?

The workflow to turn on RF heating is quite similar to the workflow for the beams described above. To turn on the RF heating module of TRANSP click on the *'Turn on RF Heating'* checkbox under the ICRF tab. This will bring up the GUI above. As with the beams, information on the RF antenna power and geometry must be provided and this can either be done automatically by reading the PPF system or manually using the GUI. To set the antenna information from the PPF system, select *'Shot'* in the *'How to drive ICRF'* drop-down menu and then click on the **Create ICRF Namelist and UFILES** button. This will set the antenna geometry information in the namelist and create two Ufiles containing the antenna powers and frequencies (extensions .RFP and .RFF). To manually configure the

antennas select '*Namelist only*' in the drop-down menu before pressing the button. This will bring up the following GUI allowing you to configure the different ICRF antennas:



Once the correct start/end times, powers and frequencies have been chosen click on **Update Namelist** to add these settings to the TRANSP namelist.

Once antenna information has been read in, a section of the GUI will appear allowing the user to set the number of toroidal modes to be simulated with each antenna and what fraction of the total antenna power to assign to each toroidal mode. It is common to simulate only the dominant $n=27$ mode with each antenna.

The other options in the RF GUI allow the user to choose which RF code to use (SPRUCE or TORIC) and configure how the code operates. There are also options to set a minority species.

Merging Antennas

Recently a checkbox has been added just above the '*How to drive ICRF*' drop-down menu titled 'Merge A2 Antennas'. If this is selected prior to pressing the **Create ICRF Namelist and UFILES** button then the four A2 antennas will be merged into a single antenna with the total power of the four. This should only be done when the four antennas have the same frequency (which is usually the case) and will result in the ICRH code executing more quickly. If this button is checked a second checkbox titled 'Merge ILA power into A2' is also available. This will also add in the ILA power to create a single 'pseudo-antenna' representing all five real antennas. Note this is not physically correct as the ILA has a different poloidal geometry to the A2 antennas. This setting is currently only used for BEAST runs where speed of execution is essential.

ACFILE

Clicking the checkbox here allows the user to specify if they wish the TRANSP run to output the beam fast ion distribution or neutral density.

Sawteeth

This section allows the user to either set a sawtooth extrapolation window such that TRANSP will not use data within a given window of a sawtooth event but will extrapolate from outside the sawtooth window to the sawtooth time or to model sawteeth based on the q profile.

Pellets

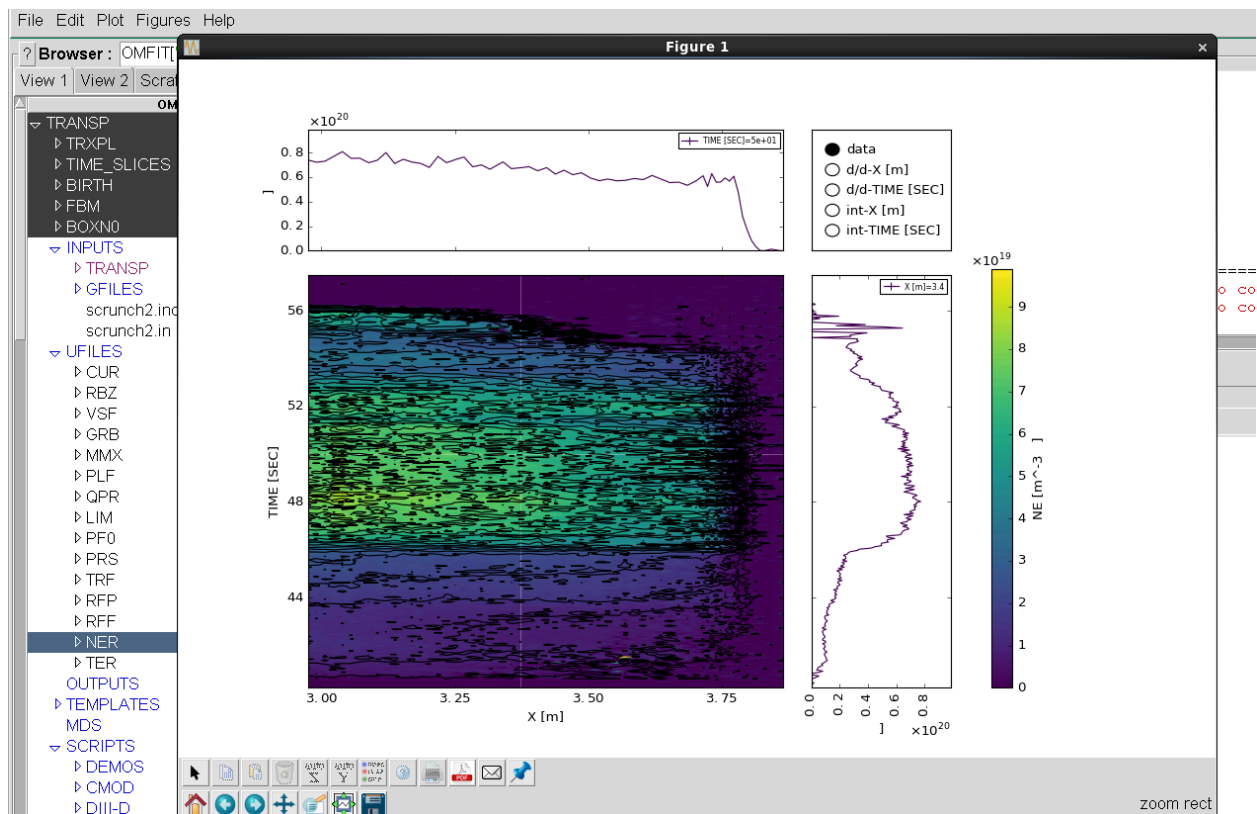
This section allows the user to either set pellet times and extrapolation windows such that TRANSP will not use data within a given window of a pellet but will extrapolate from outside the pellet window to the pellet time or set times to model injected pellets.

Reading in an Equilibrium

Even when using the TEQ internal equilibrium solver one must still read in a plasma equilibrium as the plasma boundary and q profile are needed. Having chosen which PPF to take the equilibrium from in the [equilibrium section](#) of the namelist GUI one simply clicks the button under the **main/Form Inputs** tab labelled **2. Load Equilibrium Ufiles**. This will then create an equilibrium g-file from each time slice in the simulation window before calling SCRUNCH2 to convert the input g-files to a moment Ufile that TRANSP understands (extension .MMX). After this step has been run several new ufiles will have been created in the **UFILE** section of the OMFIT tree containing information like the plasma current, q profile, surface voltage etc. Most importantly the flux surface moment representation is stored in a Ufile ending with extension .MMX.

TRANS		OMFITmodule
▷ TRXPL		OMFITmodule
▷ TIME_SLICES		OMFITmodule
▷ BIRTH		OMFITmodule
▷ FBM		OMFITmodule
▷ BOXN0		OMFITmodule
▷ INPUTS	--{ 4 }--	OMFITtree
▷ TRANSP	FILE: transp.nml (0.0bytes)	OMFITTranspNameList
▷ GFILES	--{ 22 }--	OMFITtree
scrunch2.index	FILE: scrunch2.index (1.1KB)	OMFITascii
scrunch2.in	FILE: scrunch2.in (54.0bytes)	OMFITascii
▷ UFILES	--{ 11 }--	OMFITtree
▷ CUR	FILE: OMF92316.CUR (0.0bytes)	OMFITuFile
▷ RBZ	FILE: OMF92316.RBZ (0.0bytes)	OMFITuFile
▷ VSF	FILE: OMF92316.VSF (0.0bytes)	OMFITuFile
▷ GRB	FILE: OMF92316.GRB (14.2KB)	OMFITuFile
▷ MMX	FILE: OMF92316.MMX (802.1KB)	OMFITuFile
▷ PLF	FILE: OMF92316.PLF (2.1KB)	OMFITuFile
▷ QPR	FILE: OMF92316.QPR (14.2KB)	OMFITuFile
▷ LIM	FILE: OMF92316.LIM (8.0KB)	OMFITuFile
▷ PF0	FILE: OMF92316.PF0 (2.1KB)	OMFITuFile
▷ PRS	FILE: OMF92316.PRS (14.2KB)	OMFITuFile
▷ TRF	FILE: OMF92316.TRF (2.1KB)	OMFITuFile
OUTPUTS	--{ }--	OMFITtree

Note that the Ufiles themselves can be plotted by double clicking on them. This will bring up a window like the one shown below for the electron density.



Profile Selection

QPR: Q Profile

Abscissa = Root Normalised Toroidal Flux d

Select a PPF to read:

DDA = 'OMF' d

Datatype = 'QPR' d

User ID = 'JETPPF' d

Sequence = 12 d

Or select a UFile directly:

Current Ufile is OMF92316.QPR

☒ Keep this UFile?

Pick a different UFile

NER: Electron Density

Abscissa = Outboard Major Radius d

Select a PPF to read:

DDA = 'HRTS' d

Datatype = 'NE' d

User ID = 'JETPPF' d

Sequence = 0 d

Or select a UFile directly:

Pick UFile = " Tree Local Remote d

TER: Electron Temperature

Abscissa = Outboard Major Radius d

Select a PPF to read:

DDA = 'HRTS' d

Each possible signal for which profile data can be provided has a separate section in this dialogue box and each section has the same layout. The sections allow the user to either specify a PPF to be read for that item by giving the DDA, data type name, user ID and sequence number or to directly read in a Ufile for that item if one already exists. If a Ufile already exists for that item it will be listed and a checkbox is shown asking whether the user wishes to keep that Ufile or replace it with one read from the PPF. In the picture above the q profile has already been read in during the equilibrium step and so a Ufile is listed and the 'keep' checkbox is ticked as usually the user will not want to replace the q profile corresponding to their equilibrium. If a PPF is read the user must also set the 'abscissa', i.e. what coordinate the data being read in is against.

When all required profiles have either PPF or Ufile information provided, click on the button at the bottom labelled **Make Ufiles**. This will read in any PPF data and create Ufiles from it. Then you can close the Profile window.

Reading in Time Trace Ufile Data

This step is very similar to the profile step above. Clicking on the button **4. Load Device Specific Ufiles and Settings** will open a dialogue box like the one encountered in the profile data section prompting the user to provide certain required items of time trace data. If no bolometry profile data was provided during the step above then time trace data *must* be provided. If profile Z effective data was not provided then a time trace of Z effective can be read in and a flat profile is assumed. Otherwise a flat Z effective will be set based on the value in the namelist (see the [plasma namelist section](#)). One can also read in a Ufile of sawtooth times from this window. Again once all the required information has been provided, click the **Create Ufiles** button at the bottom.

Submitting the TRANSP run

If you have completed the above steps then you should have all the data needed to submit a TRANSP run. To do this click on the button labelled **Prepare TRANSP Run (tr_start)**. This will copy all of the Ufiles that have been created and the namelist to a staging directory and tarball them in preparation for submission to the fusion grid. If this step is successful the **Submit TRANSP Run (tr_send)** button should be available and can be pressed to send the job to the FusionGRID at PPPL. If you have not already activated a grid proxy, you will be prompted to do so now. If everything works OMFIT will print 'Run Successfully Submitted' to the console. If there is a problem with the run you will receive an email from PPPL containing information about the cause.

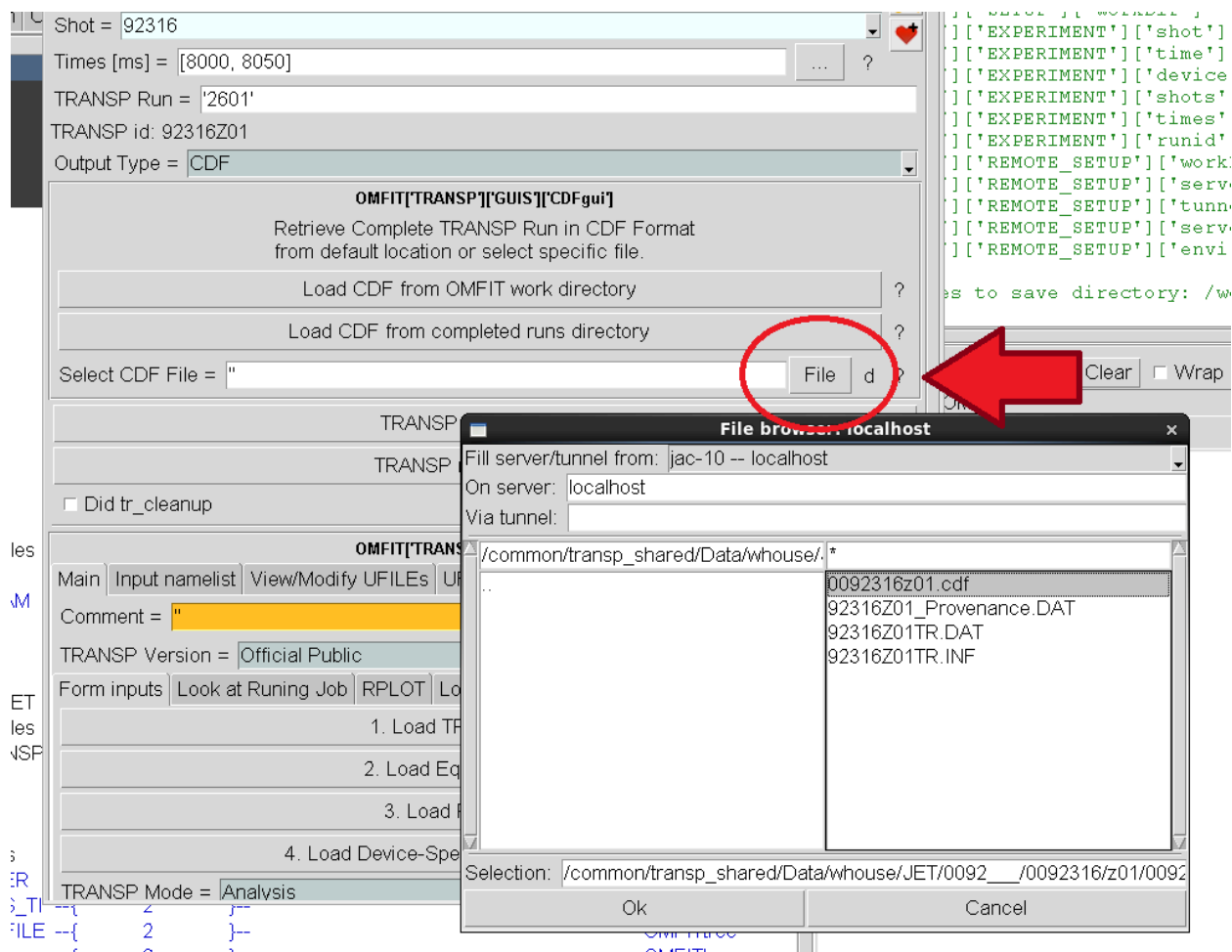
Monitoring the TRANSP run

To monitor the execution of the run you can click on the **TRANSP Monitor Website** button to bring up the PPPL grid monitor website. By entering either your user ID or the run ID into the boxes on the left pane you can search for the status of your run. When it is listed as completed you can fetch it.

Recovering the TRANSP run

Once a run is listed as having completed on the TRANSP monitor website click on the button labelled **Fetch TRANSP Run (tr_fetch)**. This will recover the TRANSP output from the FusionGrid and store the files in the correct locations on the JAC filesystem. It will also save a link to the NetCDF file in the OUTPUTS tree in OMFIT so it can be viewed.

Viewing the TRANSP run



Once a TRANSP run has been fetched it can be viewed within OMFIT. By default the CDF file is not read into the OMFIT project so if you do want to view it in this way the first step is to read it in by clicking on the 'File' button next to the 'Select CDF File' entry on the main TRANSP GUI. Navigate to the file you wish to read in (or point at the link in the OUTPUTS tree) using the dialogue box and click OK.

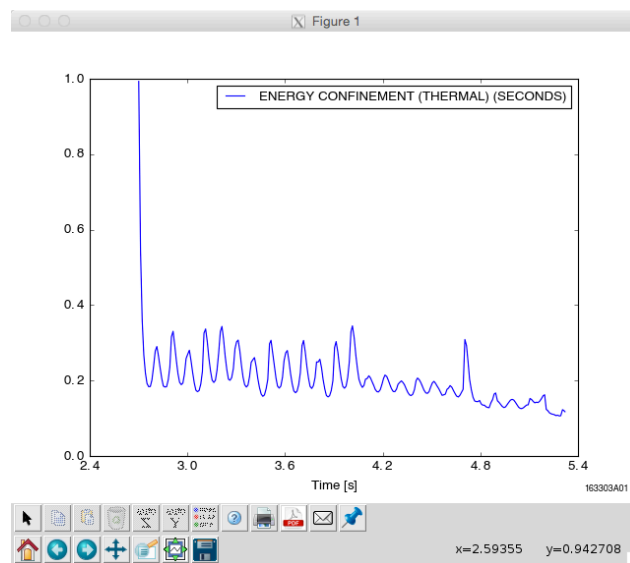
If the run has just been fetched the CDF file should be in the results directory i.e. `/common/transp_shared/Data/result/JET/<shot>/<sequence>` , if it has been archived it will be in the corresponding warehouse directory which for run 92316Z01 would be `/common/transp_shared/Data/whouse/JET/0092___/0092316/z01/`.

Using RPLOT for comprehensive plotting and calculations

Select the RPLOT tab underneath the Main tab. In the top combobox titled '**Servers**' select '**CDF**'. Once you have done this the 'Trees' entry will disappear as it is not needed. Enter the run ID(s) of the run(s) you wish to look at in the '**Run IDs**' entry. Note that this entry can be a list allowing multiple runs to be compared easily.

Plotting a Function of Time

Select 'History' in the '**Plot Type**' combobox and then in the '**Variables**' field enter a list of variable names you wish to plot together. It is possible to use the **Operations** field to perform algebra on signals if desired. To plot the signal click on the **Plot** button at the bottom.

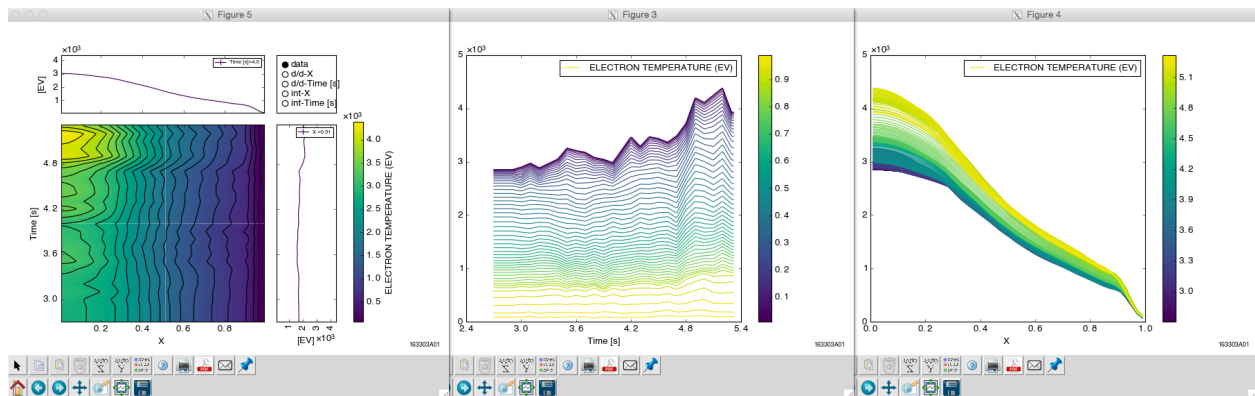


Plotting function of time and space

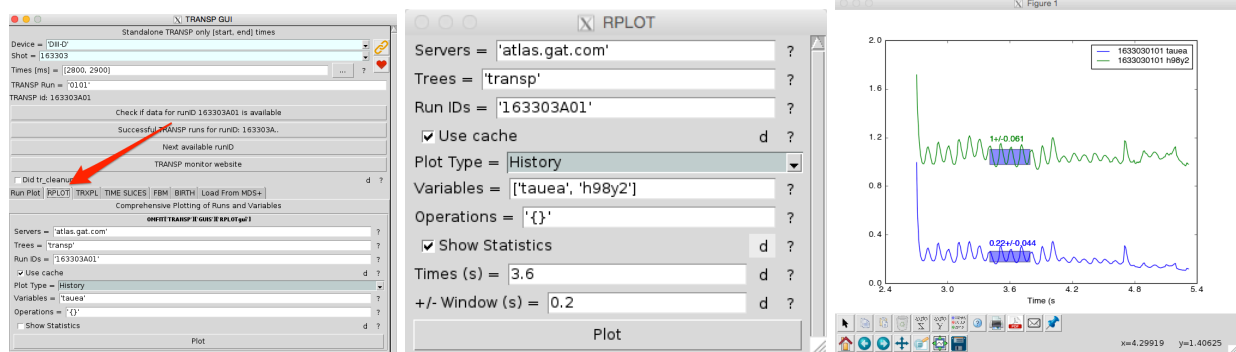
Select 'Profile' in the '**Plot Type**' combobox and then in the '**Variables**' field enter a list of variable names you wish to plot together. As before it is possible to use the **Operations**

field to perform algebra on signals if desired. One can also give lists of times in the **'Times'** field to plot a set of radial profiles at the given times and a list of radii in the **'Radii'** field to plot time traces at the select radial locations.

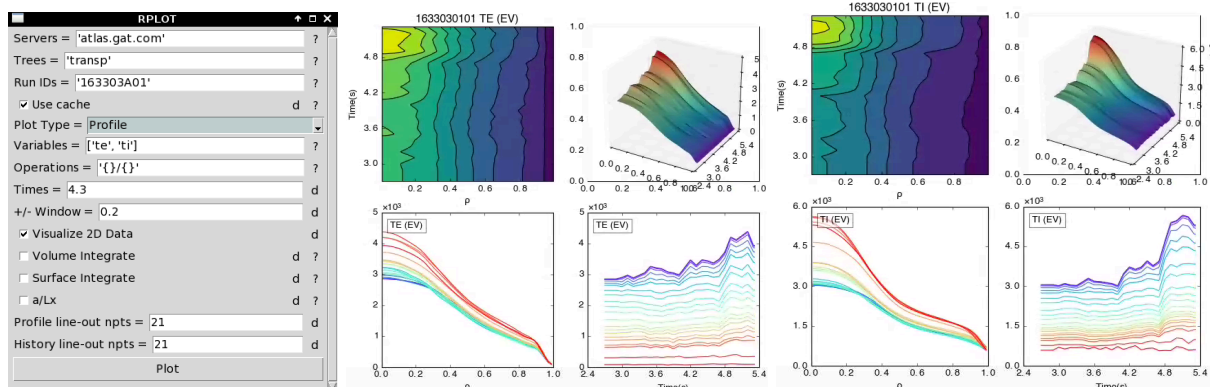
To plot the signals click on the **Plot** button at the bottom.

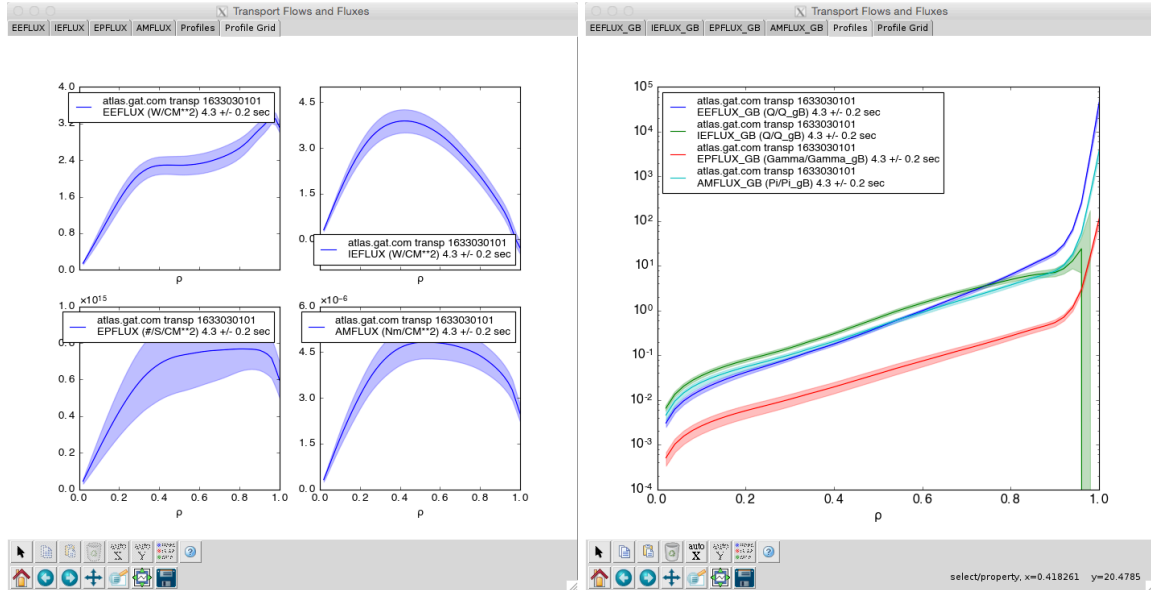


Interactive plotting, slice in X and slice in Time



Below are a few examples of the output you can view from TRANSP:



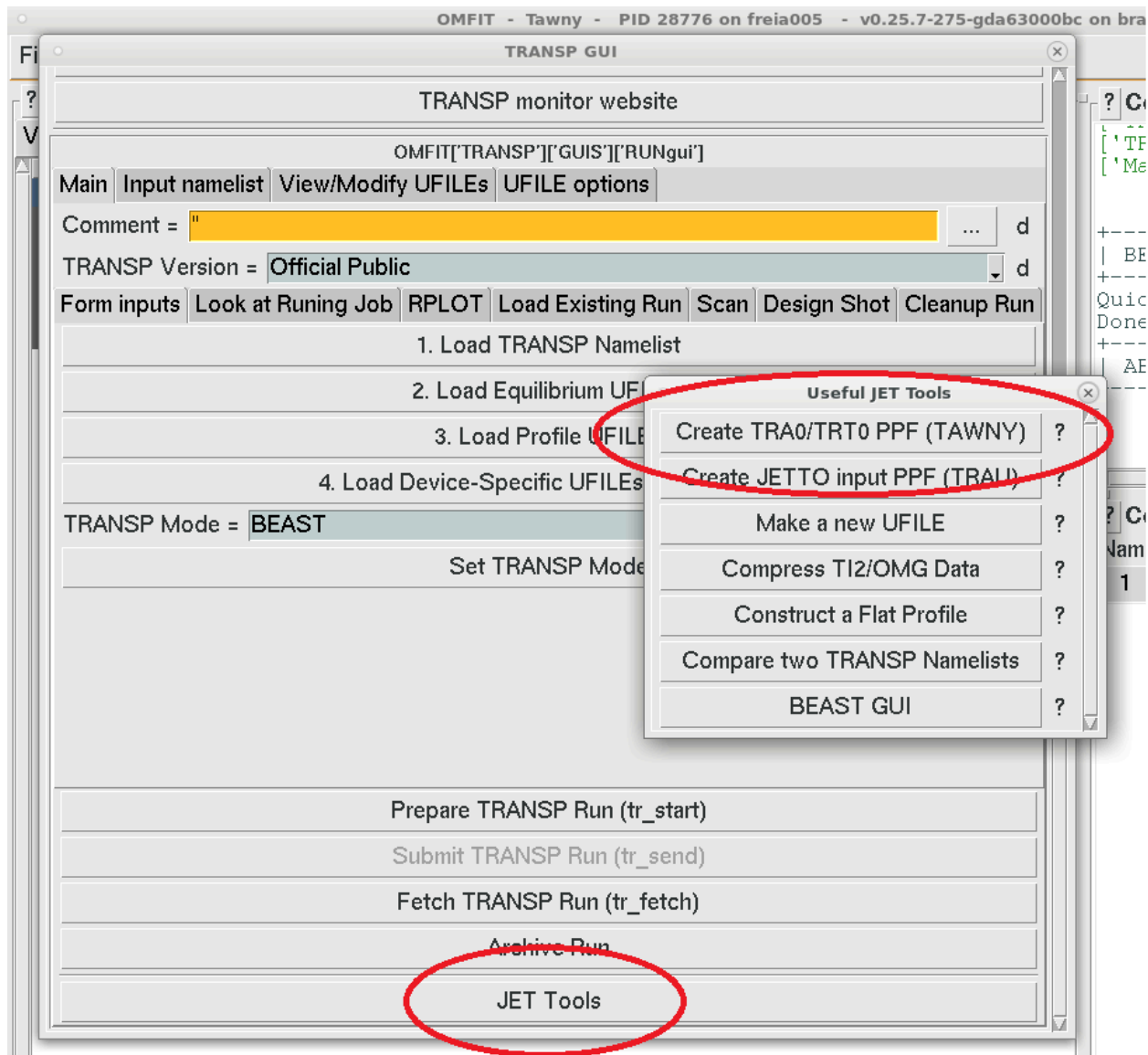


Archiving the run

In order to archive your TRANSP run you must first have made an entry in the [TRANSP run database](#). Once an entry exists, you can click on the **Archive Run** button to automatically archive your transp run.

Creating Output PPFs

In order to create a PPF containing the output of your TRANSP run, first click on the **JET Tools** button at the bottom of the main GUI and then click on **Create TRA0/TRT0 PPF (TAWNY)**. This will attempt to create PPF data from a run with the current run ID. Note you do not have to have just performed this run; you could open OMFIT, set an old shot number and sequence ID and if the run exists this program will attempt to create a PPF from it. If successful, the program will create a new PPF under your user ID and inform you of the sequence number. The PPF will have 2 DDAs: TRA0 which contains profile data and TRT0 which contains time-trace (history) data. This replicates the functionality of the older TAWNY program.



Killing a run / Removing it from TRANSPgrid

To kill a run or to remove a completed run from the TRANSP grid so it can be resubmitted use the 'Cleanup Run' tab under the 'Main' tab. Here you simply need to enter the run ID of the run you wish to kill before clicking the 'Send Cleanup Request' button. The run will then be removed.

Saving your work and trading runs

To save your work click on

File->Save Project As

You can then give the project a name (I would advise using the run ID of the TRANSP run) and leave some useful comments about it before saving it. Note that the entire OMFIT environment is saved here, all your Ufiles are saved, the namelist is saved and the settings you currently have are saved. When you re-open the project everything will look just as it did when you saved it.

If you want to copy someone else's run then it is simply a question of copying the run from their projects directory to your projects directory and renaming it something appropriate. If you followed the [First Time Settings](#) at the bottom of this document your projects directory will be:

```
/common/transp_shared/Data/work/<user>/OMFIT/projects
```

Once copied over, the project can be opened in an OMFIT session as if it was your own and will look exactly as it did for the person that created it when they saved the project.

You are then free to modify the sequence number (to use your own letter identifier) and resubmit the run with any changes you wish to make.

Useful Advice

- If you are not sure what something does, see if it has a ? mark next to it on the right. If so you can click on this for information about the entry.
- If you can't find a GUI after pressing a button, it may have appeared behind the main TRANSP GUI, try moving this.
- The first thing that must happen when preparing a run is to read in a namelist. After that you can read in data in any order you like although it is suggested you follow the order laid out. Once all data you want is read in you can submit the run.
- If you wish to manually edit the namelist this is possible. In the **INPUTS** sub-tree, right click on the TRANSP entry (the namelist) and select 'Open in Editor'. This will open the namelist for editing. Once you have finished editing it, save it and then

right-click on the TRANSP entry again and select *'Reload from File'*. It is strongly advised that any manual edits of the namelist are made immediately before submitting the run after all other preparation has been done. Otherwise there is a small possibility that a user could add an entry then use a GUI function which adds the same entry in a different location in the tree leading to the same entry existing twice in the namelist. It is also recommended that users attempt to keep any manually added entries in appropriate subsections. The subsections are structured to match the sections on transp.help on the PPPL website.

Appendices

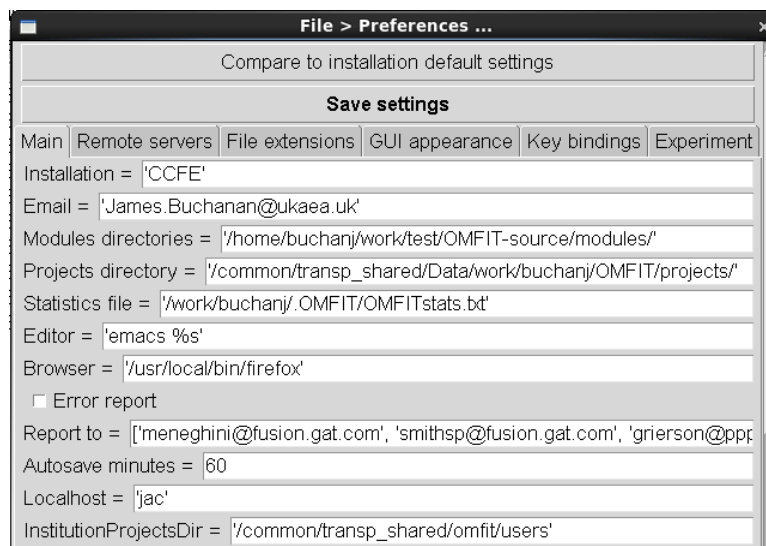
First Time Settings

There are a few settings that you will need to configure the first time you run OMFIT.

After starting the main window perform:

File->Preferences

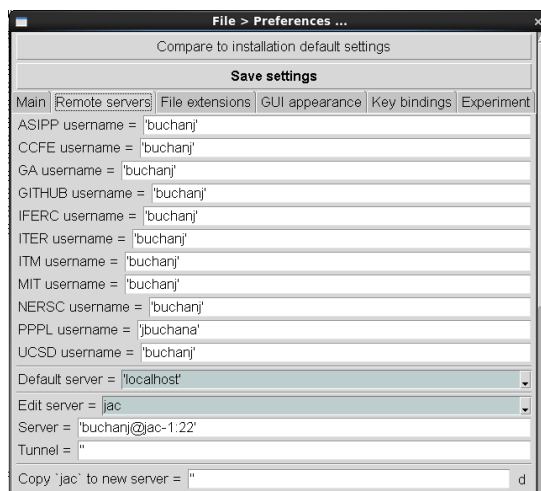
To bring up the user preferences window:



Under *'Email'* enter your email address so that you can be contacted about any errors etc. Change the *'Projects Directory'* entry so that it matches:

```
/common/transp_shared/Data/work/<user>/OMFIT/projects
```

Where <user> is your CCFE username. This is where your saved OMFIT projects will be stored. Then click on the **Remote Servers tab**:



Your username should already be correct but you should check that it is. Change the 'Server' entry to '<user>@jac-n:22' where <user> is your username on the JAC and *n* is a valid node number. From above you can see that I have chosen jac-1. Lastly make sure the 'Tunnel' entry is an empty string. Then click on **Save Settings** at the top of the GUI and restart OMFIT.

Reading an existing namelist (not the template)

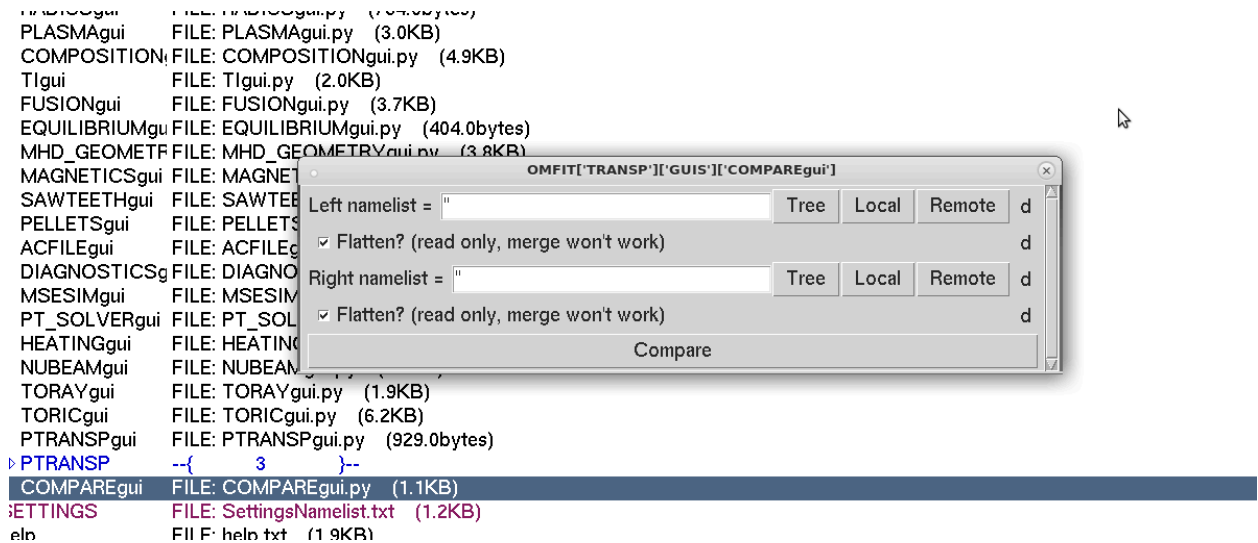
One can read in a pre-existing namelist by clicking on the **Load Existing Run** tab under **Main**. This will bring up an interface to specify the location of the namelist to read (TR.DAT Namelist field). To read in a namelist created previously using OMFIT, select the option Disk/None from the **Namelist/UFILES** drop down menu. To read in a namelist created using the old system, select JAC/PPF. If an old style namelist has provenance information in a "jim string" such as "EXTQPR='Q_0011 PPF:2:tranppf:0342:\$SDD:Q_PROFILE(PSI_NORM) :'" then the system will attempt to create Ufiles of the same data used in the original run. Note that the tools to read old style namelists are new and not rigorously tested. It is advised that you start from the OMFIT template when starting a new run rather than reading in old style namelists.

It is **strongly** recommended that you remove anything to do with ICRH in the old namelist before reading in, because the old system added antenna powers together. This will confuse the new system if you make changes. Having said that, if no changes are made to ICRH settings using the GUI, then old runs should still run in exactly the same way.

The screenshot shows the OMFIT GUI with the title bar 'OMFIT[TRANSP][GUIS][RUNgui]'. The 'Main' tab is selected. The 'Comment =' field is empty with a yellow background and a file selection button '...' and a 'd' icon. The 'TRANSP Version =' dropdown menu is set to 'Official Public' with a 'd' icon. The 'Form inputs' section has three buttons: 'Load Existing' (highlighted with a dotted border), 'Design Shot', and 'Tree'. Below this, the title bar is 'OMFIT[TRANSP][GUIS][LOADgui]'. The 'Namelist/UFILES =' dropdown menu is set to 'JAC/PPF' with a 'd' icon. The 'TR.DAT Namelist =' field is empty with a 'Tree' button and a 'Local' button, and a 'Remote' button with a 'd' icon.

Comparing two Namelists

You can compare two namelists for content by clicking on the 'JET Tools' button at the bottom of the TRANSP GUI and then on the 'Compare two namelists' button.



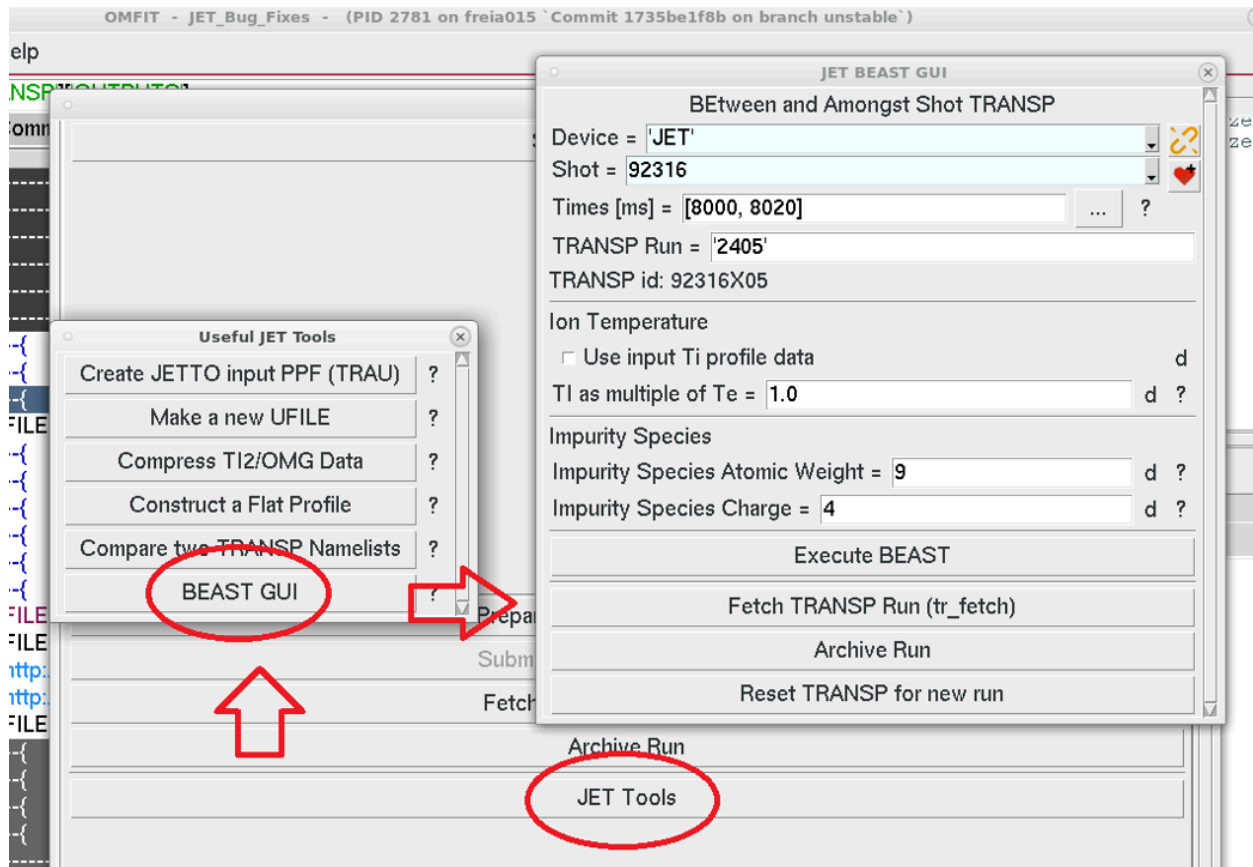
Select the two namelists you wish to compare and click the 'Compare' button. This will bring up a view showing the entries which are different in the two namelists.

Making a JETTO input PPF

To make a PPF which can be used to read TRANSP output data into JETTO click on the 'JET Tools' button at the bottom of the GUI. If the results have been fetched a button called '**Create JETTO input PPF**' should be present. Clicking on this button will make the PPF which will have the DDA TRAU. The sequence number of the new PPF is printed upon completion.

Running BEAST in the control room

A special simplified GUI has been set up to run BEAST quickly in the JET control room. To start this GUI open the main TRANSP GUI and click on the 'JET Tools' button at the bottom of the GUI. Then click on the **BEAST GUI** button.



As with a normal run one must enter the shot, execution time window and sequence ID at the top of the window. Following this one can choose whether to use TI data or simply set a multiple of TE. The user must also set the impurity species to be used. Once these are set one simply needs to click on the **'Execute BEAST'** button. All of the required scripts will be run automatically, the job will be submitted and then fetched on completion without any further user intervention. OMFIT will also automatically make a database entry for the run and then archive it if everything is successful.

The GUI also contains the buttons for manually fetching and archiving the run but as stated above, if all works correctly these should not be needed.

If you wish to submit another BEAST run, once the first has been successfully archived, click on the **'Reset TRANSP for new run'** button to start again fresh.

FAQ
