# SamSrf X – Users guide

This manual replaces the longer cookbook that was included in previous SamSrf versions. You can still find this cookbook in the *SamSrf/Documents* folder. Most of the information in there should be correct but many individual steps described are probably out of date. There is also a separate document introducing the concepts of pRF analysis.

The present manual describes the basic steps for a standard pRF analysis that you can run using the *SamSrfX* GUI.
The GUI itself also gives detailed descriptions of the various model parameters you can specify. That should help you figure out more advanced analyses.

More advanced users may still wish to run analyses directly in Matlab and code up batch analysis looping through all data sets etc. This functionality has not changed.

Since SamSrf 10.3, we also added standalone versions of several tools, including a command line interface for running pRF or CF analyses. This can be run via the *SamSrfAnalysis* function. Please refer to the specific user manual for that.

## 1. To begin using SamSrfX, either launch the *SamSrfX* standalone app or run *SamSrfX* in the Matlab command window.

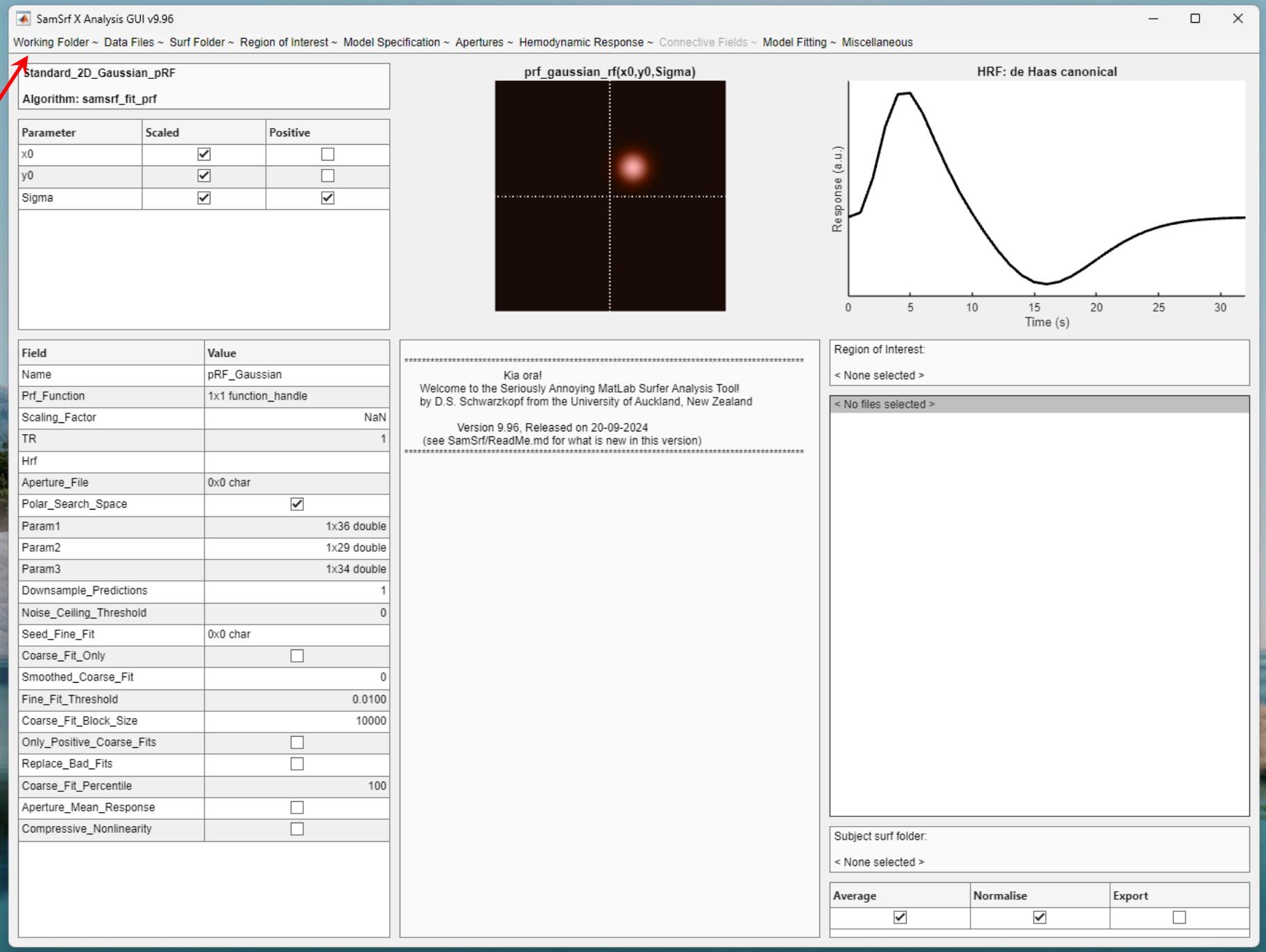
The SamSrfX GUI looks something like this. The menu bar at the top lets you access several functions.

2. For starters, you may want to use the *Working Folder* menu to navigate to the folder where you want the pRF map files to be created.

While this step is not strictly necessary, it makes things more convenient for you when selecting files.

We are assuming a directory structure used by the *SamPenDu* lab in the past, where functional data are kept in a subfolder of the subject's *FreeSurfer* folder. But this is not mandatory either; you could also have functional and structural data in separate places (as in the BIDS structure).

Here, we navigated to *X001/prf* which is a subfolder in our example dataset.



3. Next, we need to select the data. Under the *Data Files* menu, you have several options:

Your functional data should have have been motion corrected and coregistered to the anatomical T1 image already.

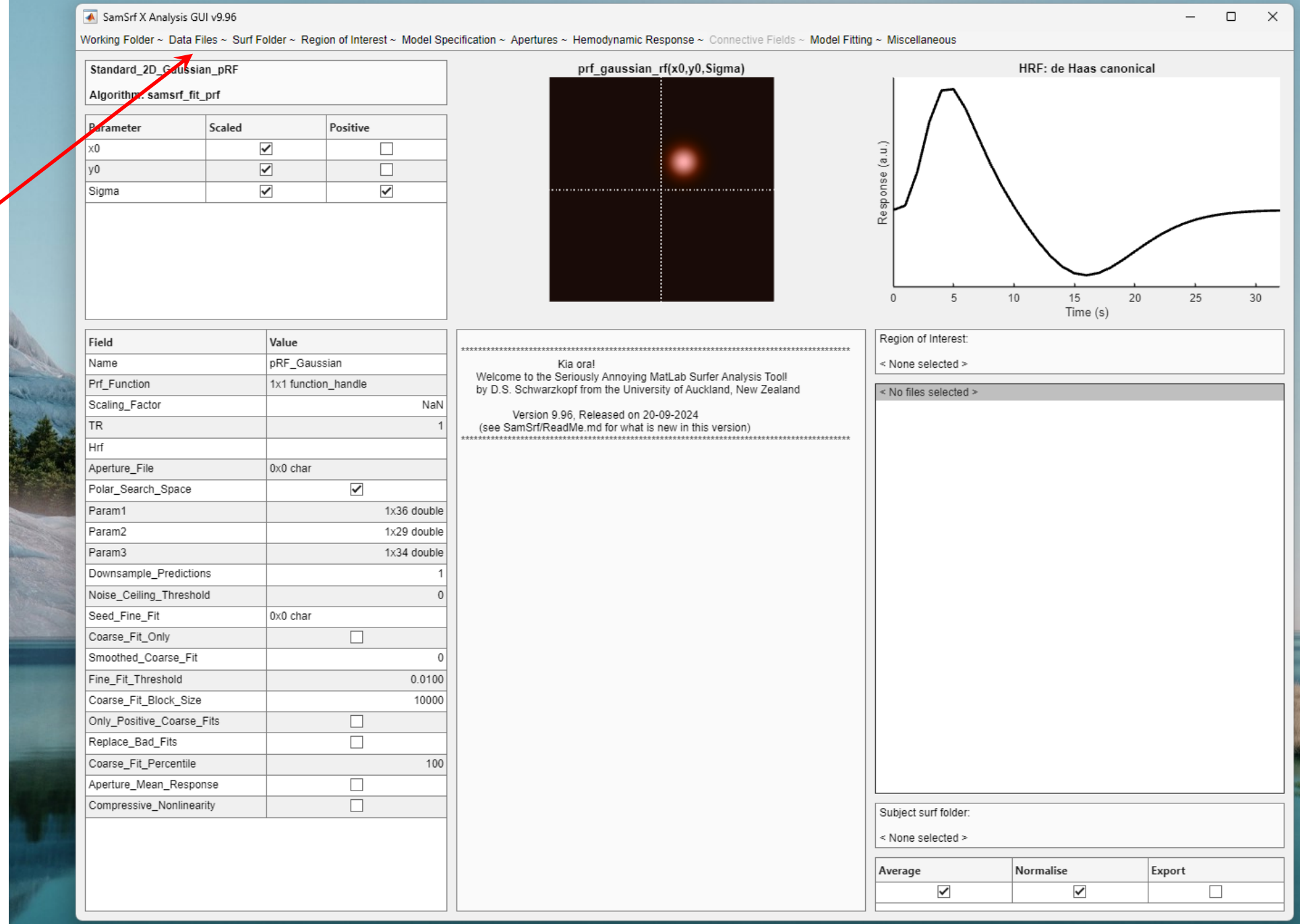
You now have three options:

- Select hemisphere *.GII* files
- Select bilateral *.GII* files
- Select volume *.NII* files

If you choose the bilateral option, a dialog will ask you to specify the *left hemisphere* files, and it will automatically combine these with the corresponding right hemisphere files.

Our functional data files are in *X001/func*.

Note: SamSrfX expects *.GII* files to be named following the same convention as *FreeSurfer* files: The prefix *lh* and *rh* indicate left and right hemisphere files, respectively.

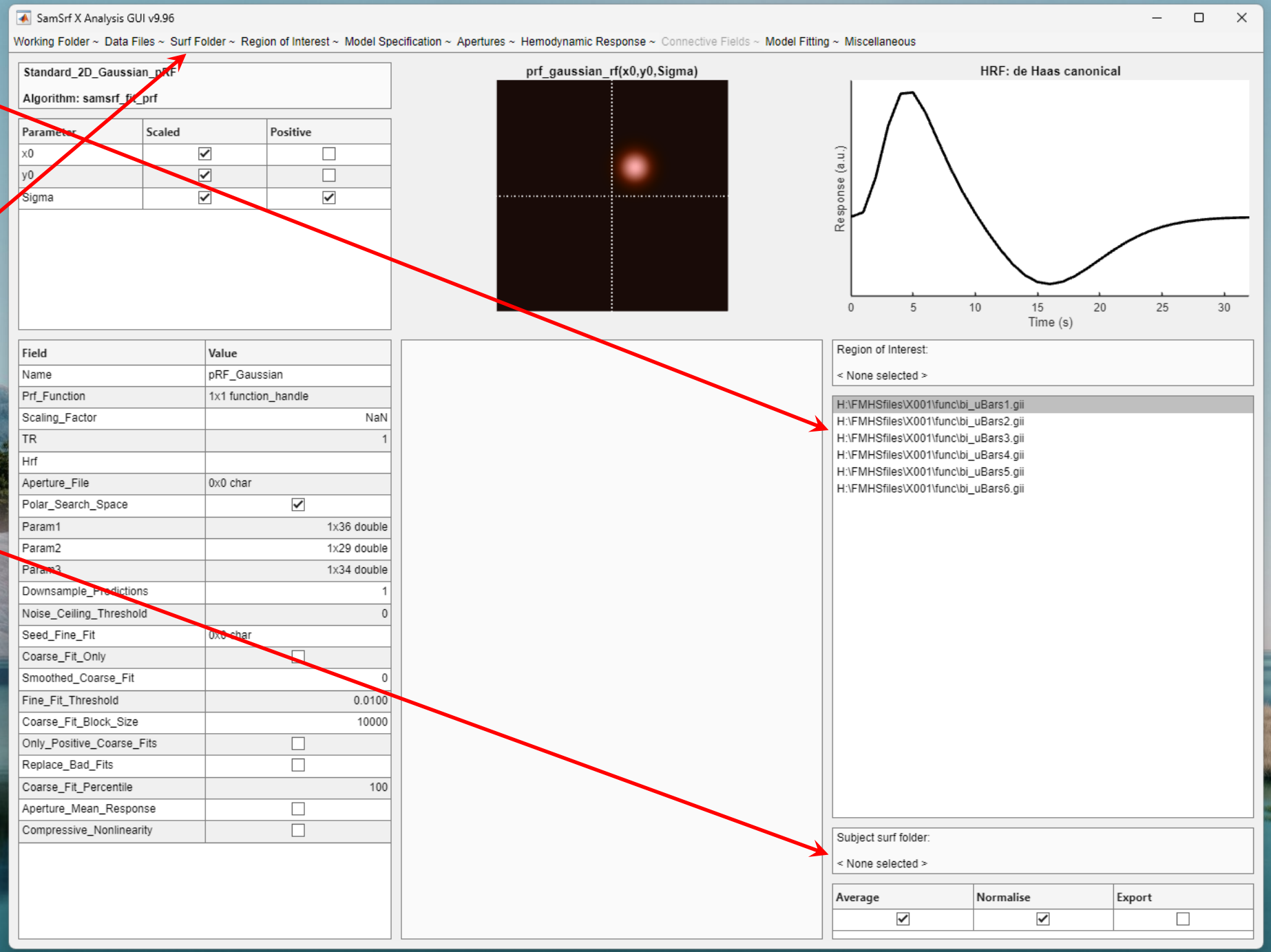


Here, we used the bilateral option. You can now see the *lh_*.GII* files in the data file list.

For surface-based analysis, we also need the *surf* folder of the subject's FreeSurfer recon.

**4. Select this via the *Surf Folder* menu.** If your data are structured in the normal SamSrf way, the dialog that opens will already point to the correct place so you just need to confirm.

Once confirmed, the surf folder will appear below the file list.



Many pRF analyses can be rather time-intensive. We therefore often restrict them to a region of interest (ROI), such as a roughly defined occipital region. This is optional and you need to decide which parts of the brain are most important to analyse.

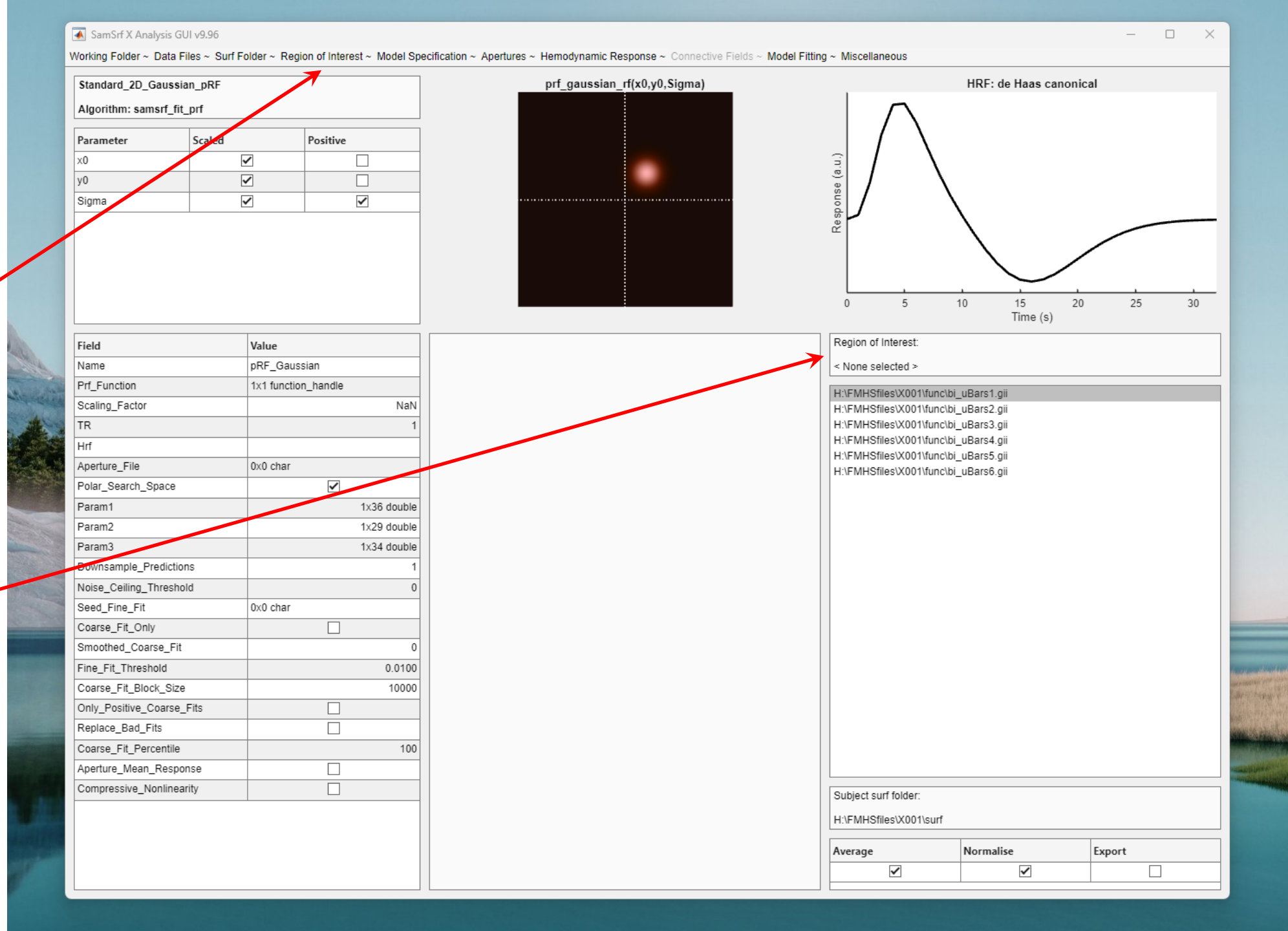
5. You can automatically generate a ROI in the *Region of Interest* menu via *Create Occipital ROIs*.

This will create a occipital ROIs for each hemisphere as well as a combined (bilateral) ROI called *occ.label*.

Alternatively, you can create your ROIs yourself.

6. Next, use *Region of Interest -> Select ROI Label* to select the ROI you want to analyse.

Once confirmed, this ROI will then appear above the file list.



Now things get real. You need to specify the model for your analysis. The model contains all the parameters and options of the analysis you want to run.

SamSrfX GUI currently supports three algorithms:

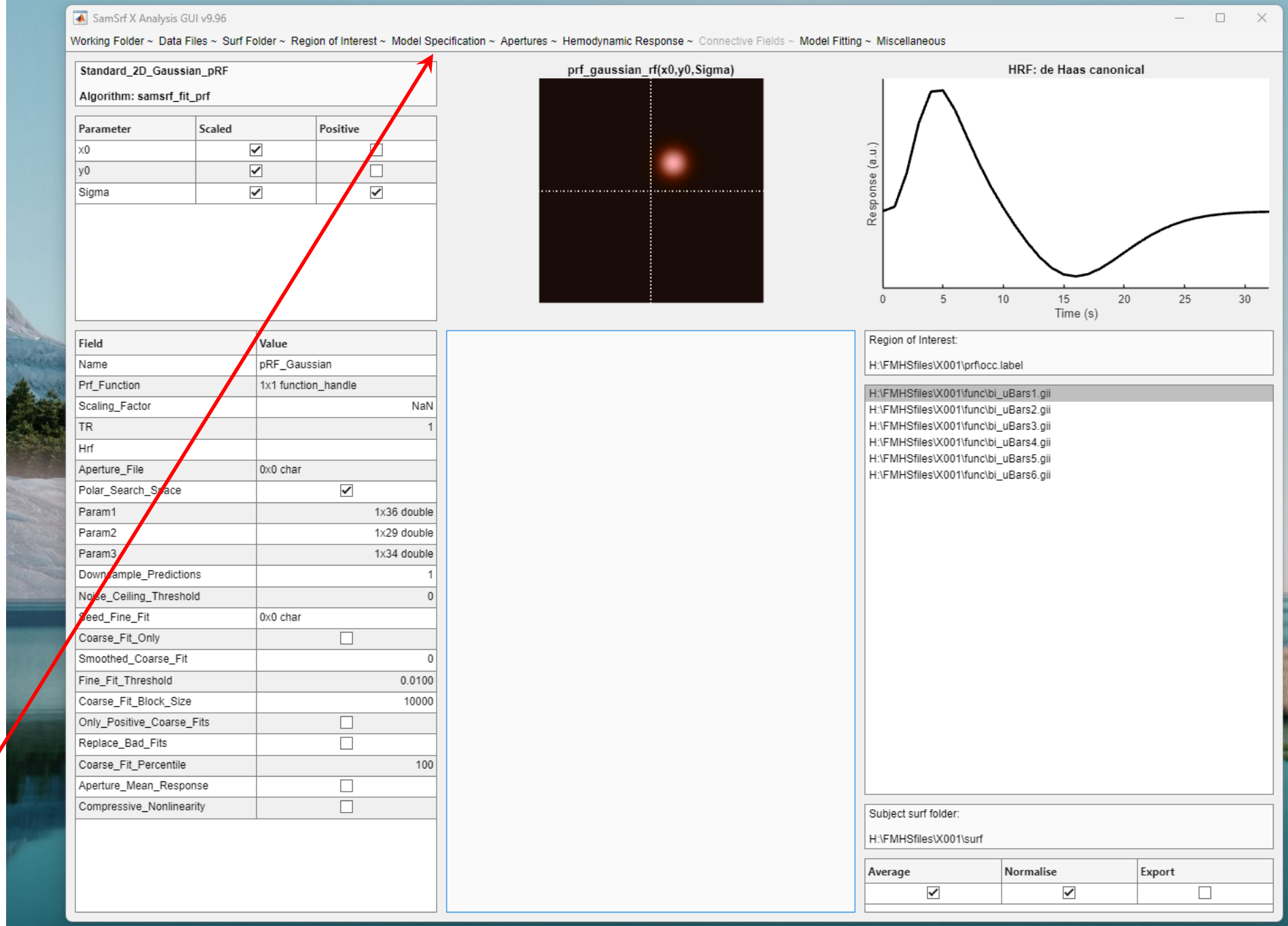
- Forward model pRF
- Reverse correlation pRF
- Reverse correlation CF

Each of these algorithm comes with different model options.

By default, the GUI opens with a standard 2D Gaussian pRF model and for many people there won't be any reason to change this.

However, you may want to use a different algorithm or use another pRF model (e.g. the difference-of-Gaussians or elliptical pRF model).

7. Choose an algorithm or predetermined model using the *Model Specification* menu.



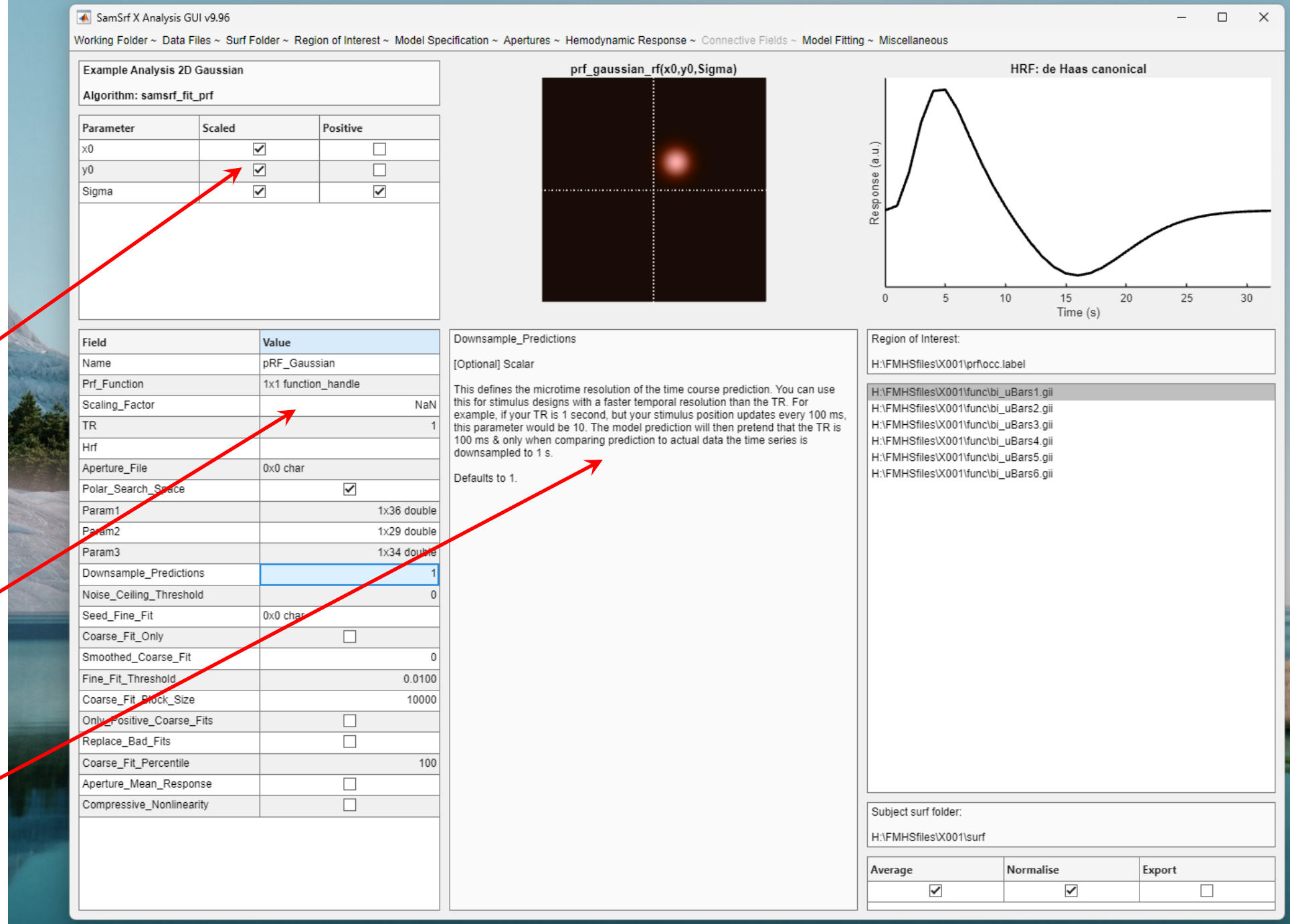
For now, we stick to the standard 2D Gaussian pRF model.

The model parameters/options are listed in the tables on the left side of the GUI.

The top table shows the free parameters of the pRF model and some check boxes for them. You can rename the parameters, but you cannot add or remove parameters here. For this you would need to load another model with a different number of parameters.

Other options are shown in the bottom table. You can edit all of the values, check boxes, and file names in the right column. Some rows cannot be edited, however (function handles and vectors).

**8. Clicking on any cells in these tables will show you some detailed descriptions about them in the info field in the centre.**

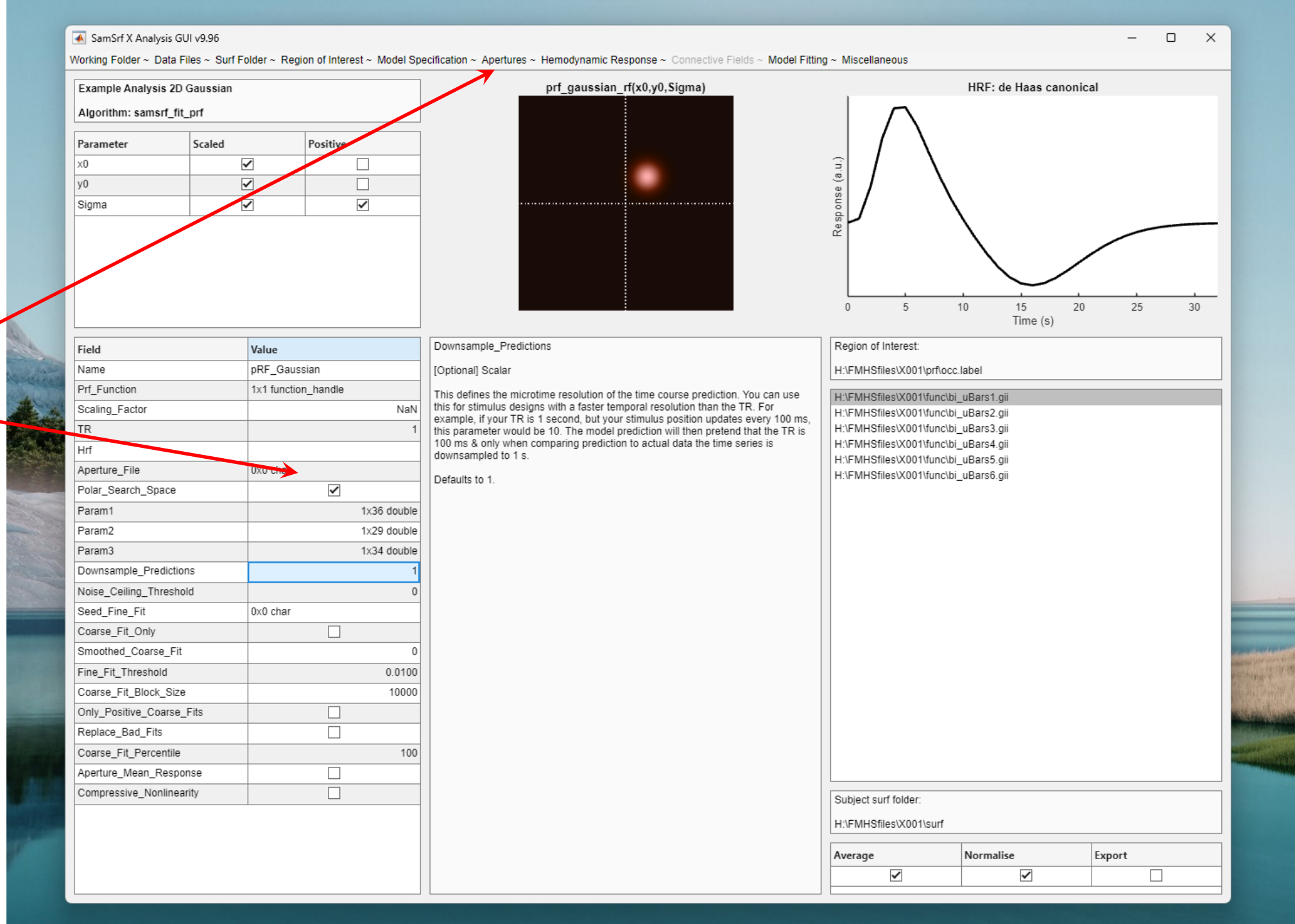


For the conventional Gaussian model, you won't need to tweak many of the parameters. There are only a few things that are mandatory to define before you can run an analysis:

**9. You must define the stimulus apertures corresponding to the sequence in your data.** You can select the aperture file either through the *Load Apertures* in the *Apertures* menu or by clicking the cell in the table.

In the menu, *View Apertures* allows you to visualise the apertures so you can check they are correct.

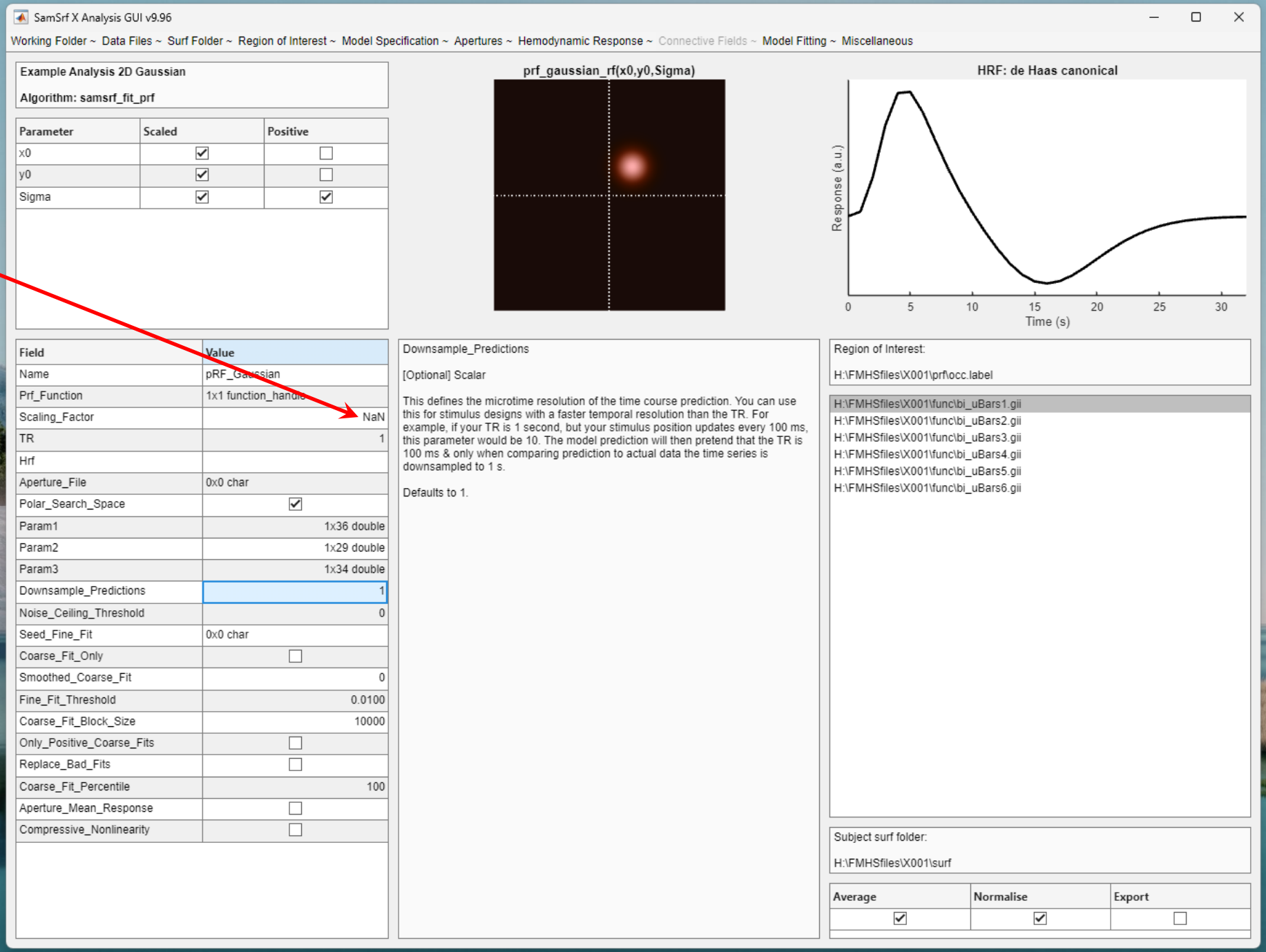
(Note: In previous versions, the forward modelling pRF algorithm expected vectorised apertures. This step is now done internally so you don't need to worry about it. You can still select vectorised apertures if you want. It won't matter either way.)



The other mandatory parameter you must define is the scaling factor. In 2D retinotopic mapping designs this is the maximum eccentricity of your stimulus.

10. Change the *Scaling_Factor* parameter to the desired value.

This is a critical parameter because the search space for the coarse-fitting stage will depend on this value. It also affects the exclusion criteria for bad pRF fits.



In theory, we are now ready to run the analysis. If you click on the *Model Fitting menu*, it will give you a completeness check of all the mandatory parameters and this should tell you that you are ready.

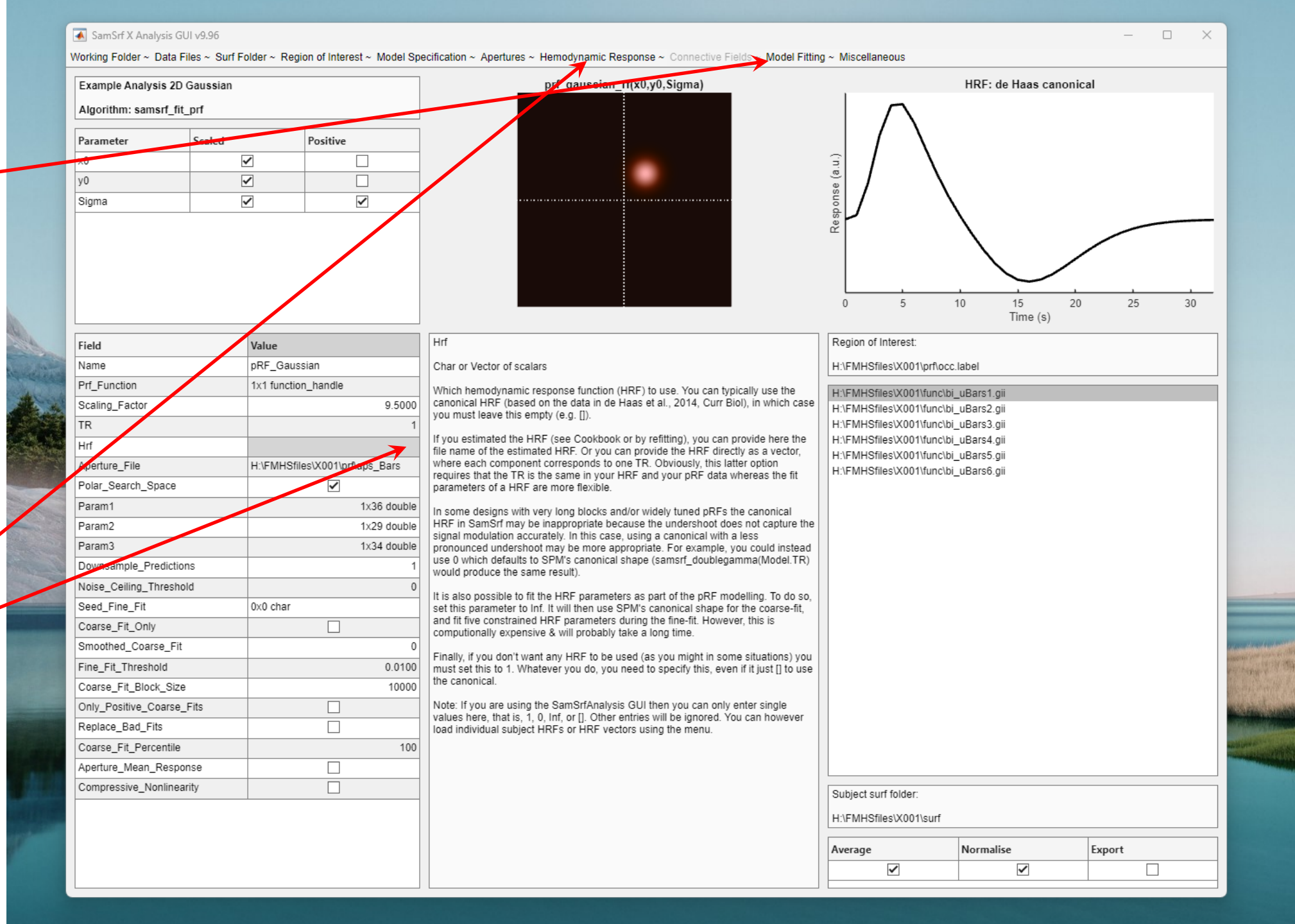
It will also warn you if you didn't define a ROI but that doesn't stop you from running the analysis.

However, there could be many other options you can define. You can also chose a different approach for the hemodynamic response function.

## 11. Set the HRF, if desired.

You can either change the value in the table (see info field for the available options) or you can load a prefit HRF from a file via the *Hemodynamic Response* menu at the top.

However, we stick with the default, an empty *Hrf* field: *de Haas canonical HRF*



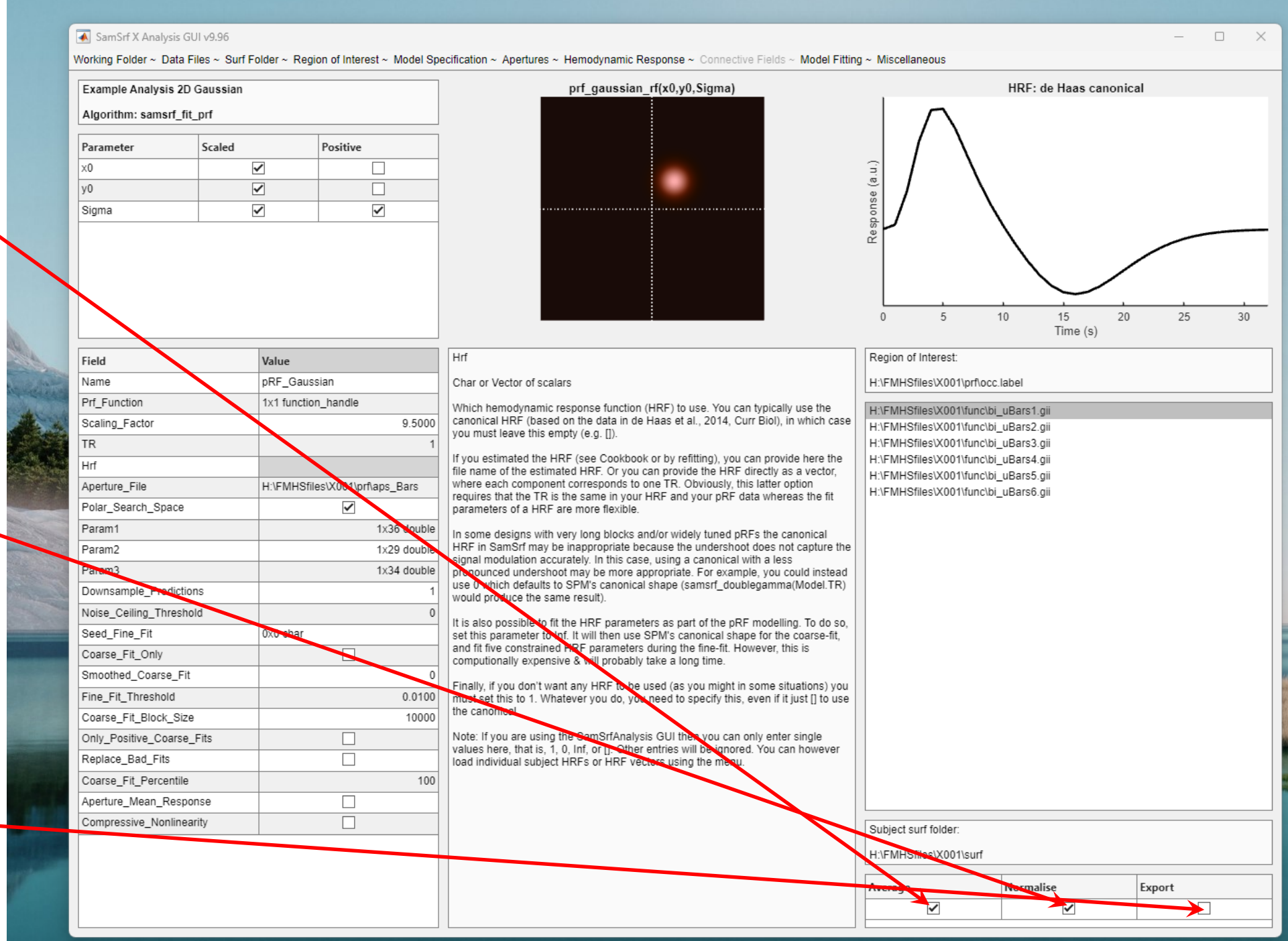
Finally, there are some options for how the data are treated prior to the analysis and what happens after pRF fitting.

**12. Unchecking the *Average* box means run will be concatenated instead of being averaged!**
Most conventional pRF studies use the same temporal sequence for stimuli in every run. But if the sequence differs between runs you must concatenate them.

**13. Usually, the time series in each run is detrended and normalised. Uncheck this box if that is not desired.**

pRF maps will be saved in a *.MAT* file inside the working folder. This format is convenient for many reasons, but you may wish to export data to be used in other tools (e.g. *FreeView*).

**14. Check this box to export data in the same format you use for input** (i.e. either *.GII* or *.NII*).

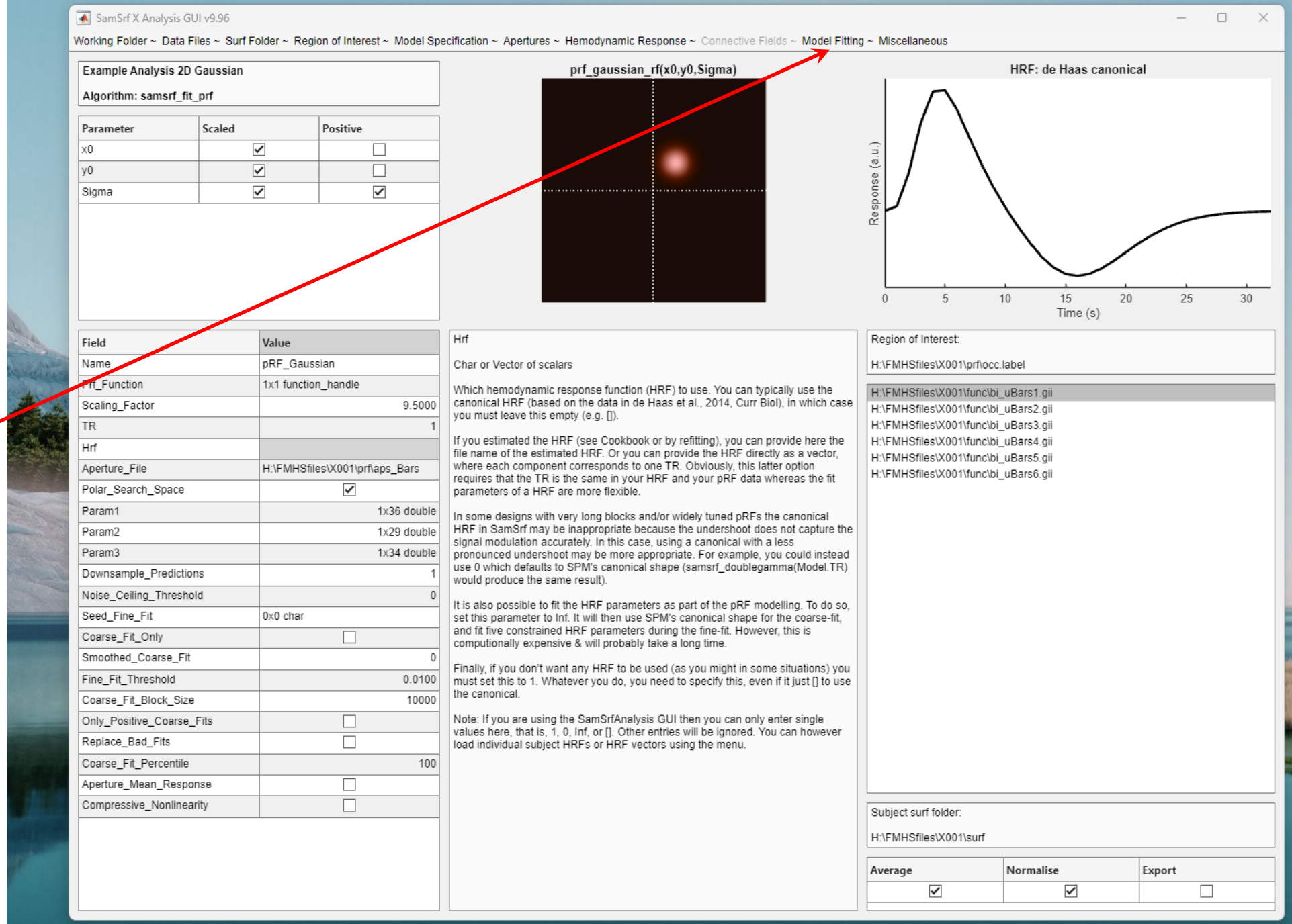


Now you can run the analysis. As already mentioned, when you click on *Model Fitting* it will perform a completeness check that all necessary information has been defined.

Moreover, as the specification is complete now, the *Fit Model* option in that menu should now be available.

**15. Click Fit Model to start the analysis.** This will then start by converting the *.GII* files into SamSrf format, in this case as bilateral surface data.

Following that, the actual pRF analysis commences.

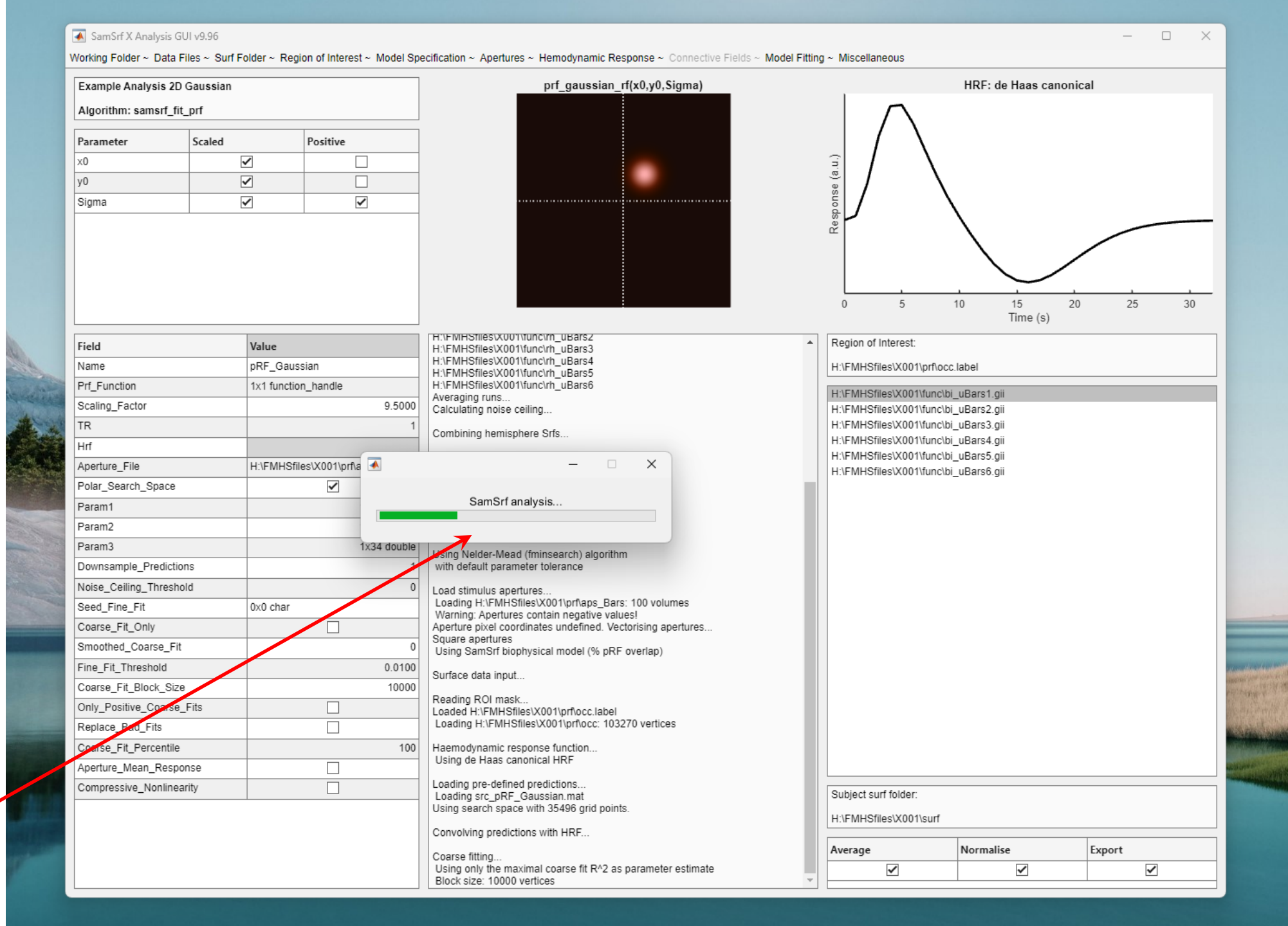


## Intermission

Some pRF analysis only takes a few minutes but other can be hours or even days. Just how long it takes depends on:

- How many voxels or vertices you are analysing (so e.g. how large the ROI is)
- How many time points in the time series (therefore concatenated data take longer than averaged)
- Whether you are filtering the data based on SNR ratios
- How many free parameters your model has
- The processing power and amount of system memory

For the protracted phases of the analysis (like fine-fitting pRFs) the progress bar will give you an idea how long it may take…



Either way, if all goes to plan your analysis should eventually be completed.

16. The *Miscellaneous* menu has a few options for you to inspect the data directly in the GUI.

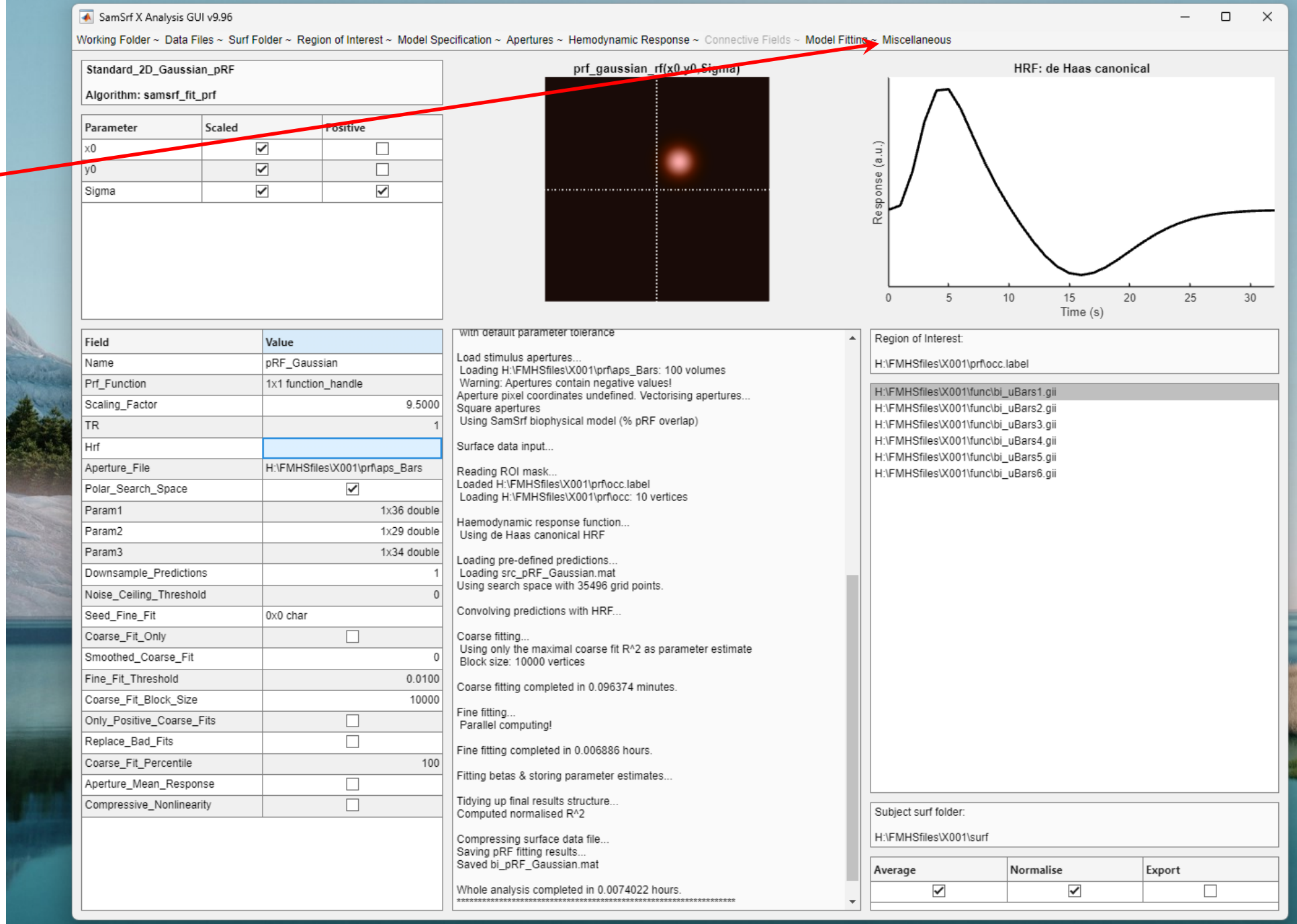
For example, you can use the *Map Display Tool* to look at the surface maps (only if using .GII input data).

You can also use the *Map Delineation Tool* to define retinotopic brain areas (refer to the tutorial document on delineations).

You can warp a normalised retinotopic atlas into native space to create ROIs.

You can use Eccentricity Plots and Visual Field Coverage to visualise pRF data from several regions of interest.

And there are other options (and more may be added in future…)



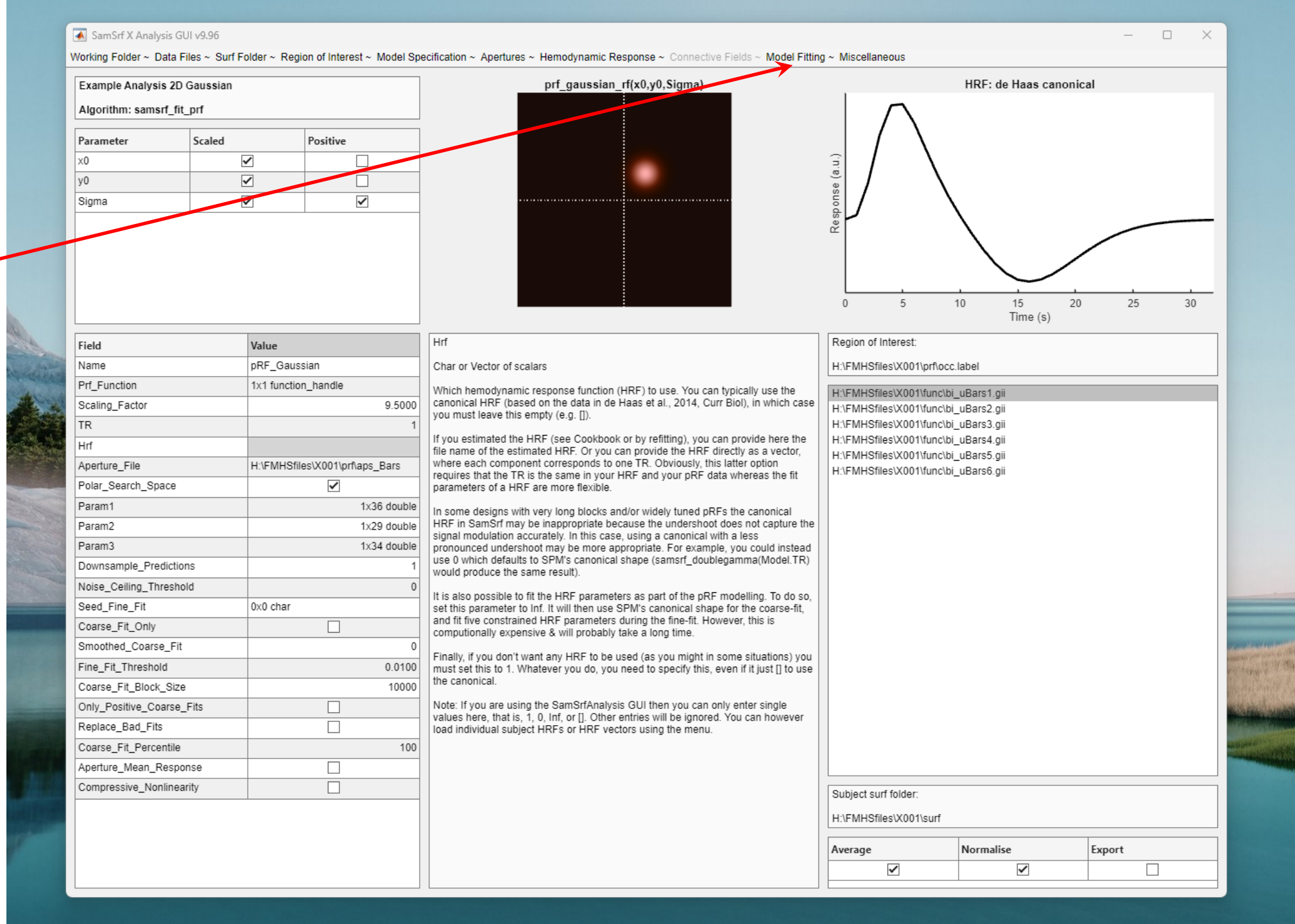
Finally, once you specified a model, and defined all the files for data and ROIs etc, you may run the exact same analysis for another participant.

17. Use the *Replace String* option under the *Model Fitting* menu to quickly replace any mention of the current subject's pathname to a new one.

For example, here we might want to replace X001 with X002. It will do this for all the data files, for the ROI and surf folders, and any mention of X001 in the table.

**Note: This will *also* replace the string in the working folder!**
The idea is that you'll be in the same subfolder for the subject, so if we were in *X001/prf* before we should now be in *X002/prf*.

**This also means you must be consistent in your naming!**
Don't name the folders X001 but some files S01 or some such.

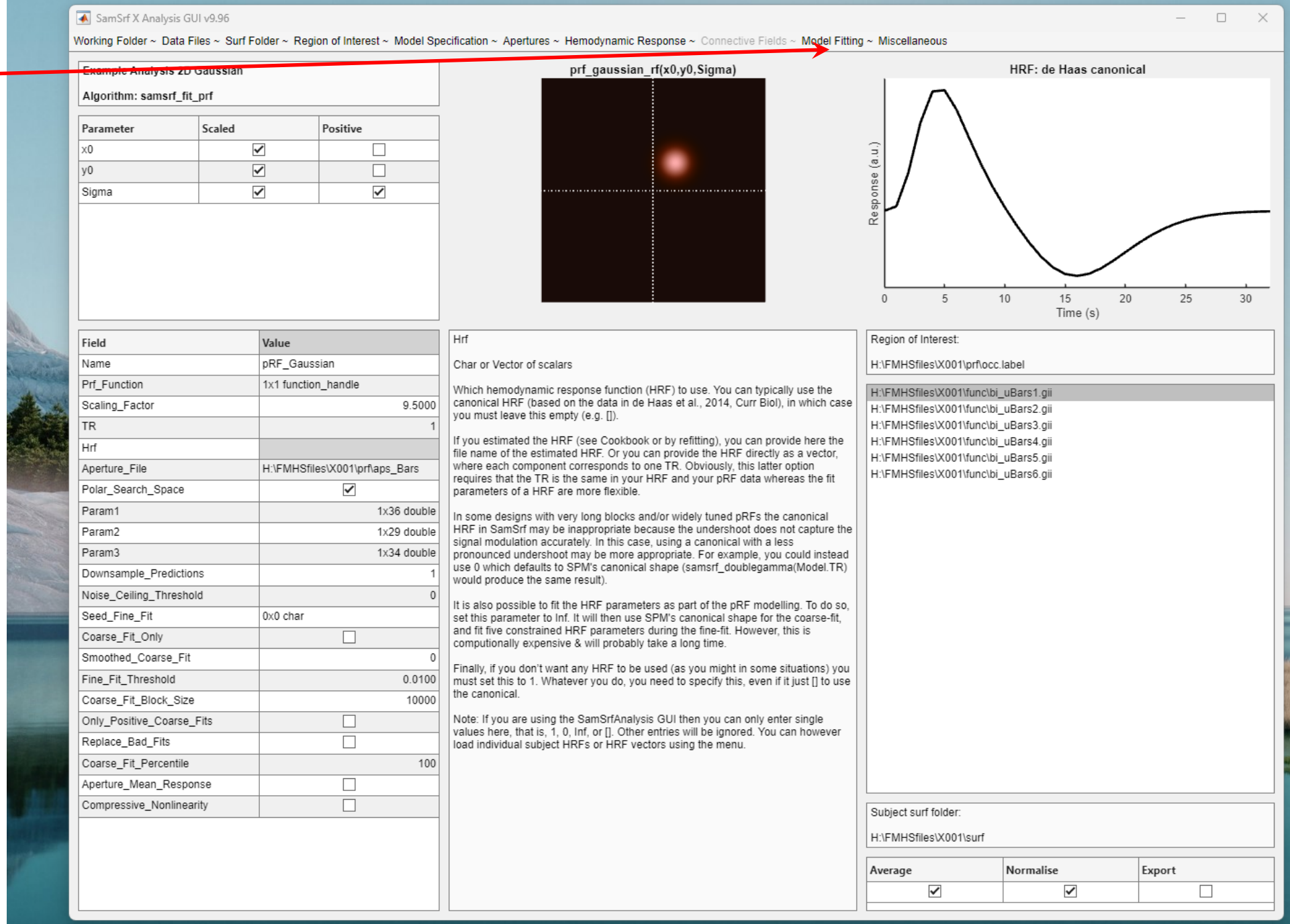


18. Related to the previous point, you can use *Run Batch Analysis* to automatically run the same analysis on a set of subjects.

This will internally replace all the instances of the subject ID with the other ones in the batch. For example, here all instances of X001 would be replaced with X002, X003, etc.

**Note: It is therefore crucial that you start this analysis in the working folder of one subject in the batch! All the names must be consistent.**

For example, you could specify your model in the working folder *X001/prf*, and then run the batch on X001, X002, X003, etc.



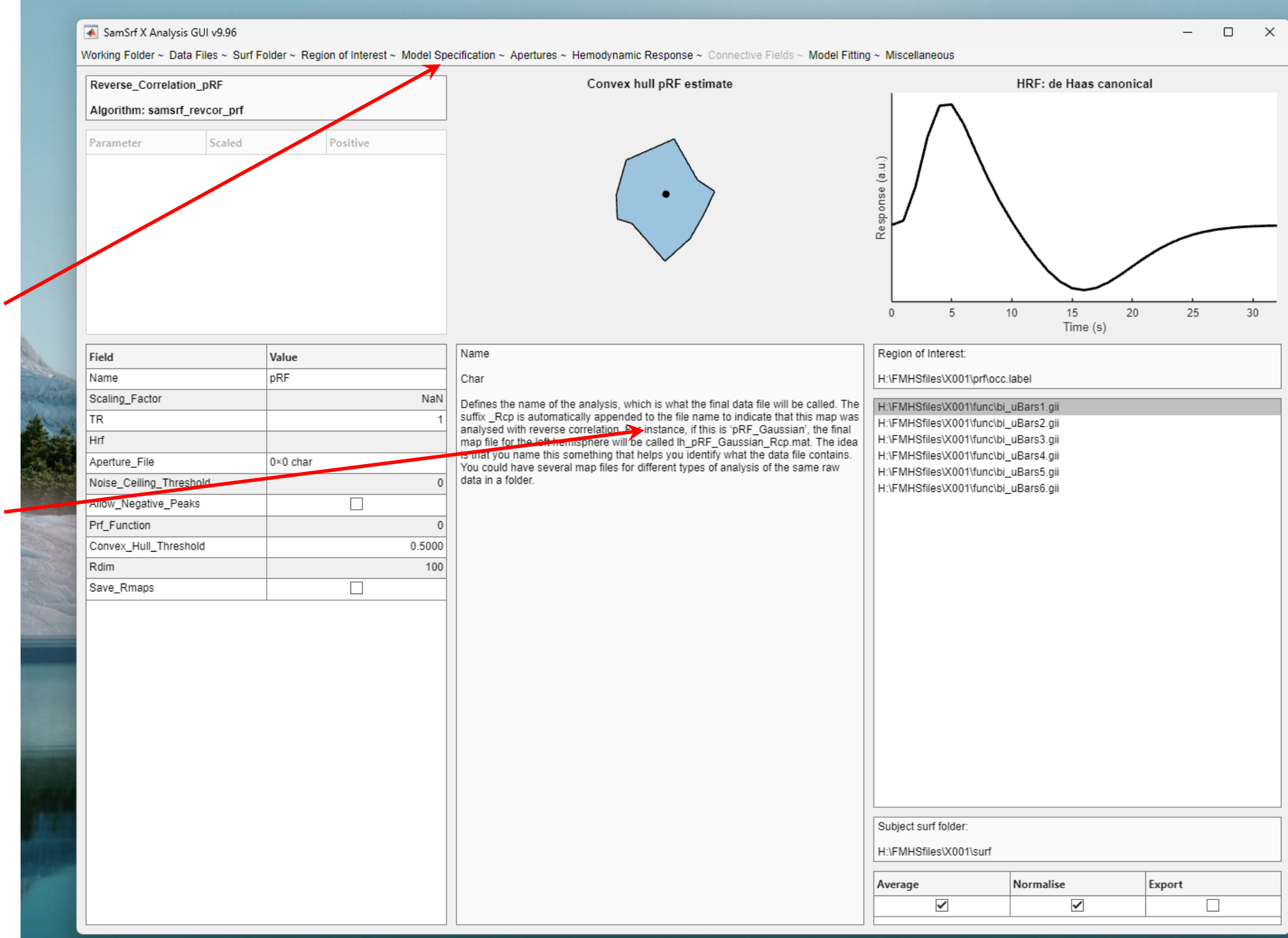
## About other analyses

As already explained, there are other algorithms and many model options you can define for each of these.

For example, you could choose the reverse correlation pRF algorithm instead. This has other model options you can define, and the GUI will accordingly look somewhat different.

This manual has no information about these but you can get some more explanation via the *Model Information* option in the *Model Specification* menu.

Finally, you can save and load previously saved model specifications. These files include the data files and ROI labels you defined so you don't have to do this every time. For use with batch analysis, you want to save these .MOD files in the working folder of your subject.



# Final Remarks

## Default FreeSurfer template

You may want to change the default folder pointing to your *fsaverage* template. You can change this path in the file *SamSrf_defaults.json* in your *SamSrfX* folder. Under a standard *FreeSurfer* installation this will already be correct, but your setup may differ. Obviously, this step only applies if you even use *FreeSurfer.* Moreover, it is only required for optional analyses that involve normalised brain templates.

## Default colour schemes

You can also change the default colour schemes for various data types in your maps in the same .JSON file.
Colour schemes are defined as .CSV files inside the *Colours* subfolder. You can add or make your own colour schemes. These are simply three-column matrices with the RGB values for each step in the colour map.

## Other default settings

There are other default settings (e.g. how much of the brain the Map Display Tool will show).
Future versions of this manual may contain more information about these.

# Questions / Comments?

*SamSrfX* is developed by Sam Schwarzkopf at the University of Auckland, New Zealand, with support from his students and collaborators. We strive to make this a user-friendly, easy-to-use tool, making it comparably straightforward for other researchers to run pRF and CF analyses. However, we receive no dedicated funding for this work, and this is not commercial product. Primarily, we developed these methods for our own research. Our capacity to support and troubleshoot other people's research is therefore limited. We cannot guarantee that SamSrf does everything you want or that it is free of bugs and problems.

Nevertheless, please contact Sam if you have questions or suggestions. He or someone from his team will usually reply and – time permitting – we may also be interested in a closer collaboration:

s.schwarzkopf@auckland.ac.nz