

Using the PIPT

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Abstract

This tutorial outlines the steps for creating a proposal with the Principal Investigator Proposal Tool (PIPT).

1 Introduction

This tutorial is intended as a gentle introduction (if there is such a thing) to the *Principal Investigator Proposal Tool*. Now that's a whopping long word, and that is why there's an acronym for – PIPT. This is only one of the tools you might want to use for creating a proposal, and you may launch some other tools from it, as you'll see later on.

Naturally, a tutorial such as this has to make some assumption about the reader. Specifically, it assumes that you are an astronomer and that you know about SALT and its characteristics. So, please don't expect any advice on how to plan your observation.

You will be introduced to the PIPT by going through the proposal creation process step-by-step for a real-world example. This won't cover all the details you can find in the PIPT, but it should be fully sufficient to get you started. Where appropriate, some remarks commenting on features not used in the example will be included. So after completing this tutorial you should be able to confidently create your own proposal.

SALT is still a work in progress, and so is the PIPT. Hence some of the things will change in the future. Hence you might want to check for an updated version of this tutorial from time to time.

Finally and most importantly, you are not on your own. If you have any questions about using the PIPT and don't find an answer on the following pages, please don't hesitate to ask the SALT Team, which you can reach via email at <mailto:salthelp@sao.ac.za>. If you have any questions or want to make suggestions concerning this tutorial, feel free to send the author a mail!

Having said all this, without any further ado let's plunge into having fun with the PIPT!

2 Downloading and Launching the PIPT

Please note that the following installation instructions do not apply if you are using the PIPT for creating your NASSP project. If you want to install the PIPT for that purpose on your computer, please send the author a mail. You can find his address above.

Before installing the PIPT, you should make sure that some prerequisites are fulfilled.

First, you must make sure that Java 5 or higher is installed on your computer. The easiest way to check this is to open a terminal and execute the command

```
java -version
```

You then should get some output of the form

```
java version "1.5.0_16"
```

```
Java(TM) 2 Runtime Environment, Standard Edition (build 1.5.0_16-b06-284)
```

```
Java HotSpot(TM) Client VM (build 1.5.0_16-133, mixed mode, sharing)
```

The important part is the version number (1.5.6 in the example); if it is 1.5 or higher, all is well. In case the version number is less (such as 1.4) or you get an error message, you'll have to update or install Java. For Windows or Linux go to <http://java.sun.com> for more information on how to do this. On Mac OS X, Java 5 should be running out of the box, but if it doesn't, have a look at <http://developer.apple.com/java/>.

Second, you need an internet connection, although most of the steps during creating your proposal can be accomplished without.

Third, depending on the complexity of your proposal and the time of the day, you might need sufficient supplies of coffee, Coke, pizza or whatever else may bribe you into continuing with your work.

As soon as all the requirements are fulfilled, you can install the PIPT. To this end, go to its download page, which is located at <https://www.salt.ac.za/wm/> and (what a surprise) download the PIPT. The details depend on your operating system.

Windows

Click on the link for downloading the version for Microsoft Windows. If you are asked whether to execute or save the application, opt for saving, as you are extremely likely to use the PIPT more than once and don't really want to download it all the time. It doesn't matter where you store the PIPT, so choose the location most convenient for you. You can launch the PIPT by double-clicking its icon. You will then be guided through the installation procedure, as described below.

Mac OS X

Click on the link for downloading the version for Mac OS X. This will download and open a disk image, so that you'll be presented with a window containing the PIPT. Move its icon to the applications folder or any other location you deem appropriate. You can then launch the PIPT by double-clicking its icon. You will then be guided through the installation procedure, as described below.

Linux and any other operating system

Click on the link for downloading the version for Linux or other operating systems. This will download a jar file, which you should move to a convenient location. If you are lucky, you can then launch the PIPT by double-clicking the icon of the jar file. Otherwise, you'll have to launch it manually from a terminal by means of

```
java -jar PIPT.jar
```

where `PIPT.jar` is the name you've chosen for the jar file, including its path if necessary. Either way, after launching the PIPT, you will be guided through the installation procedure, which will be described next.

2.1 Installation Procedure

When launching the PIPT for the first time, you will be led through an installation procedure. It starts with a welcome screen (Figure 1). There isn't much meaningful information on there, so you can proceed directly by hitting the "Next" button.

The next screen (Figure 2) lets you choose where to create the directory for your PIPT data. The suggested default is your home directory, but you may choose any location you like. A directory called `.PIPT` will be created in the chosen location. Note that under Linux and Mac OS X that directory will be hidden, as its name starts with a `.`. Also note that *you must not move or rename the directory*, as otherwise the PIPT won't find your data any more. Choose a convenient directory and click on the "Next" button.

You now have to decide whether to download the required data (such as the existing SALT partners and their institutes) from the SALT server (Figure 3). Unless there is a really good reason not to do this straight away (such as reading this tutorial in a remote place without internet access), you should choose the option "Download the data now". As usual, hit the "Next" button to proceed.

It depends on your choice of whether to download the data what you'll see next. If you opted for downloading, you will be asked to log in to your SALT account (Figure 4). In case you've got one already,

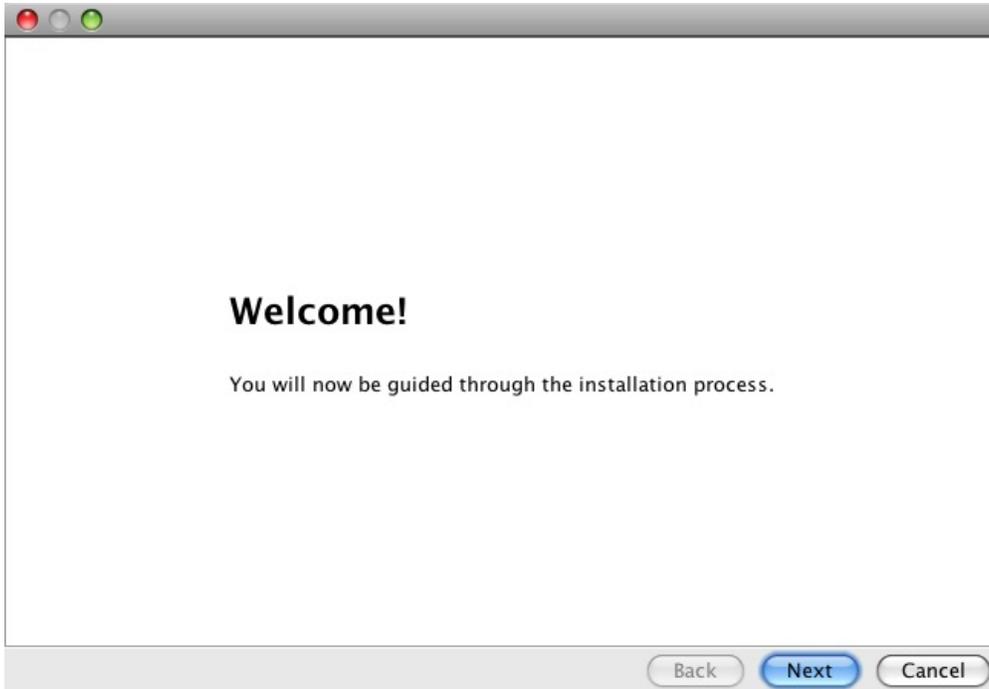


Figure 1: The welcome screen of the installation wizard.

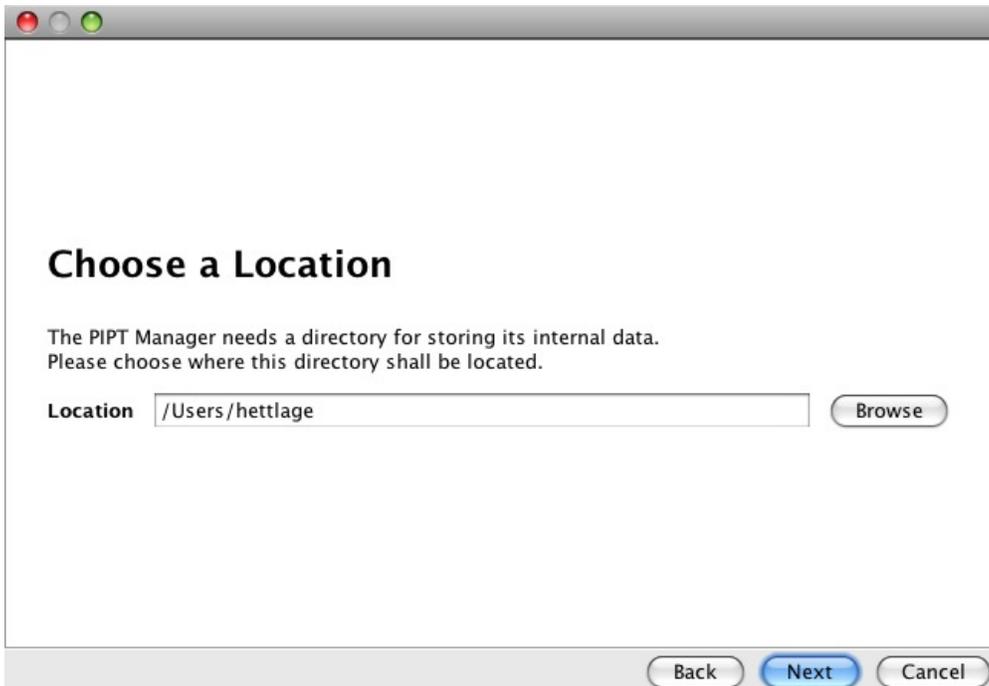


Figure 2: The screen for choosing the location where to store your PIPT data.

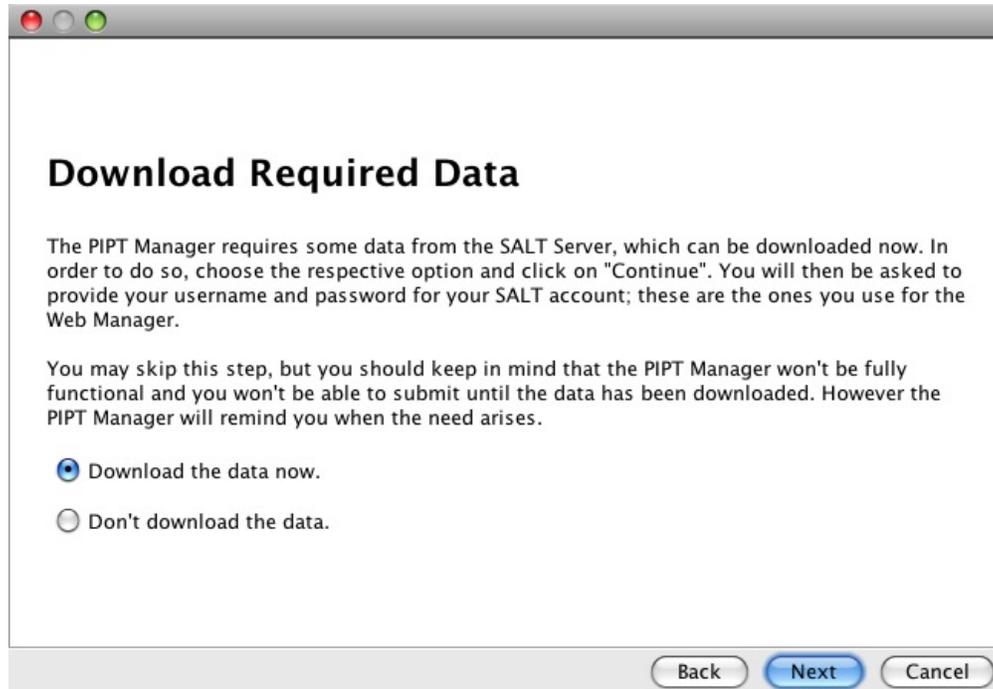


Figure 3: The screen for choosing whether to download data from the SALT server now.

enter your user credentials and click on the "Next" button. Otherwise, go to <https://www.salt.ac.za/wm/Register/> to create an account. After submitting the form on that page you'll receive an email for activating your account. You need to do this before you can log in. When you've activated your account, you can return to the login screen, enter your credentials and carry on by hitting the "Next" button.

If you have chosen not to download data, or if you've logged in successfully, you'll be presented with a summary (Figure 5). If you are happy with what you see, click on the "Install" button to start the installation. Otherwise use the "Back" button to change your choices first.

After the installation has finished, you are offered to launch the PIPT (Figure 6). Of course, if you have better things to do after the stressful installation, feel free to cancel instead. Next time you double-click the PIPT icon (or start it from a terminal), the PIPT will launch without bothering you with all the installation screens.

3 Creating a proposal

When the PIPT has started up, you might feel tempted to say that it looks somewhat empty (Figure 7), the reason being that it actually *does* look somewhat empty. But, lo behold, there is a simple way to change this: Create a new proposal!

Believe it or not, there are three ways of doing this:

1. Choose menu item "New Proposal" from the "File" menu.
2. Use the keyboard shortcut given in that menu item.
3. Right-click on the "Proposals" node you can see on the left and choose "New Proposal" from the context menu. (Not that there are any other choices in that context menu, by the way.)

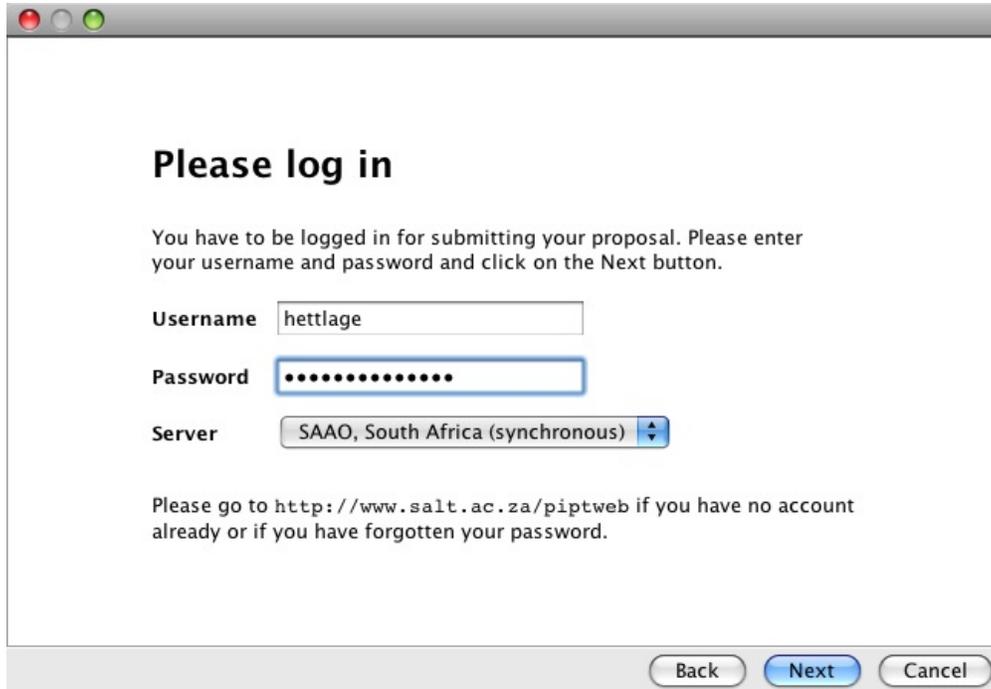


Figure 4: The screen for logging in.

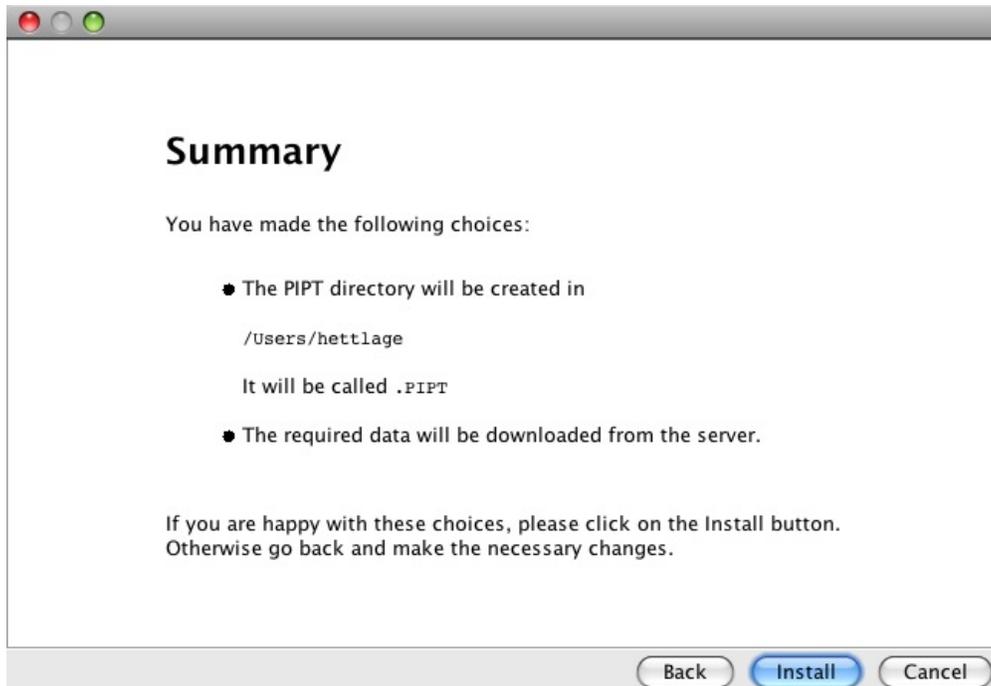


Figure 5: The screen the displaying a summary of your installation choices.

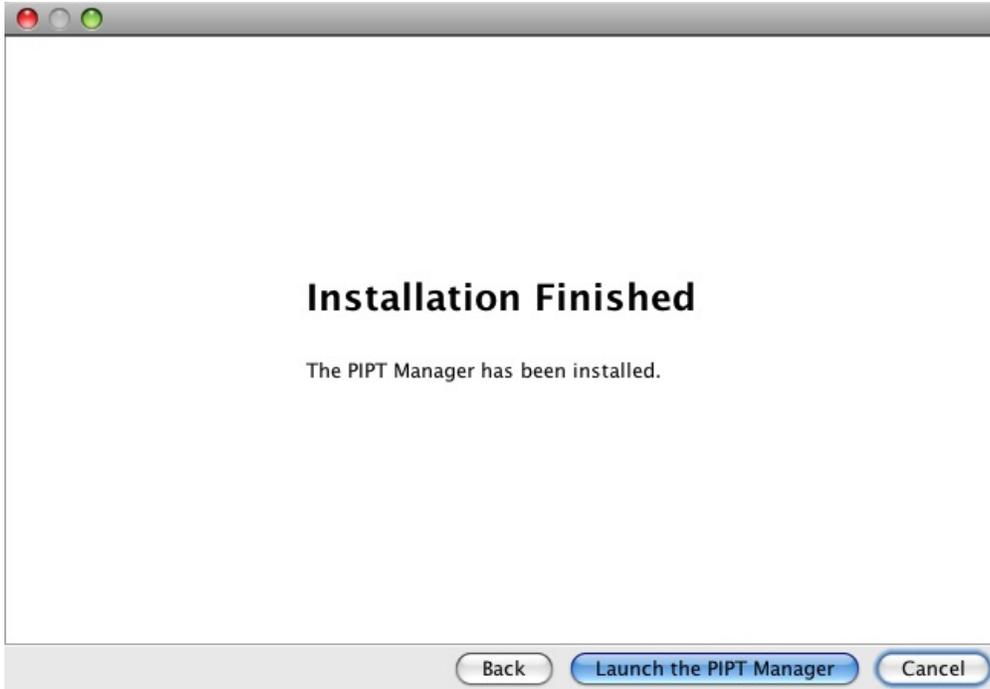


Figure 6: The screen telling you that the installation has been successful.

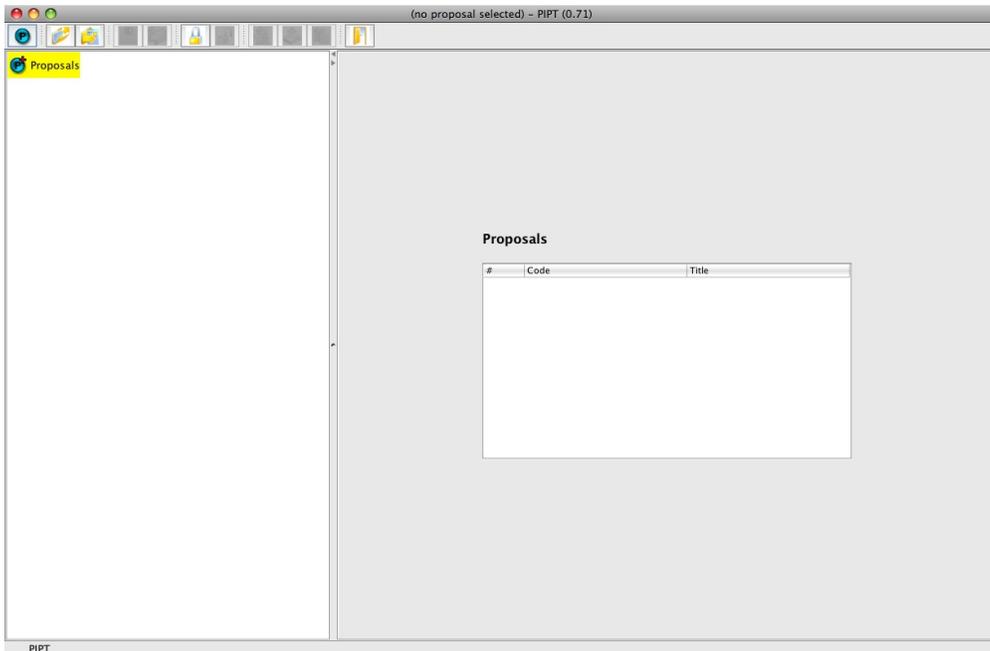


Figure 7: The PIPT after launching.

(menu)

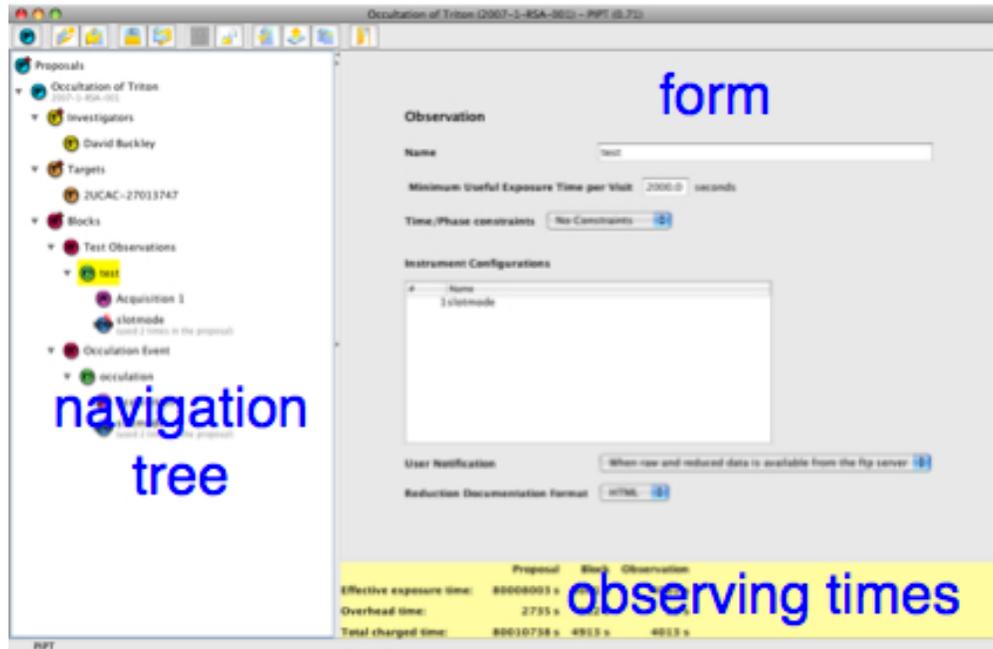


Figure 8: Overview of the PIPT. The menu isn't shown.

You will be asked whether to create the new proposal from scratch or from a template. *Do not use the template option.* Due to a bug it won't work...

As illustrated in Figure 8, the PIPT consists of various components:

Form The form allows you to enter your proposal information. Its content depends on the node you've currently selected in the navigation tree.

Navigation tree The navigation tree allows you to navigate through your proposal(s) and to add or remove elements. You can expand or collapse a tree node by clicking on the respective little triangular (or similar) icon to the left of the node label. (Double-clicking the node should work as well.)

Observing time panel The observing time panel lists exposure and observing times. We'll cover it in a little more detail later on.

Menu As most applications, the PIPT has a menu bar. Its located at the top of the PIPT window, unless you are running the PIPT under Mac OS X, in which case it can be found at the top of the screen (as you would expect from a Mac application).

If you want to remove a proposal again, you can either right-click on its node in the navigation tree or right-click on its entry in the Proposals table and choose the respective action from the context menu. *Deleting a proposal cannot be undone!* You have been warned.

3.1 General Information

Now that we've got a proposal, we need to fill it with life. Let's start with the general proposal information (Figure 9), which you enter in the form you see after creating a new proposal or clicking on a Proposal in

Figure 9: The form for defining the general proposal information.

the navigation tree. We discuss all its fields in turn.

The *title* is a title for your proposal. Try to choose a meaningful title, such as *Occultation of Triton*

The *abstract* should be a brief summary of your proposal, such as

SALTICAM in slotmode will be used to observe the occultation on Uranus' satellite, Triton, by a 13.2 magnitude star at 01:47 UT on the morning of 21 May 2008. A precursor "test" run will be carried out the previous night.

When SALT is fully operational, proposing will be a two-step process. In phase one, you will just provide basic information, and based on that information a time allocation committee will decide whether your proposal should be observed. If your proposal is accepted, in phase two you have to resubmit it with all the detail information required for observing. As currently, there is no formal time allocation in place, you always have to supply a phase two proposal, and hence the value for the *phase* is fixed in the PIPT.

The *proposal code* will be inserted automatically, so you don't have to worry about it when filling out the form.

If your proposed observation requires that you provide target information at short notice (for example as you want to observe microlensing events), tick the *target of opportunity* check box.

Arguably the most important part of the general information is the *scientific justification*, which gives you the chance to explain why your observation is of importance and why SALT is your choice of telescope for it. There are a few guidelines:

- Discuss what the scientific questions are and how SALT will help answer them.
- Provide a brief summary of the observational setup.
- Demonstrate the observational feasibility of your proposal.
- Justify the amount of time you are requesting.

And there are a few technical requirements:

- The scientific justification must be supplied as a PDF file.
- It must contain the proposal title, the Principal Investigator and the Principal Investigator's institution.
- Its text font should have a size of at least 12 pt.
- There shouldn't be more than two pages in your scientific justification.

In order to add or replace the scientific justification use the respective button in the form. Unless your PDF is too complex, you'll be shown a thumbnail, and irrespective of whether this is the case you can view the PDF in its full glory by clicking on the thumbnail window.

Finally, you have to state the *year* and *semester* for your proposed observation. Note that for January and February not the current but the previous year must be supplied. In other words, if your observation is to be carried out between, say, 1 September 2008 and 28 February 2009, choose 2008 as the year and "1 October - 28 February" as the semester.

3.2 Investigators

If you expand the navigation tree for your proposal, you'll see an "Investigators" node, and if you select this, you'll be shown an "Investigators" table as the form. So obviously you are supposed to define at least one investigator. But how do you tell the PIPT to do this?

This is a special example of a rather general question: How do you tell the PIPT to add an element such as an investigator, target or instrument configuration? There are actually two possible answers to that. First, you can use the navigation tree. If you right-click on the prospective parent element, you'll get a context menu which allows you to add the desired element. In case there exists a sibling for the new element (for example, you want to add an investigator and there is one already), you can also right-click on the sibling immediately before or after the prospective new element. Similarly, you can remove an element by right-clicking on its tree node. See Figure 10 for examples.

Second, if there is a table for the elements of the desired kind, you can right-click in that table. If you want to insert the new element at a specific location (rather than just at the end), right-click on the table row directly before or at the desired location. Removing an element is possible by right-clicking on the respective table entry. See Figure 11 for an example.

When creating a new element, you will be asked what exactly you want to do (cf. Figure 12):

- You can create a completely new element ("Define new element").
- You can re-use an existing element of the kind you are about to create. If you re-use an element, all changes you make on one instance will be reflected by all the other instances. This option makes sense for instrument configurations only.
- You can copy an existing element of the kind you are about to create. Changes you make to the copy won't be reflected by the original and vice versa.
- You can import the element from a file. This is mainly intended for being able to create an instrument configuration in the Salticam or RSS simulator, save it and subsequently load it into the PIPT.

So you can create an investigator by right-clicking either in the Investigators tree node or in the Investigators table. Either way, (left-)click on the new Investigator tree node or Investigators table entry to get the form for providing the investigator details (if it isn't shown already). This form is shown in Figure 13.

If the investigator happens to be the *Principal Investigator* (or PI for short) or the *Principal Contact*, tick the corresponding check box. There must be exactly one Principal Investigator and exactly one Principal Contact in the proposal, which may but need not be the same person.

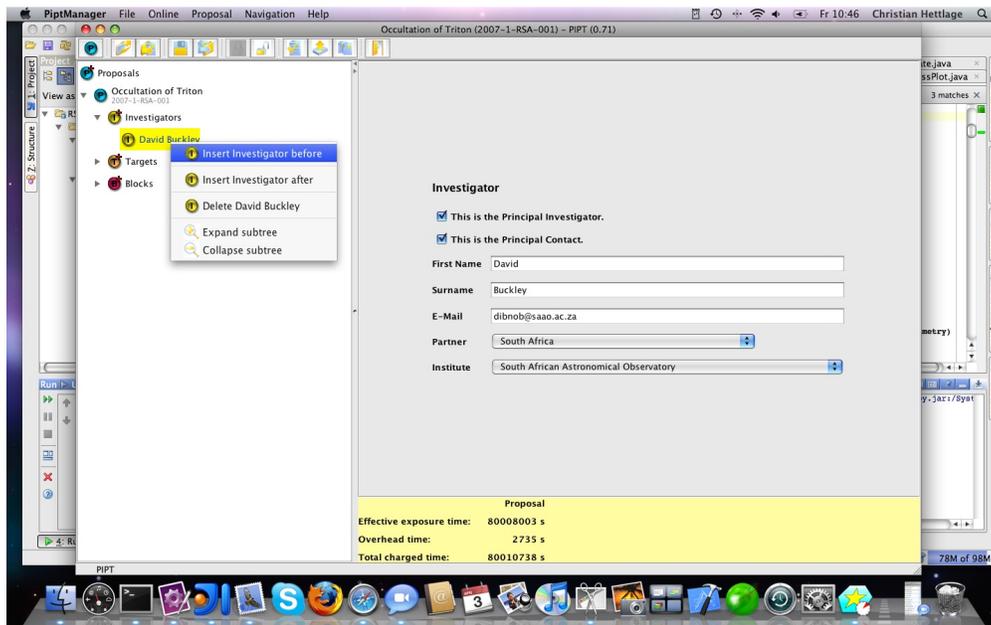


Figure 10: Adding an investigator in the navigation tree.

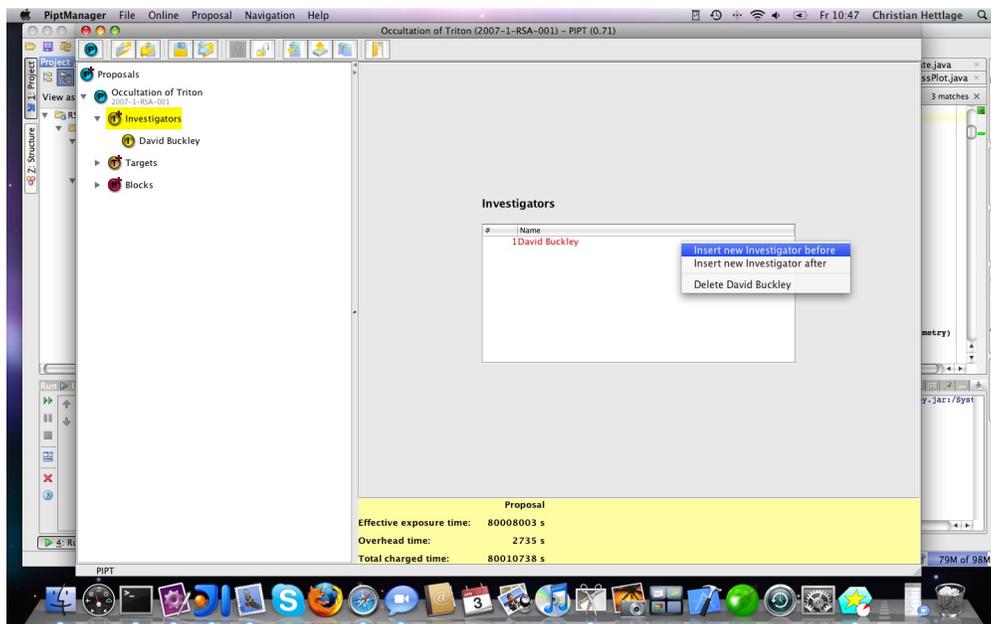


Figure 11: Adding an investigator in the investigators table.

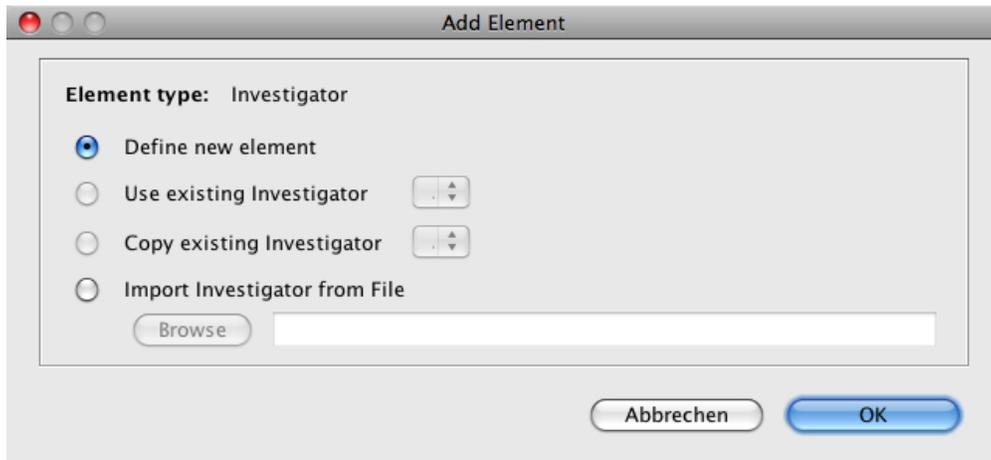


Figure 12: Adding a new element.

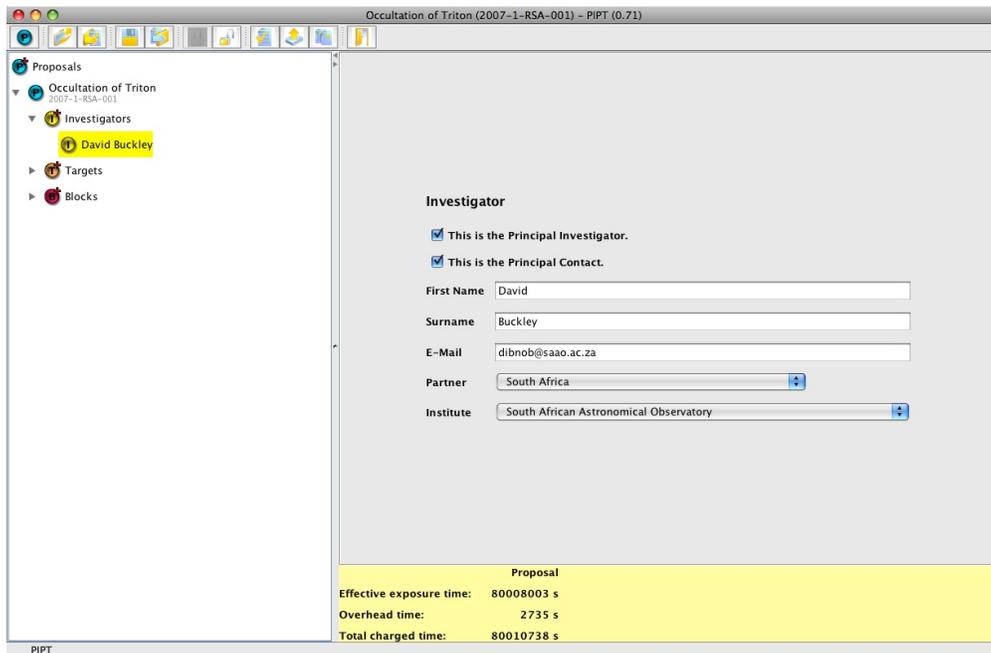


Figure 13: The form for defining an investigator.

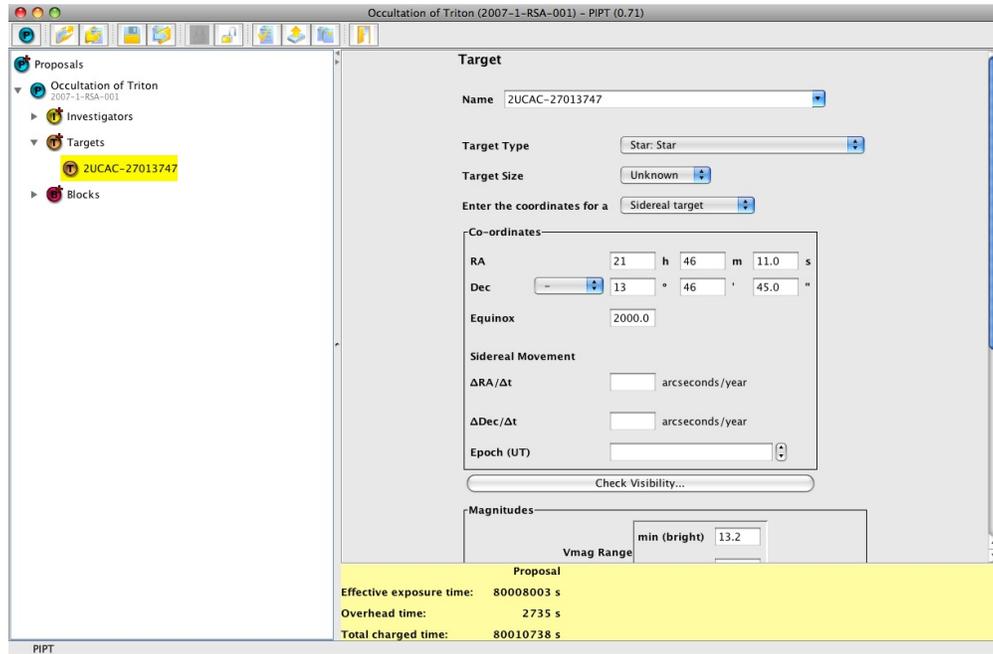


Figure 14: The form for defining a target.

The *first name* and *surname* are what you would expect them to be. The *email* address of a Principal Investigator or Principal Contact must belong to an existing SALT account, and the *partner* and *institute* must be the same as those given for the account. Otherwise, your proposal will be rejected when submitting it. Also note that a Principal Investigator must belong to a SALT partner, so that you mustn't choose "Other" as the partner in this case.

After having filled out the form completely, you may notice a subtle change in the navigation tree. Whereas the proposal as well as the investigator node were coloured red before, they are now coloured black. The reason for this is simple: A tree node is coloured red whenever its form or any of the forms for its descendant nodes is filled in incompletely. In addition you may have noticed that form fields which require input are highlighted in red. If a form component has no content but isn't highlighted, it doesn't necessarily have to be filled in. (As it seems, from time to time the tree indicates missing information, although all is complete; so if a node is read and you absolutely can find no reason for it, the tree might be wrong and you might be right. Use validation (discussed below) to make absolutely sure whether your proposal is complete.)

3.3 Targets

In the preceding section, the general mechanisms for adding elements to your proposal was explained, and you can use these to add a target. So right-click on the Targets tree node or in the Targets table (which you see after selecting the Targets tree node) to go about this business. See Figure 14 for an example of a target form.

While there is nothing to prevent you from using a *target name* like "Target 1", *you should never do this*. Use the real target name instead. The reason for this is twofold; targets are re-used in the SALT database (see below), and your observational data might be used for the Virtual Observatory at some stage. The latter clearly suggests to use a commonly accepted target name.

The *Target type* can be chosen from a list of types. If you feel that this list really doesn't cover your target, opt for "Unknown". As the *target size* may be a useful piece of information for the data reduction pipeline when reducing your observational data, you are asked for it even though it is of no concern for the

observation itself.

Targets can be broadly divided into two classes, sidereal and non-sidereal targets, and you can choose either of the two by means of a combo box. The movement of a sidereal target can be taken to be linear. Hence it can be described by providing its position (given as the right ascension (*RA*), declination (*Dec*) and the *equinox*) and, only if the target is moving, the *epoch* and a (constant) change per time in the right ascension ($\Delta RA/\Delta t$) and in the declination ($\Delta Dec/\delta t$).

The movement of non-sidereal targets, on the other hand, is non-linear and must be described by providing a file with a list of times and corresponding target positions and velocities. However, this is beyond the scope of this tutorial.

Both the minimum and maximum *magnitude* must be supplied for a target, even if the two are the same.

In case of a periodic target, you might want to provide a *periodic target ephemeris*. If so, you need to supply a heliocentric Julian *date*, the *period* at that date and optionally the rate of change for the period (*Pdot*). You can show or hide the periodic ephemeris data by clicking on the respective link ("show" or "hide"). You can only hide the data if no data has been provided.

There are several guidelines for the *finding charts*, which are used during the acquisition of your target:

- A finding chart must show black sources on a white background.
- It must have a size of $10' \times 10'$. If you need to provide more accurate information, use additional finding charts (blow-ups) for it.
- The size must be shown, for example by a bar displaying its length in arcminutes.
- The finding chart must contain the Principal Investigator and the target name.
- The orientation of north and east must be clearly marked.
- The band of the image (e.g., K-band, R-band, DSS) must be specified.
- For example, in imaging if the target lies in the centre of the finding chart, it might fall in the CCD gap. Hence the target position must be clearly marked on the finding chart.
- While colours may be useful on screen, bear in mind that all finding charts are printed as greyscale images.
- Any other observation mode dependent information, such as reference stars or the position angle, must be included.

Finding charts should usually be added to the target information. However, if there is more than one acquisition for a target and if a finding chart is to be used for a subset of these acquisitions only, it should be added to the acquisitions which use it.

You can add or remove *finding charts* by right-clicking in the finding charts table, as you know from the Investigators or Targets table.

3.4 Blocks

According to SALT terminology, a *block* is the smallest schedulable unit of a proposal. This means that all the content of a block will be observed in one go. In principle, a block may contain more than one observation, but you should group two or more observations together in a block only if there is a reason why they have to be observed without any other observation between them. So in practice, you'll usually end up with a single observation per block, which is perfectly fine.

It should come as no surprise to you that you can add a block to your proposal by right-clicking on the Blocks tree node or in the Blocks table (shown when selecting the Blocks tree node). Figure 15 shows the form for entering the block information. As usual, we'll go through the form step by step.

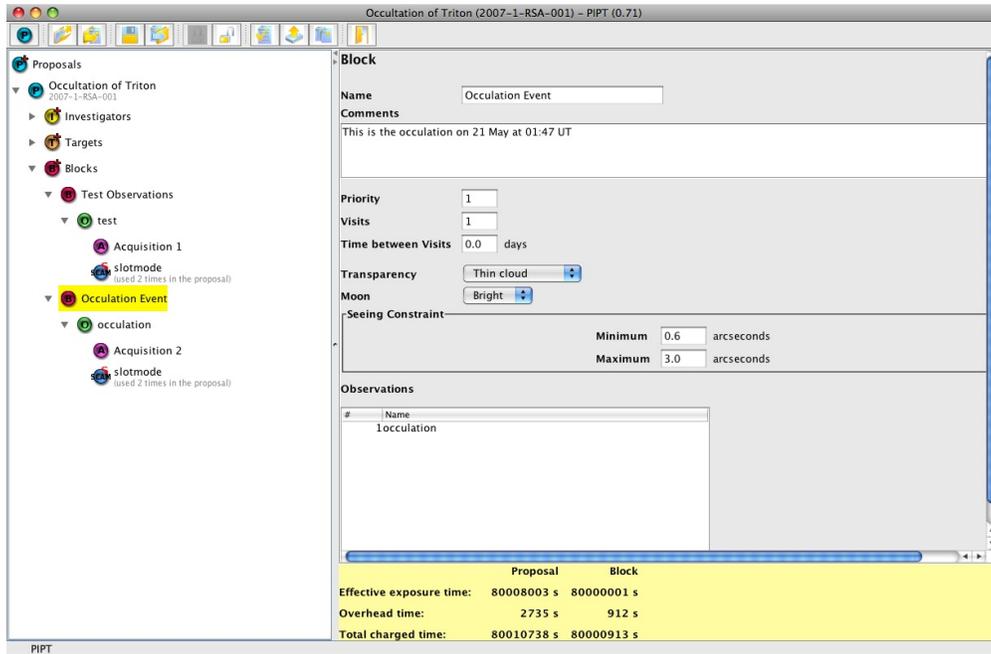


Figure 15: The form for defining a block.

It is completely up to you what to choose as the *name* of the block, but you make everybody's (including your own) life easier if you choose a meaningful one. So, for example, including the target name of the target observed in the block might be a really good idea.

If you feel that the SALT Astronomer should know about something when planning or attempting to observe your block, you should add respective *comments*). An example would be

Two visits per night (east & west tracks). 14 night campaign. Observe for total length of track, even if >3000s.

You might want to indicate that some of your blocks in a proposal are more important than others so that if there is a lack of time these rather than the other blocks should be observed. This may be indicated by setting a *priority*. But beware: *The higher the number in the priority the less important is the block!* Hence the priority value for the most important blocks will be 0.

The number of *visits* denotes the number of times you want to have the block observed. You have to specify the *time between* (consecutive) *visits*. "0" is a perfectly valid value if the time gap doesn't matter or if there is one visit only anyway. Obviously you might feel that a single number doesn't do justice to your needs, and if so you ought to add more detailed instructions to the comments, as it was done in the example above.

You also have to specify the *transparency of the sky* and the brightness of the *Moon*. And if you wonder what exactly is meant by a bright, grey or dark Moon, have a look at Table 1.

Whereas the *maximum seeing* for your observation is important, the *minimum seeing* usually isn't and you can just use the suggested default value of 0.6 arcseconds.

Finally, there obviously needs to be at least one observation in your block, and that is why the form finishes off with an observations table. You may add arbitrarily many observations by right-clicking in the table or the navigation tree. The observations will be performed in the order you define them.

Phase	Above horizon?	Brightness
< 5 %	yes	dark
5 % ... 50 %	yes	grey
> 50 %	yes	bright
any	no	dark

Table 1: Formal definition of the Moon brightness, as used in the PIPT. The brightness depends on the phase and on whether the Moon actually is above the horizon.

The screenshot shows the PIPT web interface for defining an observation. The sidebar on the left displays a tree view of proposals and blocks, with the 'occultation' block selected. The main form area contains the following fields and options:

- Observation Name:** occultation
- Minimum Useful Exposure Time per Visit:** 2000.0 seconds
- Time/Phase constraints:** No Constraints
- Instrument Configurations:** A table with one row: # 1, Name 1slotmode
- User Notification:** When raw and reduced data is available from the ftp server
- Reduction Documentation Format:** HTML

At the bottom of the form, a summary table shows time allocations:

	Proposal	Block	Observation
Effective exposure time:	80008003 s	80000001 s	80000001 s
Overhead time:	2735 s	912 s	12 s
Total charged time:	80010738 s	80000913 s	80000013 s

Figure 16: The form for defining an observation.

3.5 Observations

An observation can be added by ... Oh well, you probably can figure that out yourself by now. When you create a new observation, the corresponding acquisition will be created as well (but we'll cover the acquisition in the next section). Figure 16

As for blocks, choosing a meaningful *name* for your observation is a good idea. When defining an instrument configuration (which we'll cover later on), you have to specify the exposure time. But, alas, the world isn't perfect and it might be that the time available is less than the time you've requested. In such cases, it is useful for the SALT Astronomer on duty to know whether attempting your observation still would yield some useful result, and that is why you have to provide a *minimum useful time*.

In case your observation can be carried out at specific times or phases only, choose the options "Time Restrictions" or "Phase Constraints" from the *Time/Phase Constraints* combo box. In both cases you'll be presented with a table. As usual, table rows can be added and removed by right-clicking in the table. You can edit a value by (left-)clicking in its table cell.

The format of time restrictions depends on the language used by your operating system. Rather than guessing what it might be, click in a table cell for editing and subsequently click on the little up or down arrow next to the text field. The current date and time (in the required format) will be displayed, at least if

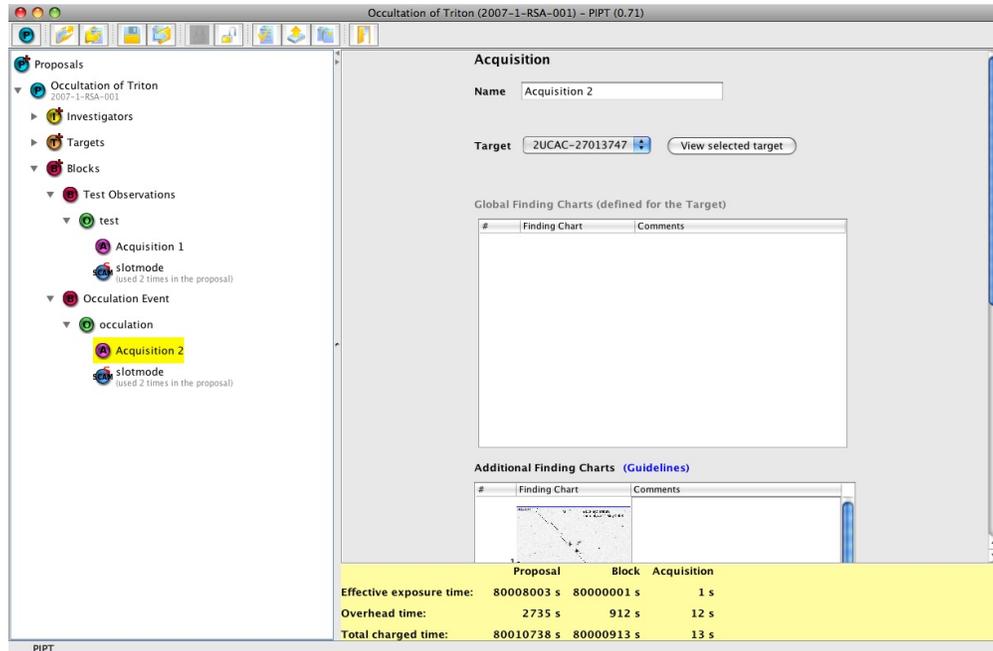


Figure 17: The form for defining an acquisition.

the text field was empty before. You may either edit the date and time by hand or you may use the arrows for changing it.

A phase constraint, on the other hand, is just a number between 0 and 1. Using phase constraints makes sense only if a periodic target ephemeris is defined for the target.

You can define an arbitrary amount of time restrictions or phase constraints, but not both of them at the same time.

The table of instrument configurations display the science configurations, but not the acquisition. You can add or remove configurations in the usual way by right-clicking in the table or the navigation tree. The instrument configurations are executed in the order you define them.

Of course, after your data have been taken, you will be informed, and you can choose when this *user notification* shall take place. If you opt for "When raw and reduced data is available on the ftp server", you will receive an email as soon as your data are reduced by means of the SALT data reduction pipeline and are put on the SALT ftp server. Otherwise, you will already be informed when the raw data are available. You will be notified again when you can download the reduced data. Unless there is good reason not to so, you should stick to the default and choose the first option.

The *reduction documentation format*, as produced by the SALT data reduction pipeline, can be either HTML or plain ASCII text. Again, it is a good idea to use the default and opt for the HTML version.

3.6 Acquisitions

The first step in every observation obviously must be to find the target and point the telescope to it. Hence it comes as no surprise that every observation must contain an acquisition (see Figure 17). For your convenience, you can (and actually have to) give it a *name*. The standard naming mantra applies: Meaningful names should be preferred.

As the acquisition is all about pointing to the target, the desired *target* must be specified. You can choose it from the list of targets you've already composed for the proposal. If you want to review the definition of

the chosen target, click on the button next to the target combo box and you will be led to the respective form.

It has been pointed out above already that finding charts may be defined for a target or an acquisition. All finding charts for the target and the acquisition are shown in the acquisition form, but only those for the acquisition can be edited. (That's why the table for the finding charts defined for the target are greyed out.) At least one finding chart must be provided.

If your target is very faint and isn't likely to be visible in the acquisition image, you might want to define a *blind offset*. To this end, click on the "show" link and enter the *magnitude*, the coordinates and (if necessary) its sidereal movement of a brighter source B, as well as the *north offset* and *east offset* of your target relative to B.

Each acquisition is performed with Salticam, and hence the definition of an acquisition includes a Salticam configuration. However, most of the parameters are fixed, and you can only fiddle with the *filter* and the *exposure time*. See the Salticam section for more information on these.

Finally, a word of caution: Never rely on the acquisition for your science. The acquisition image is only meant to allow the SALT Astronomer to position the telescope properly, and for example it might happen that your target happens to end up in a CCD gap while the acquisition image is taken!

3.7 Instrument configurations

We've finally reached the part of the proposal where you provide the nitty-gritty details of the actual observation. Which filters should be used? How long do you want to expose? Do you want to do spectroscopy? Polarimetry? And so forth, and so forth.

The main decision obviously is which instrument to use. The main ones are Salticam and RSS, and we'll cover both in the following.

Each observation must involve at least one instrument, and so (in addition to the acquisition) you have to provide at least one instrument configuration. As you might guess, instrument configurations can be added by right-clicking in the instrument configurations table in the observation form or by right-clicking in the navigation tree.

3.8 Salticam configurations

The Salticam detector (Figure 18 and `reffig:salticamImage`) features two rectangular CCD chips, which are separated by a vertical gap of 1.5 mm. Each chip has two amplifiers. The frame transfer boundary runs horizontally and so does the slot for slot mode observations. You can find detailed information on <http://www.salt.ac.za/telescope/instrumentation/salticam/> and <http://www.salt.ac.za/telescope/instrumentation/salticam/specifications/>.

You can use the detector in three different modes: In normal mode, the full CCDs are exposed. In frame transfer mode, only the upper half of the chips is exposed. After the exposure, the electrons are moved to the lower half and are read out while the next exposure is done. This allows for a time resolution of a few seconds.

Even higher time resolutions can be achieved in slot mode. Here only a 144 pixel wide slit adjacent and parallel to the frame transfer boundary is exposed, and as in the case of frame transfer the electrons are moved to the lower half of the chips, which takes about 15 ms. During an exposure the electrons in the lower half are moved 144 pixels further to the detector. So the lower half usually contains the electrons of several exposures, separated by 144 pixel wide gaps.

Before we can give the time resolutions for frame transfer and slot mode, we need to mention (pre-)binning. Neighbouring pixels on a CCD chip can be grouped together into a kind of super-pixel. The electrons located in such a super-pixel are read out together, which reduces the overall readout time. Unfortunately, it also reduces the resolution.

Any number of pixels between 1 and 9 can be binned both in rows and in columns, but usually the number is the same for both. You'll normally choose a binning of at least 2×2 .

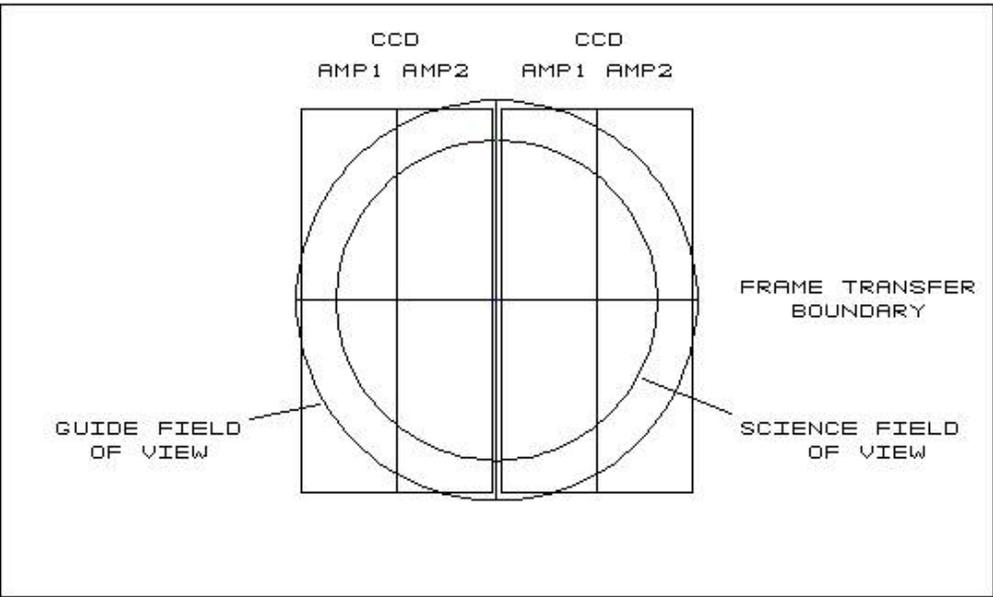


Figure 18: The CCD chips in the Salticam detector.

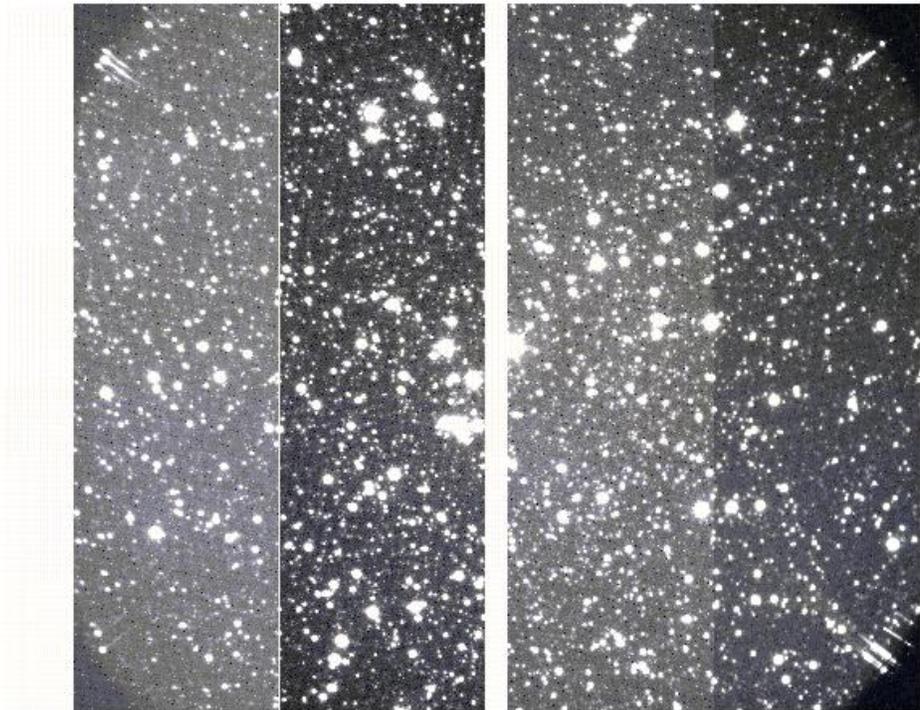


Figure 19: Example of a Salticam image. You can clearly see the two CCD chips. As different bias levels were used, you can also see that there are two amplifiers per chip.

Binning	Frame transfer (sec)	Slot mode (sec)
1 × 1	15.90	0.70
2 × 2	4.70	0.30
3 × 3	2.80	0.20
4 × 4	2.00	0.15
5 × 5	1.70	-
6 × 6	1.40	0.08
7 × 7	1.30	-
8 × 8	1.10	0.07
9 × 9	1.10	0.05

Table 2: Minimum frame transfer and slot mode exposure times for the valid binnings.

Gain	Readout speed	e/ADU	Typical use
faint	slow	1.00	default for faint target
faint	fast	1.55	faint target and high time resolution
bright	slow	2.50	unusual
bright	fast	4.50	bright target

Table 3: Electron ADU ratio and typical use for the various combinations of gain and readout speed. A faint target has a magnitude of 18 or higher.

Table 2 shows the achievable time resolutions for frame transfer and slot mode. Note that an exposure time mustn't be less than the time resolution. Also note that for slot mode the binnings 5×5 and 7×7 are forbidden. This makes sense, as the slot width (144 pixels) can be divided neither by 5 nor by 7.

You may choose between fast and slow readout for the detector. The former entails a higher readout noise, but this may be completely acceptable if your target is sufficiently bright.

Table 3 lists the electron to ADU ratio for the various combinations of gains and readout speeds, and states what the typical use for the combinations would be.

By default, the top of the CCD chips points due north, so that the frame transfer boundary lies in east west direction. However, quite often this proves inconvenient. A typical example would be a slot mode observation of a target and a reference star. Here you have to ensure that both the target and the reference star lie in the slot – and this will usually imply that you have to rotate the detector by some angle.

This angle is known as the position angle and is measured from north towards east. In other words, a position angle of 0° is equivalent to north, a position angle of 90° is equivalent to east and so forth. For SALT, the position angle is taken to be the angle of the slot, so that a position angle of 0° actually means that the slot lies in north-south direction. Figure 20 shows an example. It should be stressed that the default position of the detector does *not* correspond to a position angle of 0° , but to an angle of 90° .

Another potentially mind-boggling feature of a Salticam configuration is the filter arrangement. Fundamentally, you have to provides a filter sequence, which defines the order in which filters should be used and how long the exposure time should be for each filter. The exposure time denotes the length of time for which the shutter is open for a single exposure. It doesn't include any overhead such as the time required for reading out the CCD chips or moving to the next filter. More pragmatically, it is the time actually spent on obtaining science data (per exposure). An example of a filter sequence might be:

$$U (3 \text{ sec}) - B (5 \text{ sec}) - V (4 \text{ sec})$$

The available filters comprise the standard Johnson UBVRI filters, a clear filter, a filter with a central wavelength of 340 nm and a FWHM of 35 nm, and a filter with a central wavelength of 380 nm and a FWHM of 40 nm.

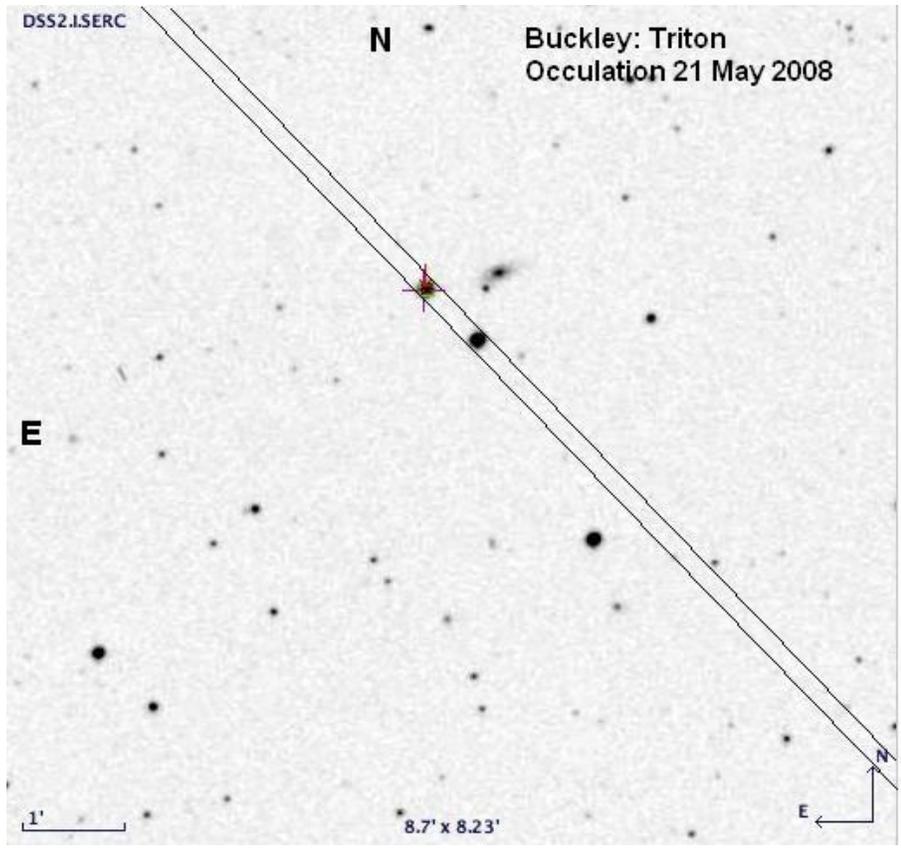


Figure 20: A finding chart for a slot mode observation. In order to cover both the target and the reference star, the slot must have an angle of 45° relative to north. In other words, its position angle must be 45° .

Now you might want to take more than one exposure for each filter. If so you have to set the iterations per filter to the desired number of exposures. So, for example, if the iterations per filter is set to 3, our filter arrangement becomes

U (3 sec) – U (3 sec) – U (3 sec) – B (5 sec) – B (5 sec) – B (5 sec) – V (4 sec) – V (4 sec) – V (4 sec)

Alas, iterations per filter aren't supported by Salticam yet, and hence they will always be 1. However, you can specify the number of iterations of the filter sequence. Sticking to our example and assuming the number of iterations of the filter sequence is 4, we end up with the filter arrangement

UUUBBBVVV – UUUBBBVVV – UUUBBBVVV – UUUBBBVVV

When defining your filter arrangement, you should keep in mind that each filter change takes about 15 seconds. Many filter changes thus imply a significant overhead, i.e. telescope time which isn't used for obtaining data. Another important source of overhead time naturally is the detector readout time, unless you are using frame transfer or slot mode.

The exposure times as well as the overhead times (and the resulting total requested time, which is just the sum of the two) are displayed underneath the form. In case of a Salticam configuration, the times are given per iteration of the filter sequence.

The times for a block are given per visit. They essentially are obtained by adding up the respective times for the acquisitions and instrument configurations in the block, but there is another important contribution to the overhead: Pointing SALT to a new target takes about 15 minutes, and these are added to the block overhead.

The times for the proposal result from adding up the respective times of the blocks; so there is no surprise here.

A healthy dose of distrust is in order when looking at the overheads: First, the given overheads are to be understood as rough estimates only. Second, there is at least one known bug: If you consider a filter sequence of one filter only, the readout times won't be multiplied by the number of iterations of the filter sequence when the block and proposal overheads are calculated. Also note that the overheads calculated in the simulator tools may differ from those calculated in the PIPT.

This does *not* mean that you should ignore the overheads. They can be a strong hint that a filter arrangement is ineffective, as it requires far too much overhead, perhaps as there are unnecessary filter changes.

We may now finally turn to the form for defining a Salticam configuration. As (almost) always you are asked to provide a (meaningful) *name* for the configuration. At the moment, neither a *guide star* nor a *guide method*, so don't provide a guide star and choose "None" as the guide method.

The filter arrangement is defined by giving a *filter sequence* in the respective table and by specifying the *number of iterations of the filter sequence*, as described above. Each row in the filter sequence table contains a *filter* and the *exposure time* for that filter. As usual, rows can be added by right-clicking in the table. In principle, you could also specify a number of *iterations of a filter in the filter sequence*, but the value of it is fixed to be 1.

The *readout mode*, *prebinned rows*, *prebinned columns*, *gain* and *readout speed* have been explained above.

As currently the point spread function, background and stray light vary rapidly, defining a signal-to-noise ratio would be meaningless. For this reason, the *minimum signal-to-noise ratio* is fixed to be 0.

You may tell Salticam to use certain areas ("*CCD windows*") of the CCDs only, but this is beyond the scope of this tutorial.

While you can launch the Salticam Simulator Tool from within the Salticam configuration form, you are likely to run into memory problems. A sign of these is that the simulator is completely unresponsive when you click a button. Thus launching the simulator as a separate application is recommended, even though this means that you have to copy values by hand.

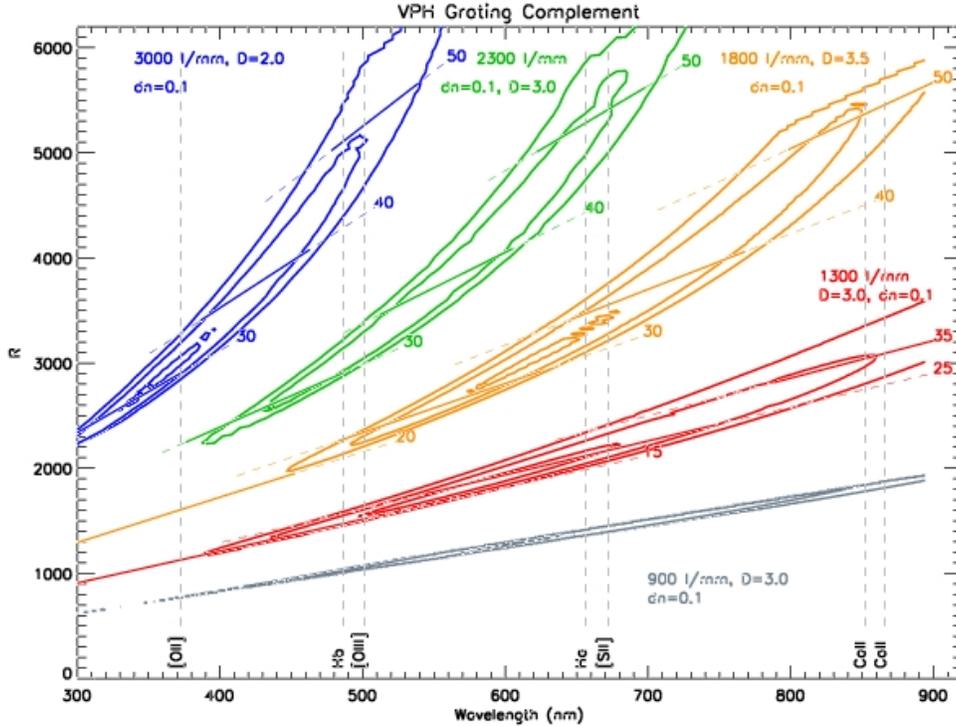


Figure 21: Efficiency curves for the VPH gratings used in RSS. The wavelength range for various grating angles are indicated as well.

3.9 RSS configurations

The Robertson Stobie Spectrograph (RSS), which is named after the late Dr Robert Stobie, a director of the SAAO and the first chairperson of the SALT board, can be used in three different modes.

See <http://www.sal.wisc.edu/~ebb/pfis/observer/> for an observer's guide for RSS. (RSS is called PFIS in the guide, which was its former name.)

3.9.1 Imaging

While RSS is not primarily intended as an imaging instrument and in particular isn't optimised for broad-band imaging, narrow-band imaging can be performed by using one of the Fabry-Perot filters.

3.9.2 Spectroscopy

Volume phase holographic (VPH) gratings allow you to cover a long wavelength range efficiently by turning the grating relative to the incoming light beam. In addition to a standard surface relief grating with 300 g/mm (where g/mm stands for "grooves per mm"), RSS contains five such VPH gratings (with 900 g/mm, 1300 g/mm, 1800 g/mm, 2300 g/mm and 3000 g/mm). See Figure 21 for their properties.

As the maximum of a grating efficiency usually is reached if the angle relative to the grating is the same for the incoming and outgoing light beam, it is clear that it must be possible to rotate the RSS camera. However, due to technical constraints, there are only 133 possible positions for the camera, which in SALT terminology are known as camera stations. The corresponding camera angles range from 0 to 100 degrees. The grating angle also affects the resolution; the resolution increases with an increasing grating angle.

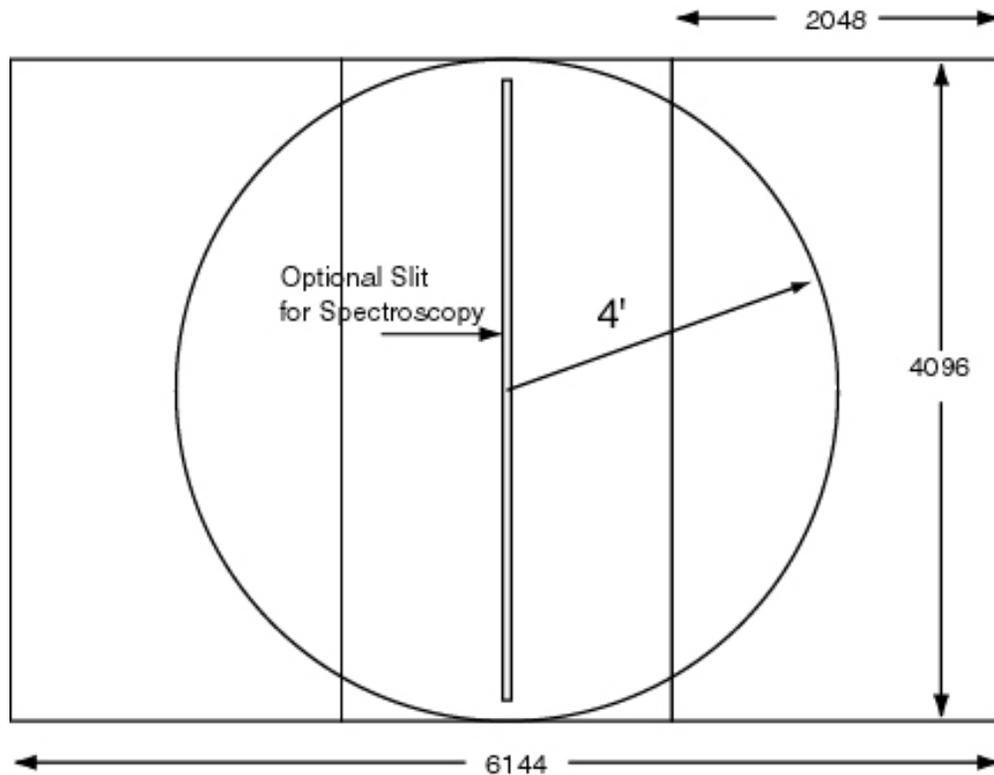


Figure 22: The CCD layout of the RSS detector.

In order to exclude higher orders, an order blocking filter is used. Plots showing the transmission curve for these filters are linked from <http://www.sal.wisc.edu/~ebb/pfis/observer/spectroscopy.html>.

Spectroscopy can be performed with a longslit, a slit mask for multi object spectroscopy (MOS) or polarimetric mask. For the former, you have to choose from a fixed set of slits, the available widths being 0.6 mm, 0.9 mm, 1.2 mm and 1.5 mm. For the latter, you have to use the Slit Mask Tool to create the required slit mask. This as well as the topic of polarimetric masks is beyond the scope of this tutorial, however.

The choice of the slit width is a trade-off between resolution and throughput. A narrow slit gives a good resolution, but at the same time lets through less light. The slit throughput actually doesn't depend only on the slit width, but on the seeing as well. As one might imagine, a better seeing leads to a greater throughput.

You should bear in mind that there are two CCD gaps in the RSS detector, as illustrated in Figure 22. Their locations are indicated on the spectroscopy tab of the RSS Simulator, which also tells you the wavelength range covered by the detector and the resolution for your instrument settings (Figure 23).

3.9.3 Fabry-Perot

There are four different resolution modes for a Fabry-Perot observation with RSS: tunable filter (TF), low resolution (LR), medium resolution (MR) and high resolution (HR). Both TF and LR use a single etalon and an interference filter for filtering out the desired interference order (and thus wavelength). A list of the interference filters can be found at <http://www.sal.wisc.edu/~ebb/pfis/observer/FilterData.htm>. For MR and HR two etalons are used; the LR etalon and the interference filter select the desired interference order of the MR or HR etalon.

When planning your observation, you should make sure not to choose a higher resolution than necessary, as the total observing time varies as the square root of the resolution. For your convenience, Figure 24 shows

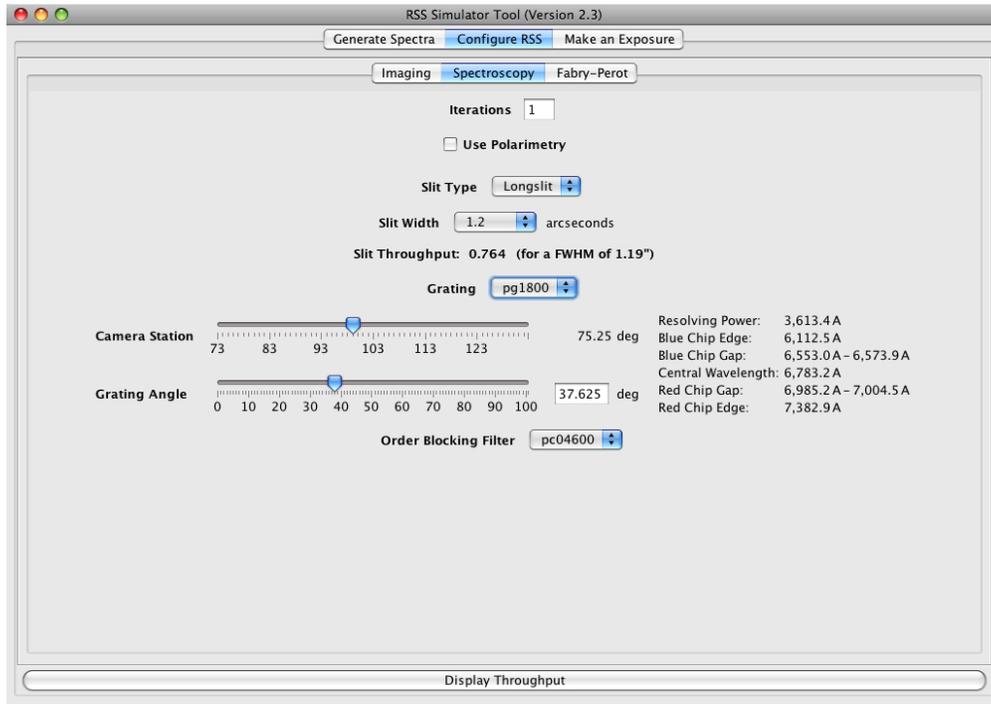


Figure 23: The spectroscopy tab of the RSS Simulator Tool.

the resolution curves for the various resolution modes discussed above.

Whereas a whole sequence of filters could be defined for a Salticam configuration, an RSS configuration can contain a single filter only. However, a configuration may very well contain various separate steps (and thus exposures). An example would be a polarimetric observation involving several wave plates. You can ask RSS to repeat the whole sequence of steps several times. The number of such repetitions is known as cycles.

You may also request a number of detector iterations, i.e. an number of exposures made during each step in the sequence. Or, to be more precise, you could if the feature was implemented at the telescope already. But it isn't and so you are stuck with the value 1 for the detector iterations.

To give a simple example, imagine your configuration contains two wave plates (let's call them "A" and "B"), and you request 3 cycles and 4 detector iterations. Then the sequence of exposures will be

AAAABBBB – AAAABBBB – AAAABBBB

What has been said about the exposure time, position angle, (pre-)binning of rows and columns, the gain and the readout speed when discussing Salticam remains true for RSS as well. Concerning readout modes, RSS has two more modes on offer, namely shuffle and drift scan, but for the time being these should be ignored.

Let us turn to discussing the RSS configuration form. The *name* is the name to use for the configuration. The *cycles* and the *position angle* have been explained above. As for Salticam, currently neither a guide star nor a guide method are used and hence you should define no guide star and choose "None" as the guide method.

The *RSS modes* are the modes explained above. You may define the settings for your desired mode by choosing the mode from the respective combo box. Note that each modes comes as a version with and without polarimetry.

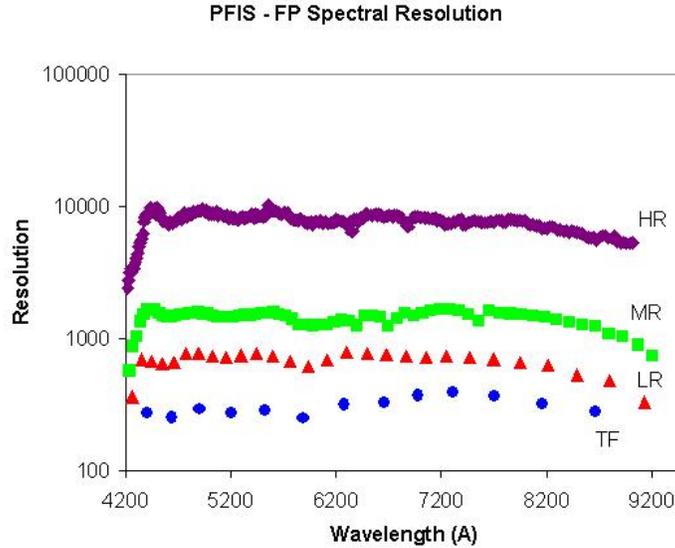


Figure 24: Fabry-Perot resolutions for RSS.

In imaging mode, you just have to specify a *filter*.

In spectroscopy mode, you have to define the slit type (long slit (characterised by a *slit width*), MOS (characterised by a *slit mask file*) or none), the *grating*, the *camera station* (or, equivalently, the *camera angle*), the *grating angle* and the *order blocking filter*. All of these have been discussed above. The PIPT doesn't constrain the combinations of values you enter for them and hence makes it fairly easy to come up with complete nonsense. In order to avoid this pitfall, *always use the RSS Simulator Tool to figure out what values to use*.

In Fabry-Perot mode, you must specify an interference *filter* and the resolution (by choosing the corresponding *etalon configuration*). You may also define an *etalon pattern*, but this won't be discussed any further here.

Irrespective of the mode, if you opt for doing polarimetry, in addition you have to supply a wave plate pattern. You may do this either by choosing a predefined pattern or by defining your own pattern. You can do the latter by choosing "User-defined" from the polarimetry pattern combo box.

At the current stage, don't worry about the *exposure type*; just choose "Imaging". The *exposure time*, *detector* (or readout) *mode*, *detector iterations*, *prebinned rows*, *prebinned columns*, *gain* and *readout speed* have been discussed above.

You may tell RSS to use a specified part ("*detector window*") of the CCD, but this is beyond the scope of this tutorial.

The *focus position* shouldn't be changed, so don't worry about it.

Finally, as for Salticam, defining a signal-to-noise ratio wouldn't make much sense right now, and hence its value is fixed to be 0.

While you can launch the RSS Simulator Tool from within the RSS configuration form, you are likely to run into memory problems. A sign of these is that the simulator is completely unresponsive when you click a button. Thus launching the simulator as a separate application is recommended, even though this means that you have to copy values by hand.

4 Submitting your proposal

When you've finished your proposal, you need to submit it. The submission wizard for doing this can be invoked by clicking on the Online > Submit menu item.