

Nodule Mapping with MAX

1. Answer for MAX Installation Questions.

The best way to know if the installation is correct is to enter the following command:

```
./max.pl --help
```

If it shows the in-line help text (over 800 lines of text), the installation is correct. If some of the Perl modules are missing, you will see errors that look like...

```
Can't locate Math/Polygon/Calc.pm in @INC (@INC contains: /usr/lib/perl5/...  
/usr/lib/perl5/5.8.0 /usr/lib/perl5/site_perl/5.8.0/i386-linux-thread-multi ...
```

```
BEGIN failed--compilation aborted at ...
```

MAX is written in Perl.

2. Additional Perl Modules Needed for MAX.

It looks like there are some Perl modules that need to be installed. And, yes, you can get them from CPAN (cpan.org):

```
XML::Twig
```

```
Tie::IxHash
```

```
Math::Polygon::Calc
```

(These are referenced by the "use" statements in the Perl code.) After installing these 3 modules, you should be able to get the correct output when you type `./max.pl --help`.

>I downloaded XML-Twig-3.32.tar.gz, I'm using version 3.16, but I don't think this will be a problem.

Twig might have some dependencies; if so, you'll have to install some other modules. For example, if you see an error message that says that it couldn't find XML/Xpath.pm, that means that you would need to download and install XML::XPath also.

>Tie-IxHash-1.21.tar.gz and Math-Polygon-1.00.tar.gz.

These are the same version that I'm using.

3. Install Additional Perl Modules in User Specified Directory Instead of the System Directory

You can actually install the Perl modules anywhere -- for example, in your home directory, but maybe even better is to install them in MAX's directory. This article... <http://tnerd.com/2008/10/26/perl-how-to-install-perl-modules-in-few-quick-steps/> looks like it has a pretty good procedure for doing this using CPAN, but it does look a little complicated. I've never done it quite this way; instead, I just install modules manually. If you want to do it manually, read the section of this article under "Manual installation of the module as a normal user under home directory". Before doing this, you should decide on a directory that will hold all the Perl modules. Then read this section: "set the environment variable PERL5LIB pointing to the home directory" to tell Perl where the new modules will be located.

4. Using MAX

MAX will analyze the XML files and will perform nodule matching. I believe that the XML files that you get from us are in the form of a single file that contains the unblinded reads from 4 LIDC sites merged into one file. If so, here's an example of how you would run MAX to do the matching: `max.pl --fname mergedfile.xml --skip-num-files-check`

`--pixel-size=0.7 --slice-spacing=1.0 --xml-ops=none` or since MAX lets you abbreviate most of the command line options, this also works... `max.pl --fname mergedfile.xml --skip --pixel=0.7 --slice=1.0 --xml-ops=none` A couple of comments:

* You might need to include a path on MAX depending on how and where it was installed.

* You might need to include a path to the merged file. But you will probably run MAX from the directory that contains the file.

* Instead of the values shown above, you will have to get the "true" pixel and slice spacing for the series that corresponds to the merged file. ****MAX will not work properly unless you have the correct values for both**** You can get the values from looking at the DICOM files. Note that you'll have to look at two adjacent files to get the slice spacing; there is no single DICOM tag that gives this value.

* Just for testing, I recommended that you run MAX with "`--xml-ops=none`" as shown above which prevents any XML files from being written. We can talk about this later. So for now, all the results (along with A LOT of other info) will be printed to the screen.

5. slice-spacing

Error (6501) results if the slice spacing is wrong. Here's one way to get the slice spacing from the DICOM images: The most reliable DICOM tag to use is "Image Position Patient" (0020,0032). A typical dump of this tag from an image looks like this:

0020 0032 34 // REL Image Position
Patient/-209.800003-193.600006-72.199997

It is a Type 1 tag, so it's always going to be present and should be reliable. Since CT images are axials, the z position of each image is the final coordinate number: -72.2mm in this case. The most reliable way of doing this is to extract the z coordinates from all the images, sort them, and then see what the delta-z value is.

(Watch out when parsing these lines: The "\" can cause problems if the numeral immediately following it is a 0 (zero). In many programming/scripting situations, "\\0" represents a null which could signal the end of the string!!)

6. pixel-size

Here's a dump from a DICOM file:

0028 0030 30 // IMG Pixel Spacing//007.421880e-01\007.421880e-01 Once again, watch out for the "\"!! Note that this tag gives the spacing in both in-plane directions, but our pixels always seem to be square, so we don't need both numbers.