

# 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](http://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.