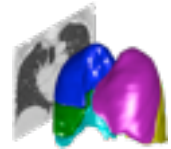


# Pulmonary Toolkit



<http://code.google.com/p/pulmonarytoolkit/>

## Installing the Pulmonary Toolkit

Version 1.2

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### Overview

This tutorial covers installing the software you need to run the Pulmonary Toolkit.

### Topic covered

- Installing Matlab and the Matlab Image Processing Toolbox
- Installing a C++ compiler
- Installing a Subversion (SVN) client
- Downloading the Toolkit using SVN
- Updating the Toolkit using SVN

### Requirements

A general understanding of the concepts of version control, Matlab and C++ compilers. You will need a licence for Matlab version R2010b or later, and the Image Processing Toolbox.

# 1. Installing Matlab and the Matlab Image Processing Toolbox

The Pulmonary Toolkit requires **Matlab version R2010b** (also known as release 7.11) or later. The add-on **Matlab Image Processing Toolbox** is also required.

If you don't currently have Matlab installed

Matlab is available for Windows, Linux and Mac. Your IT department may have Matlab licences which you can use on your own machine. You will first need to install Matlab and the Image Processing Toolbox from the Mathworks website (<http://www.mathworks.co.uk>) - this may require you to create a free Mathworks account. You then need to link your account to the licence keys or licence servers provided by your institution.

## Installing the Pulmonary Toolkit

If you already have Matlab installed

You can check the Matlab version by typing

```
>>ver
```

in the Matlab command window. You should see something like

```
-----  
MATLAB Version: 8.2.0.701 (R2013b)  
Operating System: Mac OS X Version: 10.8.5 Build: 12F45  
Java Version: Java 1.7.0_11-b21 with Oracle Corporation Java  
HotSpot(TM) 64-Bit Server VM mixed mode  
-----  
MATLAB                               Version 8.2           (R2013b)  
Image Processing Toolbox              Version 8.3           (R2013b)
```

If your Matlab version is less than 7.11, you will need to update. Click on the **Help** menu, and **Check for Updates**.

If your licence is due to expire, you can check for licence updates. In the current version, this is found on the **Home** tab. Click the arrow underneath **Help**, select **Licensing** and click **Update Current Licenses**.

## 2. Installing a C++ compiler

Some parts of the Pulmonary Toolkit require a C++ compiler. Unfortunately, Matlab does not provide a built-in C++ compiler, so you will have to install one yourself. Free compilers are available for all operating systems - see details below.

If you do not install a compiler, some parts of the Toolkit will be very slow, and other parts will not function at all.

### Windows

Windows users can install the free Microsoft Visual Studio Express at <http://www.visualstudio.com/downloads/download-visual-studio-vs>

### Mac

Apple provide a C++ compiler as part of its free **Command Line Tools**. You can download them through from the Apple developer site here: <http://developer.apple.com/downloads>. You may have to create a free developer account.

Alternatively, you can download the tools using XCode, if you have this installed. XCode can be installed for free from the Apple App Store. To install the Command Line Tools, launch XCode and go to the **XCode** menu, then select **Preferences, Downloads** and click **Install** next to the **Command Line Tools**. Some more information is available here: <http://stackoverflow.com/questions/9329243/xcode-4-4-and-later-install-command-line-tools/9964905#9964905>

Warning: there is an issue using the compiler if you are using XCode 5. You may need to modify the mexopts.sh file. See this article for details: <http://www.mathworks.com/matlabcentral/answers/103904>

### Linux

You probably already have the gcc compiler installed - you can check where it is installed by typing the following in a terminal window:

```
>>which gcc
```

### Verifying your C++ compiler (optional)

Once you have a C++ compiler installed, you can check that Matlab can find the compiler. To do this, launch Matlab and type the following:

```
>>mex -setup
```

Matlab will attempt to find your compiler. If it successfully finds one or more compilers, they will be listed in the command window. Press the number of the compiler you wish to use.

### Compilation problems

The first time you run the Pulmonary Toolkit (see Tutorial 1), it will attempt to run the above command to ensure the C++ compiler is correctly set up. Then it will attempt to automatically compile the C++ files it requires. If there are problems, errors will be reported to the command window. Compilation be attempted a second time when you next run the Toolkit, but if this fails again, then further compilation will not be attempted. Once you fix the compiler you can force the Pulmonary Toolkit to recompile the files using the following commands:

```
>>ptk_main = PTKMain;  
>>ptk_main.Recompile;
```

### 3. Installing a subversion (SVN) client

The easiest way to download the Pulmonary Toolkit is by installing a **subversion client**. This allows you to obtain the latest version of the Toolkit from the internet server where it lives. You can then easily keep your version up-to-date with new features and bug fixes.

There are a number of subversion clients (some free, some paid) for all operating systems.

#### Windows

Tortoise SVN is free and easy-to-use, and builds directly into Windows Explorer - <http://tortoisesvn.net>

Alternatively, SmartSVN has a free version (which is perfectly fine for normal use) and a paid-for version (more features). <http://www.smartsvn.com>

#### Mac

If you have installed the **Command Line Tools** (see Installing a C++ Compiler above), you will already have a command-line subversion client. You can also install subversion using MacPorts. However, you may find it easier to install another client with a graphical interface.

SmartSVN has a free version (which is perfectly fine for normal use) and a paid-for version (more features). <http://www.smartsvn.com>

Another alternative is SVNX, which is free but a little more confusing: <http://code.google.com/p/svnx/>

#### Linux

Linux users can install subversion from <http://subversion.apache.org/packages.html> or using

```
$ sudo apt-get install subversion
```

## 4. Downloading the Toolkit using SVN

### Using SmartSVN

- Open SmartSVN.
- From the **Project** menu, click **Check out**
- Choose **Quick checkout**
- For the URL, enter `http://pulmonarytoolkit.googlecode.com/svn/trunk/`
- For the Local Directory, choose where you want the Toolkit code to be stored
- Click **Finish** and follow any further prompts

### Using Tortoise SVN

- Using Windows Explorer, navigate to where you want the Toolkit code to be stored
- Right-click in the window and select **Tortoise SVN**
- Select **Checkout**
- For the URL, enter `http://pulmonarytoolkit.googlecode.com/svn/trunk/`
- Click **OK**

### Using a command-line subversion client

You can download the Toolkit into a folder called “pulmonarytoolkit” using the following command:

```
$svn checkout http://pulmonarytoolkit.googlecode.com/svn/trunk/  
pulmonarytoolkit
```

## 5. Updating the Toolkit using SVN

You can update the Toolkit at any time using your subversion client. Updating will obtain the latest changes to the code, including new features and bug fixes. Updating will preserve any changes you have made to the code on your machine.

```
$ svn update
```

### Using a SmartSVN

- Open SmartSVN.
- Select the Pulmonary Toolkit project from the “Welcome to SmartSVN” dialog.
- Click the “Update” button

### Using Tortoise SVN

- Using Windows Explorer, navigate to the folder showing the main folder of the Pulmonary Toolkit code (“pulmonarytoolkit”)
- Right-click on the main folder (“pulmonarytoolkit”)
- Select Tortoise SVN
- Select Update and follow the prompts

### Using a command-line subversion client

To update the Toolkit to the latest version, navigate to the main folder of the Pulmonary Toolkit code (“pulmonarytoolkit”)