

# Import of Patient Data

Importing Patient data from other systems (such as legacy systems) is possible in GECAMed. To do so, we have defined an [XML Schema](#), defining the syntax of XML files that can be imported into GECAMed. The current version of the XML schema is available here:

[n/a: No match]

The tricky part of the process consists in extracting the data from the legacy system. Be sure to respect the conditions of the XSD Schema. Check whether your XML file fits to the XSD. You can do this in GECAMed or simply use an online validator. There are a lot of online XML validators. E.g. you can search for “check xml to xsd online” at Google or use this one: [decisionsoft XSD validator](#)

For a better understanding how the XML files should look like, you can download this example: [GECAMed patient import example](#)

## **Please Note**

### **Quotations**

The elements' attributes' text must be separated with either apostrophes (*attribute\_name='attribute text'*) or quotation marks (*attribute\_name="attribute text"*). Make sure the attribute text doesn't contain apostrophes or quotation marks, respectively that they are escaped (escape apostrophes with *&apos;* and quotation marks with *&quot;*;). As you can see an ampersand (&) is used to escape quotation characters. Therefore you need to escape the ampersand itself if you want to use it in text values (escape ampersand with *&amp;*;).

### **One file per patient**

Even though our XSD specification would allow it, you can't put more than one patient in one single XML file. There must only be one patient per XML file. This is required by the import procedure, which goes through all import files in a directory and moves the ones that have been imported correctly into a subfolder. You can however select several files or a folder in the import procedure, so that more than one patient can be imported during an import run.

### **Attached Files**

If you want to import files that are attached to a patient you need to make sure that they are available at the place specified in the XML import file. You can define where to find a file in the XML (as you can see in the example *patient\_1.xml*) using the *filename*- and *filelocation*-tag. The *filename*-tag specifies the name of the file. If you want to put your files into a subfolder, like done in the example, you need to specify the path to the file in the *filelocation*-tag, starting at the folder of the XML file. E.g. if, like in the example, the file is called *medical\_finding.pdf* and the subfolder, the file is located at is called *files*, the file name must be *"medical\_finding.pdf"* and the filelocation must be *"/files/"*.

### **Referencing Physicians**

You can refer to physicians using the UCM code. If you do so, the physicians you refer to must already exist in the GECAMed system into which you import the patients.

### **Import the Data**

Once you have generated the XML files containing the patient data, you can perform a *test-run* of the import process to check whether everything is okay or not, and do the actual import. More information regarding the import process can be found in our user manual:

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