



Heart Fenics Graphical interface

User manual and developer manual

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Motivation

This interface is intended to help the group in the automation of the heart simulation process using FeniCS-HPC. The graphical interface has been designed by Carmen Alonso Montes (BCAM), thanks to the contribution and requirements provided by Jeanette Spühler (KTH).

This version is still under a very preliminary phase, with basic functionality.

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User manual

In this section, an example will be used to show the main functionalities of the GUI¹.

To use this GUI, some basic information must be taken into account. You always need to create a project to start working with the GUI. This project will contain the main information that can be saved, and loaded later on. Please, at the moment, follow this instructions, since this is really a preliminary version. If you find any bug, please, go to the website, and communicate to calonso@bcamath.org.

This GUI has been developed in C++ and Qt, using QtCreator

Installation

Create a project

You will need to create a new project, to start working with the GUI. You can create a new project or open an existent one.

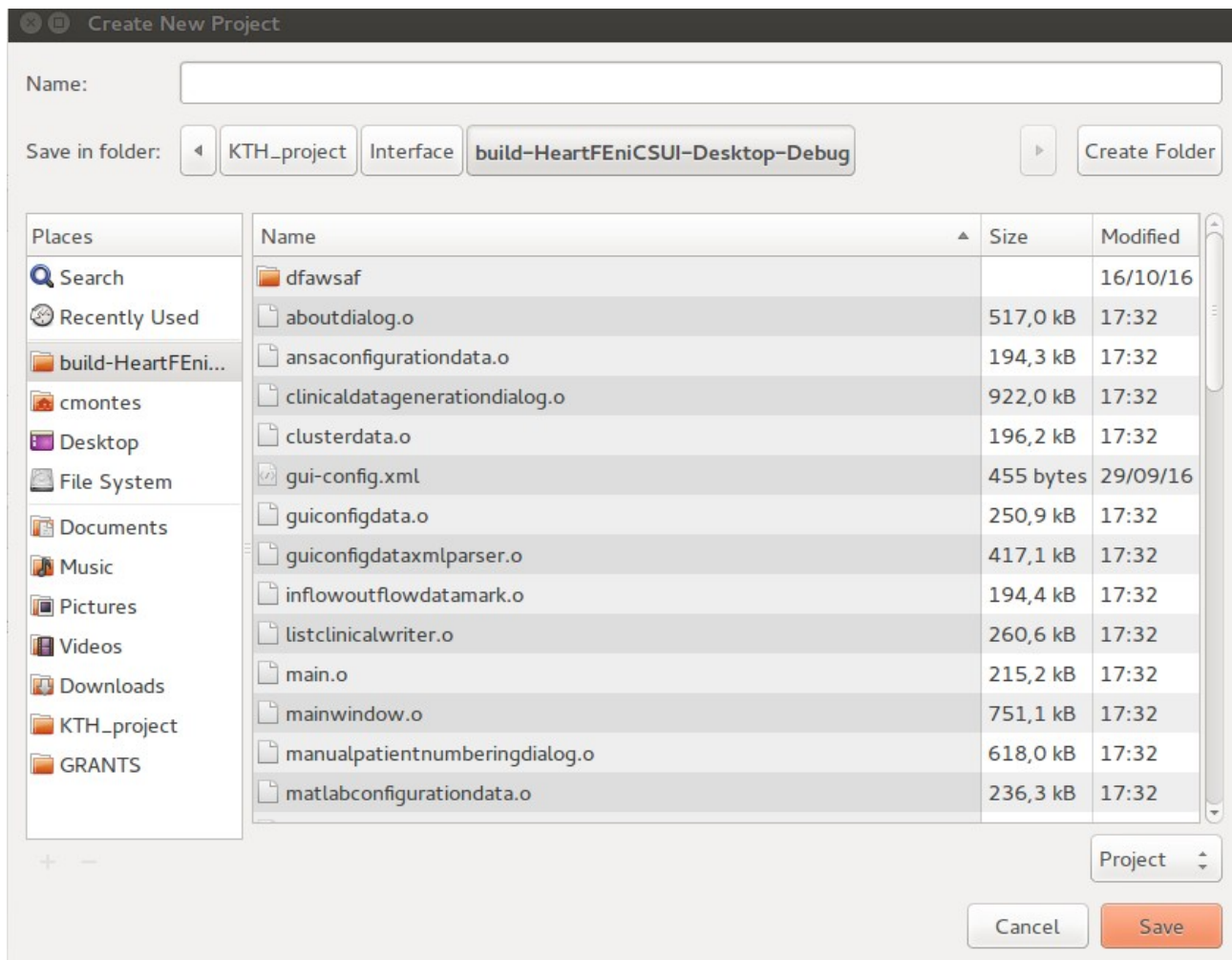


Create a new project

When you create a new project, you need to provide a name and a location where you want to store the basic information of your project. Remember, that a new folder with the name of the project will be created, storing there all the information.

¹**Note:** At the moment, only the functionality related with the simulation tab is available. So, although, some elements of the interface (like the preferences) can be already set up by the user, they don't affect currently in the process for the simulation process.

Project Subject(edit in document properties)



Open an existent project

You only need to go to the folder of an existing project and open the correspondent .prj file. All the information of the project will be automatically loaded in the different menus.

Creating and selecting the patients

Once you are in a project, you can go to the Simulation Tab.

Project Subject(edit in document properties)

Heart FEniCS simulation pipeline

Heart Model Generation | Heart Simulation

Step 1. Create the Clinical Patient file

Check clinical data

Step 2. Please Set up the cluster Information

Remote Cluster Path Set up

Patient Data Path ...

CPP File Path ...

Cluster Information

Cluster IP or name (e.g. beskow.pdc.kth.se)

Your login name in the cluster

In the simulation Tab, you have several information to be filled in. This information will be used to create the two main scripts: launcher.sh and execute.sh

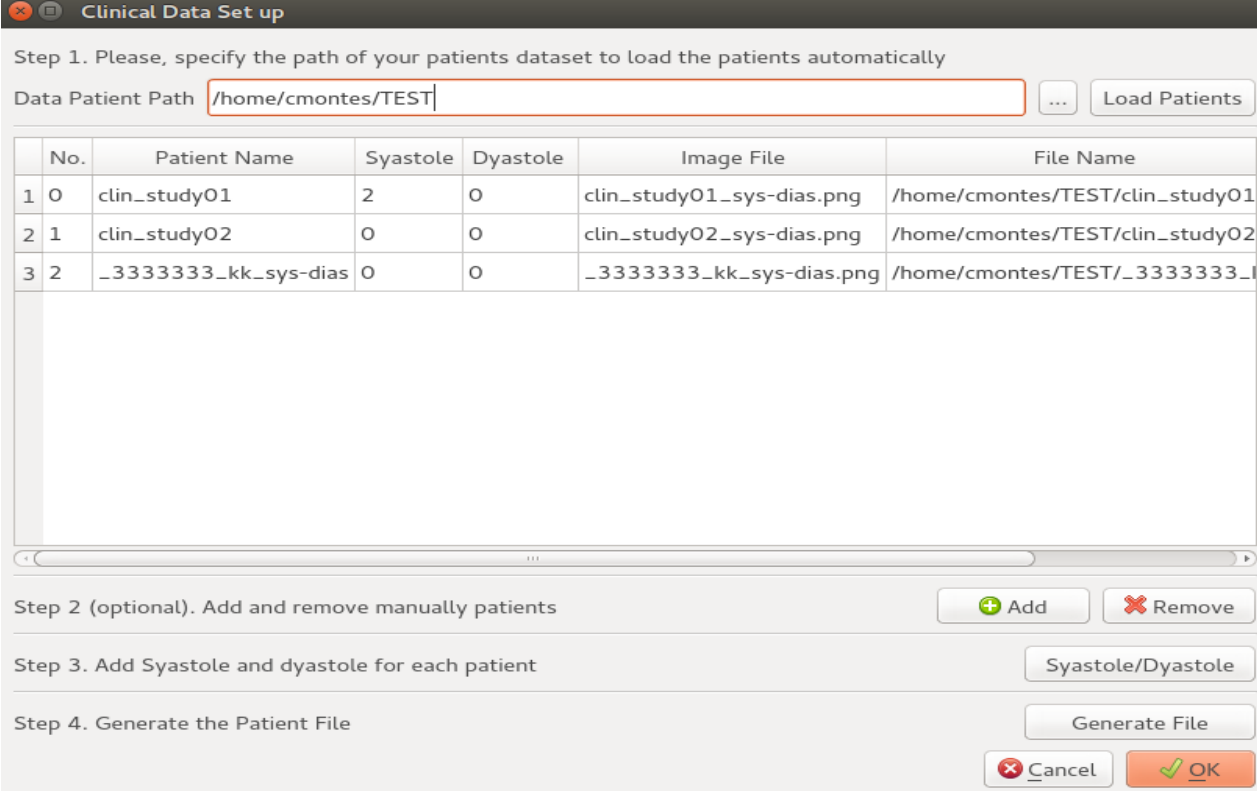
Step 1. Create the Clinical Patient File

This step indeed, is the one that will allow you to select those patients that you want to include in your simulation. Press Create/Update Clinical File Button

Note: The listClinical.txt file will be created in your client data root path. So, it is suggested, that you have all your patient data in a common folder, e.g. /home/Data/ (and inside Data, will be a folder for each patient). The listClinical.txt will be created in Data/listClinical.txt

When you press the button, a new window appear. Please, go for all the steps in order.

Project Subject(edit in document properties)



Clinical Data Set up

Step 1. Please, specify the path of your patients dataset to load the patients automatically

Data Patient Path ... Load Patients

	No.	Patient Name	Syastole	Dyastole	Image File	File Name
1	0	clin_study01	2	0	clin_study01_sys-dias.png	/home/cmantes/TEST/clin_study01
2	1	clin_study02	0	0	clin_study02_sys-dias.png	/home/cmantes/TEST/clin_study02
3	2	_3333333_kk_sys-dias	0	0	_3333333_kk_sys-dias.png	/home/cmantes/TEST/_3333333_kk_sys-dias

Step 2 (optional). Add and remove manually patients + Add - Remove

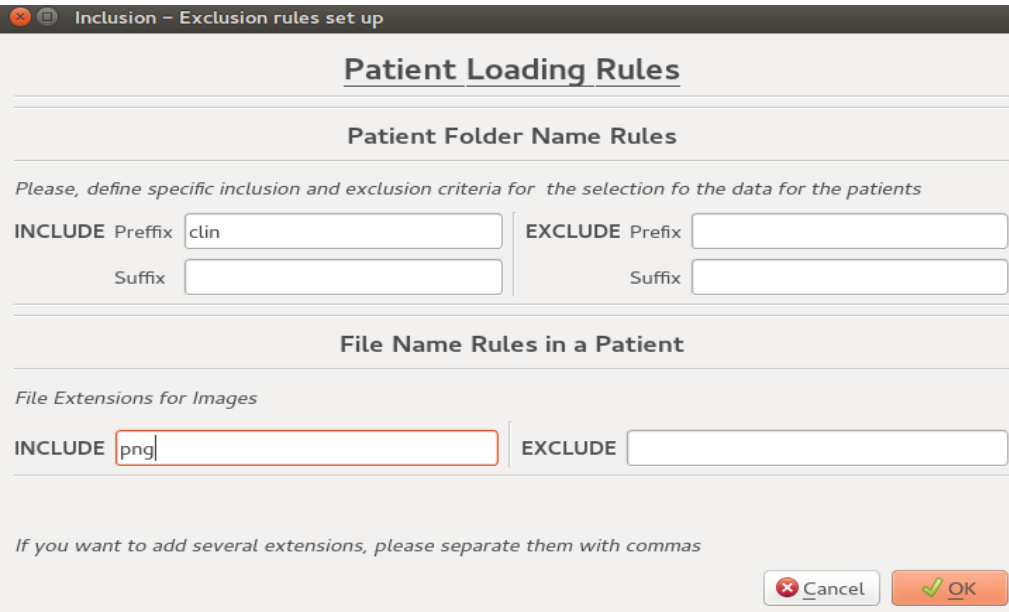
Step 3. Add Syastole and dyastole for each patient Syastole/Dyastole

Step 4. Generate the Patient File Generate File

Cancel OK

Step1. You need to select the folder where you have your client data (e.g. /home/Data) so press the tool button

Then you need to push Load Patients, to define the rules of inclusion/exclusion to select those patients that must be included in your study. A new window appear.



Inclusion - Exclusion rules set up

Patient Loading Rules

Patient Folder Name Rules

Please, define specific inclusion and exclusion criteria for the selection of the data for the patients

INCLUDE Prefix	<input type="text" value="clin"/>	EXCLUDE Prefix	<input type="text"/>
Suffix	<input type="text"/>	Suffix	<input type="text"/>

File Name Rules in a Patient

File Extensions for Images

INCLUDE	<input type="text" value="png"/>	EXCLUDE	<input type="text"/>
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If you want to add several extensions, please separate them with commas

Cancel OK

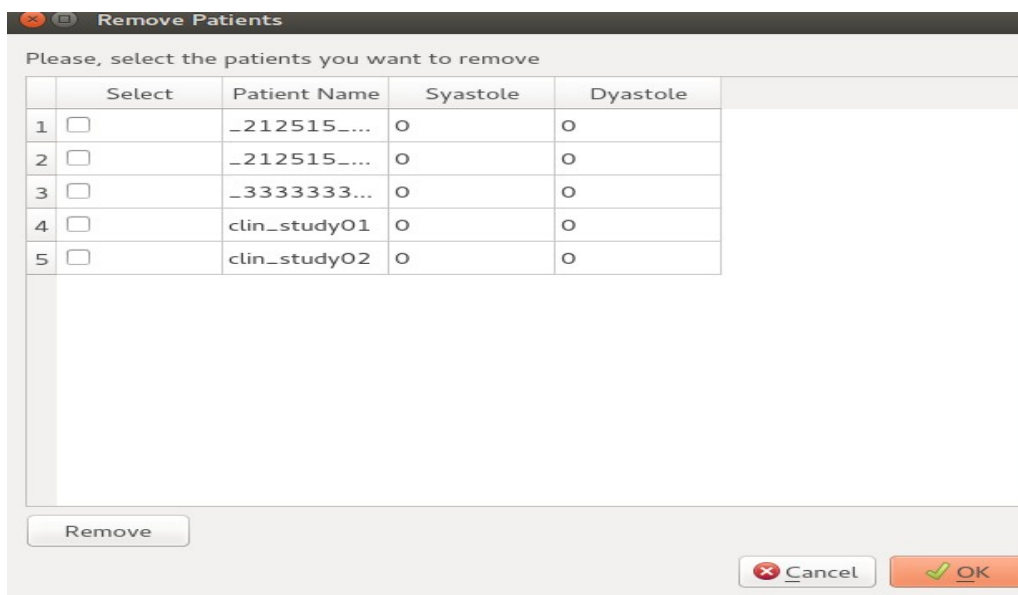
Project Subject(edit in document properties)

In this window you must select:

1. Prefix and suffix for the patients names (those names that are used in the patient folder name) that will be included in your study, and those to be excluded
2. Select the file extension for include/exclude the type of systole/diastole file image per each patient.

Note: The systole/diastole file image must be inside each patient folder in this format (and only 1 image per patient):/home/Data/mypatient/mypatient_systole_diastole.png

Step 2 (Optional) You can add manually patients, and also remove them.



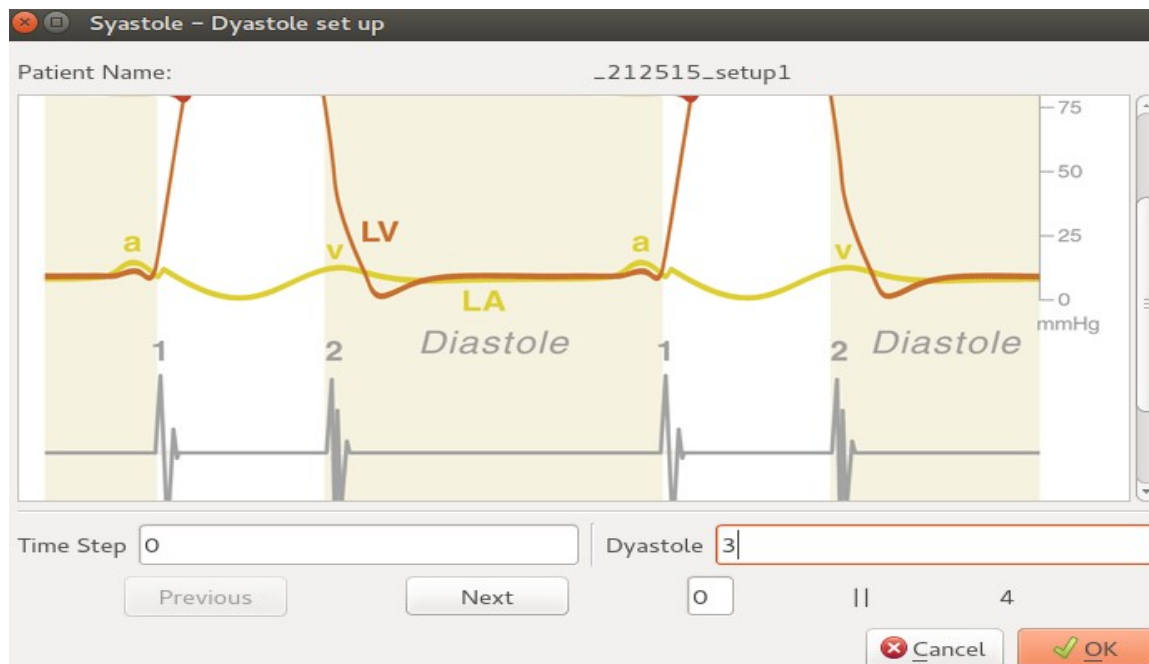
Please, select the patients you want to remove

	Select	Patient Name	Systole	Diastole
1	<input type="checkbox"/>	_212515_...	0	0
2	<input type="checkbox"/>	_212515_...	0	0
3	<input type="checkbox"/>	_3333333...	0	0
4	<input type="checkbox"/>	clin_study01	0	0
5	<input type="checkbox"/>	clin_study02	0	0

Remove

Cancel OK

Step 3. You must check the values for diastole and systole of each patient. If you click the button, a new window appear. You will see the image of each patient and you can change the values accordingly.



Step 4. You MUST generate the file, otherwise, all your changes will be lost. When you click, the file will be create at the root folder of your Data path. In the example: `/home/Data/llistClinical.txt`

Step 2. Cluster information

This information is needed to create the scripts correctly to launch the simulations in the cluster. You need to set up the paths of your data and cPP files in your cluster, and the cluster basic information (IP, and your login name)

Creating the files to execute the simulation

You need to click the create scripts button in the Simulation Tab.

Once you click, this step creates two scripts in the folder of your project (where the .prj file is stored):

1. * launcher.sh
2. * execute.sh

Launcher.sh → Is the basic script you will need to launch in conslde mode, in a console with the ticket information (in our case, Kerberos) to be able to communicate with your cluster. It contains the instructions to:

1. Copy all the files of the data patients in the cluster, reproducing the same structure than in your local computer

2. Copy ListClinical file into the cluster computer in the correspondent folder of the patient data
3. Copy Execute.sh file into the CPP folder in the cluster
4. Ssh into the cluster, so you will be able to launch your simulations.

Execute.sh → This file contains the basic information to build all the files needed to launch the simulation in the cluster.

Developers manual

Check Doxygen documentation generated.