chatter plant

PLANTLABCO

SOFTWARE TOOL

UNIVERSITAT POLITÈCNICA DE VALÈNCIA

VALENCIA UPV iGEM

1. INTRODUCTION

During the development of ChatterPlant we found several problems when working in synthetic biology of plants. We realized that, when carrying out an experiment, it took us a long time to collect all the information. The main problem was that there were not many experiments uploaded and they were very dispersed in the network. After going through this step and performing the **experiment**, in some cases, we did not obtain the desired result. What we found after squeezing our brains was that the experiment had **previously** been performed in the same laboratory where we worked, obtaining the same results. Lack of good communication had us spending time and resources that we could have used better if that experiment was properly recorded anywhere. When we spoke to other laboratories and researchers involved in plant's synthetic biology, we realized that this was not only happening in our lab, it was a **global** fact, so we decided to develop PlantLabCo.

PlantLabCo arises to **unify** all this information in a website and offers the possibility to register all kind of **experiments** in this field, establishing a **metadata standard**. Since synthetic biology in plants is a field that is in its beginnings, we have seen the need to set that record model. A **forum** has also been presented so that researchers will be able to participate providing information about the topics related to this field. In order to unite this information, a magazine will be created so that it will help the **dissemination** of this science by publishing papers by researchers, institutions and other stakeholder. Last, but not least, a mathematical **modeling tool** will foster research in synthetic biology in plants, as well as facilitate the work of current researchers in conducting experiments.

2. WORKING FLOW

The Software tool is composed by two main developers. An efficient way of working was established by following a sprint methodology of 2 weeks where at the end of each sprint each developer submitted a deliverable with the obtained results. Furthermore the planning of these periods were done following the scrum poker technology, with it defining the user cards to be done. A time estimation was attached to each card and a structure each week with 30 hours. Throughout the development the Secure Development Life Cycle was taking into consideration for having security on all the different parts of the system. Also a peer revision was followed, when a developer submitted a piece of code for the main repository the other was in charge of testing it. This way the developer and tester are disambiguated and security is reinforced.

3. DESIGN CONSIDERATIONS

3.1. DEFINITION OF REQUIREMENTS

To do this, we made a list of everything we thought our software should have, and then we interviewed them to test if our ideas and specifications where enough, or we should include more. We were open to any change and suggestion. Two main ideas blossomed thanks to that useful feedback. The first one was section in the forum called "customer support" where users can give us feedback of what they need to enjoy the tool better and create a sense of community. The second one is a FAQ and an email account where any user can contact us and inform about any problem occurred using our tool.

These changes have been made in order to make the user as comfortable as possible and build a reputation that will make people recommend us.

3.2. STRUCTURE

When developing PlantLabCo, the MEAN technology was used, MEAN is a full-stack Javascript solution that helps to build fast, robust, and maintainable production web applications using MongoDB, Express, AngularJS and Nodejs. This is a modern and young technology backed by Google. This allowed us to work with the Frontend and Backend structure. Having this dichotomy allows for a more agile tool, eases the scalability and the possibility of attending more petitions with the same resources, because we throw computational task to the Frontend and by doing this the computational load on the Backend is reduced.

3.3. GRAPHIC DESIGN

In order to realize the personal computer interface of PlantLabCo, we have started a structure already predesigned by paid professional website-designers. This template is programmed in boostrap 4, which allows us to adapt the design to any device with internet connection, in addition is also compatible with the most popular web browsers like Internet Explorer, Chrome, Firefox and Safari. On this structure, we have worked with our graphic designers, to establish an appropriate visual adaptation to what we offer in PlanLabCo. Every single image and icon has been specifically designed for providing a unique experience while navigating through the template, providing the website its own personality. If you want to know more about the visual line of PlanLabCo we recommend that you visit the section of the Graphic Design in the wiki.

After this process, we have validated the design of PlantLabCo posting it in a forum where expert marketing users gave us feedback about our interface and, after that, we adjusted the design to make it more comfortable for the user. This has improved PlantLabCo by giving it a professional image.

3.4. INTEROPERABILITY

Although the main the focus of PlantLabCo is serving the community an open service is provided for others to make profit from, in contemplation of the Elixir program, an API is available. With this other tools and platform from the environment and out of it can throw queries to the database and obtain the experiments. Also a unique metadata model was developed for our platform following the Data Management Plan project. Thanks to this the online searches can be done semantically showing the fullness of the results.

The John Papa's indentation standard was followed to ease the understanding and reuse of the code.

4. PLANTLABCO TOOLS

One of the decisions that had to be made while developing PlantLabCo was that there would be both open-source tools and others only for registered users. The main reason of this is that we want to have a register of who uses a determined tool for future development. Down below we are going to present the different sections and tool.

4.1. EXPERIMENTS

We want every experiment to be upheld in the repository, even if it does not work as it should, so there are unified and accessible to everyone.

Two parts can be differentiated:

- **Experiments viewer**: Any anonymous user can scroll down a list with all the experiments that have been performed and registered during the development of a project. The section contains also a name searcher and a categories index so that searches can be optimized.
- **Experiments repository**: Only those users that have previously registered can upload an experiment. In this part, the Principal Investigator has to fill up a questionnaire with the information of the experiment. The experiment also needs to be endowed with a unique code, which connects the intellectual property of the experiment with the author and the consent for being used by the community.

Something that needs to be highlighted about this service is that a unique metadata model for dividing the experiments has been created according to FREME DMP, a European project about how to guarantee public access to scientific publications and data searching. This project stablishes some steps when creating metadata for this kind of content.

In order to create scientific metadata, we thought about the different parts an experiment can be subdivided into. This streamlines the reach the desired content for the user. Searching engines search for words in a document, so they do not have the capability to know what they are working with. With metadata, extra information is added to the word they are working with, increasing the robustness of the search, because it will not only work with the word provided, but also with the relationship between the word and the content.

4.2. MODELING

A modeling software tool was developed to ease the mathematical modeling. The main purpose of this section is to construct a genetic circuit and having as an output a set of scripts that can be runned directly on Matlab. Concerning on how to introduce the circuit a study on the most used pieces was performed and 4 main pieces were selected. This allows the recreation the vast majority of circuits. In order to do so an interface was developed. On it there is the visual representation of the different pieces used, when clicked a modal appears on screen and the user has to fulfill all the different fields, to add it to the general circuit the user has to use the create button at the

bottom. By repeating this steps the whole circuit can be build. The user can see all the different pieces below the images as it is being built, a dependency matrix can be shown on demand to facilitate the viewing of the connections between the different pieces. If during the construction the user was to make any mistake there are two buttons for editing a piece and deleting it from the circuit. Once it is finished the user can click on the button model. Afterwards the only step left is to download the scripts that   run   on   Matlab.

When designing the translation from a visual representation to a script, the state of art was studied. After the proper research being performed, we decided to start our algorithm from an already existing one from "F Siso-Nadal, JF Ollivier, and PS Swain, BMC Syst Biol 1:36 (2007)". This algorithm in particular was chosen due to several reasons, after looking deeply on it, we realized that it had the potential to act as middleware between our reactions and the Matlab output desired. It also has the advantage, that it is completely open-source. Having the key elements selected we started to work on the translation. The resultant algorithm can convert the simple input of the parameters in a set of related and interconnected formulas that work as the input of the python script to a Matlab compatible one.

4.3. FORUM

PlantLabCo Forum is composed about free-to-access threads regarding plant's synthetic biology. In this section, all the researchers will be able to participate if they are registered in the platform by discussing topics, asking for help and post anything

they consider relevant. As this forum will be one of the first ones containing useful information about synthetic biology in plants, it will become one of the referents in this field.

Among the different sections in the forum, one will be only about transgenic plants. This section has been created so that specialists in the subject can shed light on the stigma that has been created around this issue and that transgenics are more accepted in our society.

Finally, as previously stated, there is also a consumer help section, which deals with issues related to the use of the platform.

4.4. MAGAZINE
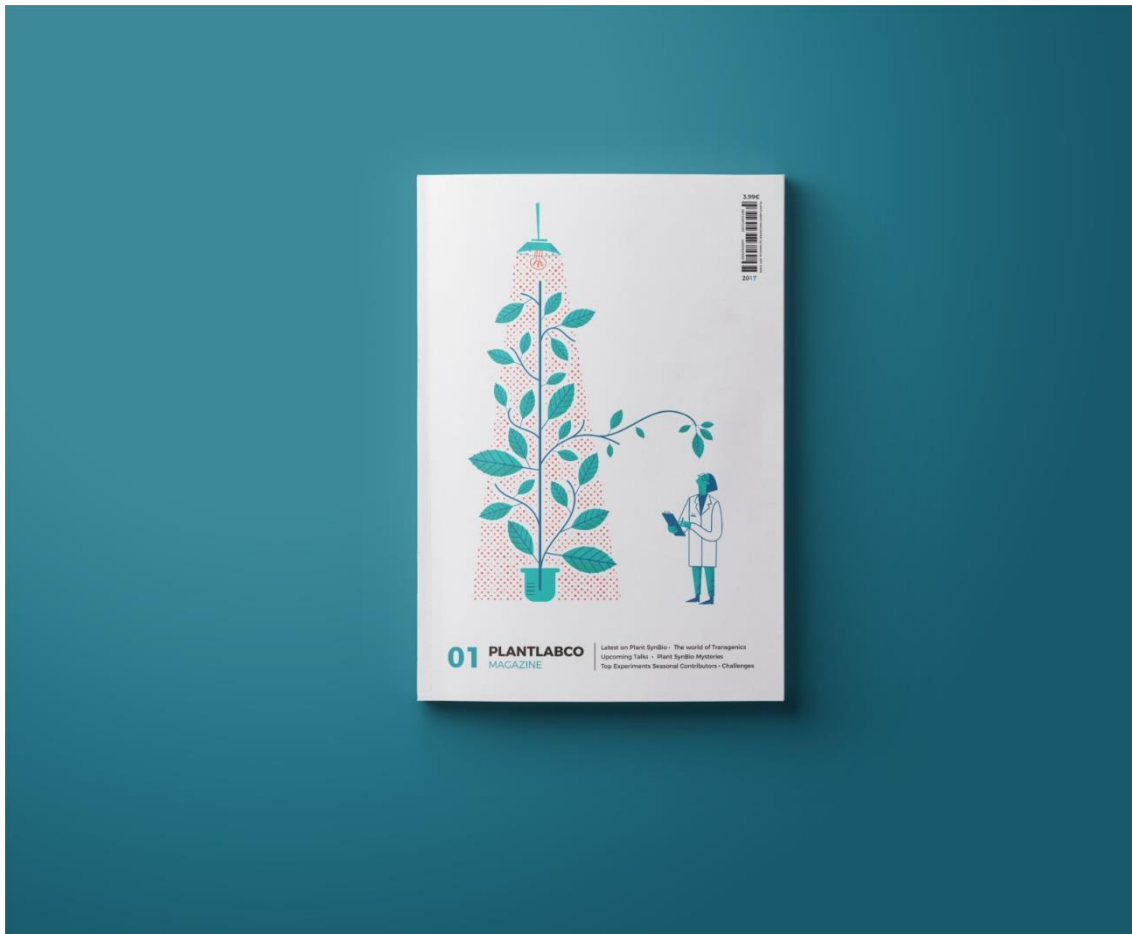
Divulgation is also present in PlantLabCo. We see as a mandatory task educate people about the wonders synthetic biology can contribute to humankind with.

Any user can benefit from the articles in this section. Those publications will be uploaded b the administrators of the website, but will be written by any person that wants to participate, from researchers, professors, institutions, research centers or others. Only a certain amount of people will publish depending on the results or the topic so that scientific quality is not lost. PlantLabCo – Magazine will compile those filtered articles. This magazine will be printed seasonally and sent to the all the interested subscribers.

5. PLANTLABCO FUTURE

As a reference in plants synthetic biology field, PlantLabCo can continue evolving in different ways, for example, developing more functions in the modeling tool and

making it compatible to the European intergovernmental organization ELIXIR standards. This service could not only provide the scripts for its execution, but also, a visual way for showing the results (with graphs and equations) could be computed for a certain price. The chassis for this modeling system would be MathWorks as it has the resources for complex calculations.

We could also make a collaboration with iGEM in order to create a division in the experiment's section. Modifications in the metadata provided will be useful in a hypothetical repository where the teams can upload their projects, and we think that this is an important point to take into account, as it will help in data mining. Many teams have participated in iGEM during the past years, and there is plenty of information regarding the topics and experiments that can't be accessed easily. Those facilities can be crucial in the creation of new teams and consolidation of the ones in their rookie year, as they can be surpassed by the huge amount of information in iGEM. That is the reason why we think our project can contribute in giving some order to this useful (but sometimes inaccessible) information.

6. GITHUB

https://github.com/igemsoftware2017/Valencia_UPV/releases/tag/1.0.0