

Welcome to our newsletter.



Dear All,
Here comes the sixth issue, a special issue about software.

This issue consists four parts:
Project Update From DRY Teams;
Open Questionnaire About Software;
Project Update From WET Teams;
& Human Practices About Collaboration & Problems.

Thanks to the following twenty-one teams:
(in alphabetical order)

Birkbeck, Colombia, EPFL, ETH-Zürich, HFUT-Software, Missouri S&T, NJU_China,
Paris Bettencourt, Purdue, SJTU-Biox, SJTU-Software, SYSU-Software,
SYSU_China, Tianjin, TecCEM, Toulouse, TU Eindhoven, USTC-Software,
Valencia UPV, WHU-China and WLC -Milwaukee.

Thanks to all of you for your contributions!

If there are any questions, please reach us at igemxmu@gmail.com

All the best! Cheer for the summer!

iGEM Amoy

2015-7-28

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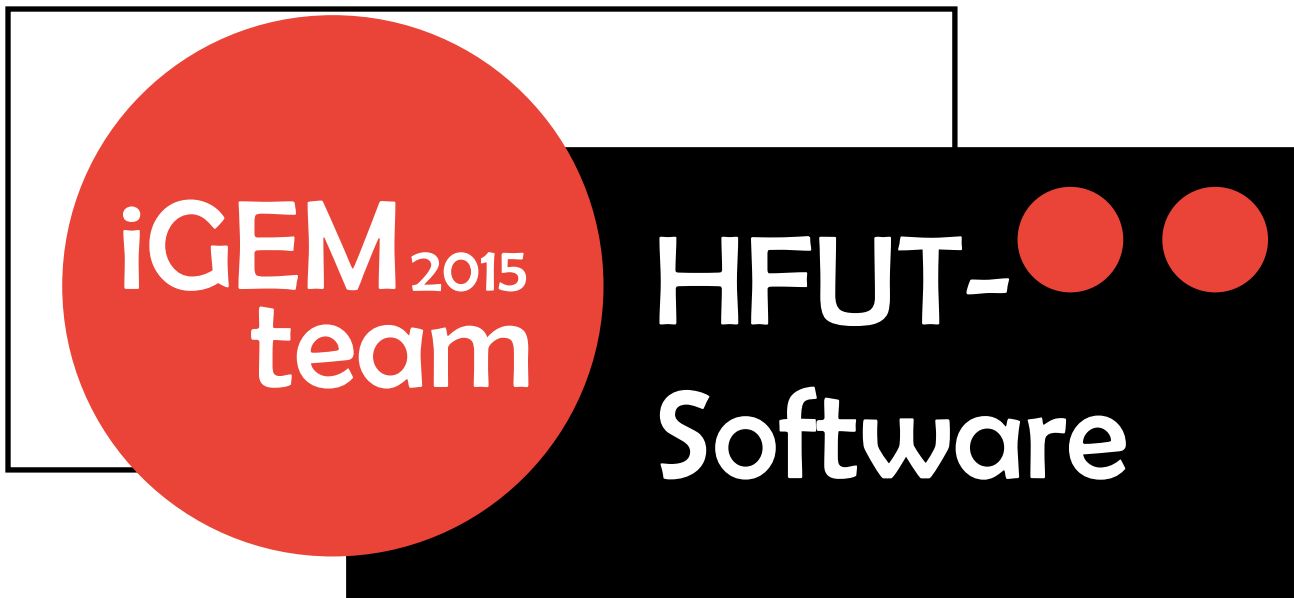
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**PRO
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By: Four Software iGEM
Teams

DRY



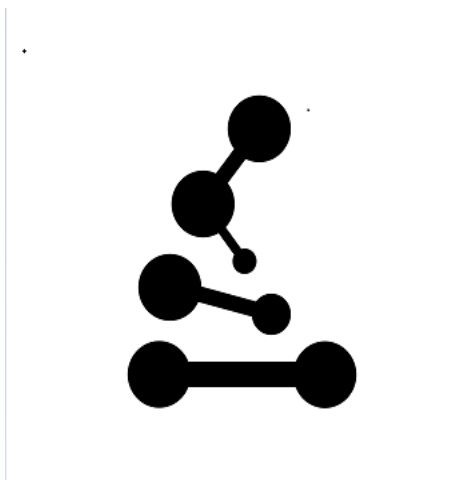


iGEM Project Description

Synthetic Biology has developed for many years, but the Synthetic Biology workflow still remains in a traditional way. People need to do their design based on lots of paper reading and information search. To determine which parts and BioBricks to use, even more repetitiously work needs to be done. After all that works the gene express results are still unclear. All those things leads to tons of works, makes the creative work become kind of boring. All those works can be completed with today's advanced computer technology. So we develop the BioDesigner, a computer assistant for Synthetic Biologist.

With BioDesigner, Synthetic Biologist can get recommendations. We will generate two types of recommendation. One is based on the parts that has already been used, the other is based on the last part in the designing chain. User can choose one to use, check information for part, or just ignore them.

Our product also provide gene express simulation. The system will simulate the gene express process and show the productions through time. With the simulation system, user can have a glance of their design before they put them into real Biology testing.



Team logo-HFUT the black logo

For the system scope, BioDesigner also can give recommendation about systems that might be useful. Also, BioDesigner can form the Pathway based on the input material and output productions, which can help the user gets a better view about their design. By comparing the current pathway with the entire gene pathway graph, Some interesting recommendation can be shown to the user.

The main purpose of BioDesigner is to develop an assistant for Synthetic Biology and makes Synthetic Biology design process to be more robotized. We are doing it and we are doing it well.

Team 2015 HFUT_CHINA is composed of 15 young members. HFUT, Hefei University of Technology, is a national university in Anhui province, which is famous for its beautiful landscapes and great history of Chinese building. HFUT is known for its study in vehicle, architecture and computer. With 'technology' in its name, HFUT is a fantastic place for students who major in engineering. We are very proud of representing our university and competing with wonderful students in other universities in iGEM. We are a group of students with different professionals like software, informatics and biomedicine. We see this competition as an opportunity to foster scientific innovation among undergraduates. Everyone in our team lives and breathes our passion! This project would never be possible if any single person from the team was lacking. And also, we deeply appreciate every friend who has ever helped us!

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Team logo-HFUT the white logo

**iGEM₂₀₁₅
team**

**SJTU-
Software**

Hello, everyone! We are SJTU 2015 Software team. Last year we had the first software team who won the golden medal and we believe we can do better this time. Most of us are studying bioinformatics, some are from Media and Design Academy or School of Electronic Information and Electrical Engineering.

We are inspired by our project last year and a game, FIFAonline. FIFAonline is a worldwide soccer game which is famous for its adjustment designed by changing your battle array. The AI in this game could help you to score your battle array. In our project, we focus on the adjustment and scoring system for the biosystem with biobricks you have collected. With our project, users, mostly the wet-lab, may judge your biobrick system which help you get rid of plenty of redundancies.

We have four main functions:

1.Upload:

after experiment work, user may find or create a perfect biobrick that may is not in our database now. Then they can upload the information of the new biobrick into our database. And you can use our web to upload your parts into iGEM official database if you are a iGEMer. With your help, our application will become stronger and stronger.If the

discount of the parts in the database is big enough, I believe the accuracy rate of our application will amazing.

2.Search

In this function, users can find the desired biobrick, before that, you can pretend the redundancy result by choosing the simple brick or the complex brick.(simple brick is a single biobrick, on the contrary complex brick means the combination of simple brick) The result of our searching will be the basic information of biobricks, such as ID, type, description, quoting time(simple brick), composition(complex brick)


3.Comparison

Comparison of simple biobricks or composite biobricks

Comparison of replaced composite biobricks components with before

4.Evaluation

This is the core part of our app. User can customize composite brick, during which user can choose whether to use the push function. For composite bricks, our app can evaluate them intelligently and give the overall score, meanwhile, the app will provide some suggestions for revision: each brick will be evaluated and then get different colors based on its evaluation,user can click on user can click on the brick to get the list of bricks we



recommend as replacement.

Moreover, our software will be based on website so users do not need to download our software but use them online. We believe with the help of our software, users can save a lot of time searching for a better and suitable biobrick and creating their own biobricks easily.

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A black circle containing the text "iGEM 2015 team" in white. The "iGEM" is in a large, bold, sans-serif font, "2015" is smaller and to the right, and "team" is below "iGEM".

iGEM₂₀₁₅
team

A red, tilted rectangular banner containing the text "SYSU-Software" in white. "SYSU-" is on the top line and "Software" is on the bottom line, both in a bold, sans-serif font.

SYSU-
Software

A solid red vertical bar.

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Captain QQ: 296754370

Introduction of project

For long designs in synthetic biology has been hindered by the lack of logical methods; on the contrary, many mature and useful principles have been applied to engineering disciplines. These principles are promising guidelines in pushing forward the field of synthetic biology. However, it is hard for synthetic biologists to master both experimental techniques and engineering methods.

Our project aims at realizing the potential of computer-aided design in synthetic biology. According to their needs, users define the functions of a system, and then use our software to find the functional component for assembly. The software makes use of the ordinary differential equations to connect each component, leading step by step to a synthetic system with the defined function.

To this end, we base our software on the analysis of existing devices and systems. Utilization of ordinary differential equations helps to resolve the existing design into basic units of different levels (i.e., devices or systems). Now we can endow the original system with new functions using this basic units.

A red circle containing the text "iGEM 2015 team" in white. The "i" is lowercase and the "GEM" is uppercase. The year "2015" is smaller and positioned to the right of "GEM". The word "team" is lowercase and positioned below "GEM".

iGEM₂₀₁₅
team

A black rectangle containing the text "USTC-Software" in white. "USTC-" is on the top line and "Software" is on the bottom line.

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Background

Synthetic Biology, a mixture of Biology, Engineering and even Computer Science, is one of the cutting edge of today's Biology. The main idea of it is decomposition, decoupling, encapsulation and assembling on simple biological parts. In this process, many data is generated. We need a way to store, organize and use these data, or, unless, some aspects of these data.

Aim

Our primary aim is to create a platform. In this platform, every thing is abstracted as a module, which only has input port(s) and output port(s). Synthetic biologists can easily grab modules' data from databases, and then quickly express their designs through some simple mouse drags, nally test these ideas in our simulator. We also want to promote the communication among synthetic biologists. They can also update their module designs to the database for other synthetic biologists to use as building blocks in their own constructions.

Work

Untill now, we have already coded a prototype of the stochastic simulator and some logic gates (include AND, NOR, NOT etc.) as the test modules. In the meanwhile, our database design is nished, and the above test modules are to be loaded in. Front End and Wiki design are also in progress.



Outlook

While developing our software, we will keep eyes on the latest core journal of synthetic biology. By reading the latest research progress, we may find some new computer-needed topics that synthetic biologists are interested in. Some could design small functions as plugins of our software.

Our Team

This year, USTC-Software consists of 23 undergraduates in USTC. As a practice, in order to recruit new members and set up a new team, former members put up posters and held introducing meetings to attract students interested in the iGEM or Synthetic Biology.

During the winter vacation, with the help of former members of USTC Software, the new members were introduced to the basic biological knowledge, the core of Synthetic Biology and fundamental skills of developing a software product. At the end of the winter vacation, captain, vice-captain and manager of a new team were elected. The captains are in charge of team management and overall direction of the team project, and the manager is in charge of arrangement for the Giant Jamboree including registration, visas, travelling, accommodation etc.

This year, our team | USTC-Software 2015 is made up of students from different departments, Physics, Mathematics, Earth & Space Sciences and Computer Science. The diverse knowledge backgrounds of our team can be a double-edged sword. For one thing, we could come up with the new ideas by brainstorming, and everyone could find some relationship between Synthetic Biology and their majors. Meanwhile, the new idea is always original and novel. For another thing, due to the lack of professional biological knowledge, sometimes brainstorming may mislead our direction, and we have to spend more time seeking out the right access.

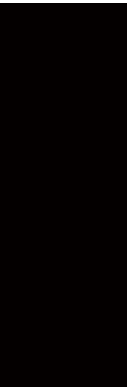
Besides, most of our members are freshmen or sophomores. In USTC, the heavy schoolwork often makes it difficult for us to spare sufficient time for iGEM, but we insist on a conference every weekend to exchange our ideas and biological knowledge timely. In each conference, one or more members are invited to make a presentation on their recent progress.

It is worth mentioning that we also cooperate closely with the USTC team. We offered them some assistance in modeling and experiment data analyzing. USTC-Software and USTC team held activities for human practice together in campus during Science & Technology Week. It proved to be a huge success through two teams' common efforts. In a word, every team member is highly motivated and greatly interested in the iGEM and Synthetic Biology. We will unite together for the same goal and solve the problems along the way no matter how difficult we may encounter. If you want to know more about our project and our team, please don't hesitate to contact us! The iGEM would be a wonderful journey and it is very nice to have your company!

OPEN

Open Questionnaire
About Software By
Fifteen iGEM Teams

Questionnaire





SnapGene[®]
Software for molecular biology



Office



Top Software

what we use, what we need, what we want

What we use

Birkbeck iGEM 2015, like all other teams past and present, make copious use of freely available software for the generic purposes familiar to non-iGEMers, and especially synthetic biology software indispensable to participants and researchers worldwide. We took to some of our most industrious software whiz kids – Sean, Luba, Barbara and Elliot – to find out just what pieces of soft kit they rely on most day to day to accomplish tasks for our first ever iGEM entry this year.

The crown, unsurprisingly, was earned by SnapGene software for molecular biology who have supported iGEM teams once more by offering free licences to all team members. "I have used SnapGene for looking at plasmid sequences and planning cloning," Sean mentioned as his most used software. Unanimously, Luba, Barbara and Elliot put forward SnapGene as their first, blowing any competition out of the water. SnapGene is the go-to programme for synthetic biology.



Birkbeck

Sean continues “Sublime text for writing the Wiki page. Microsoft office for general keeping tabs on things (such as our materials). Copasi for metabolic/genetic modelling.” Reaching out for everyday software such as Microsoft Office, Microsoft Paint, Adobe Photoshop, Adobe Acrobat Reader and web browsers goes without saying for the upkeep necessary in running an iGEM team, sharing information and staying organised.

A noteworthy runner up in the scientific software section was Arduino, which Elliot and Barbara found indispensable.

What we need

A lot of what we use, no matter what it may be, perhaps in a different conversation, is inherently also what we need. When it comes to software, we can develop a love-hate relationship with anything that we do not enjoy using, but have no choice regardless if it happens to be the only niche software for a specific task. Many tasks can be achieved by using alternative software if our first choice lets us down. Since iGEM is niche as an emerging technology, it is quite common to have these indispensable pieces of software that we absolutely cannot do without.

Elliot put forward SnapGene yet again as the chief software, while Barbara and Luba took a more attached approach to their software choices, by stating that most or all of their used software is at the same time their most needed software. Sean, our wiki master, nominated Sublime text for helping him develop our iGEM website, alongside experiment-related analytical and processing software SPSS, Excel and Word.



What we want

We all have our software dreams – that button we wish existed, that function or that command. The moment we scramble through tabs and settings to find what we think surely exists as an option, only to eventually realise that it simply does not, illustrates this perfectly. What does Birkbeck iGEM 2015 want from its software?

“I am looking forward to styling the web page” Sean described his frustration with existing wiki editing options which do not allow for very accessible visual design of our pages. Both Luba and Elliot wished there were additional SnapGene options that cover image production and editing related to the genetic information displayed. Specifically, Elliot wanted “a template for illustrating the process of digestion and ligation in a presentation.”

The worst case of wishful thinking was summed up by Barbara, half-jokingly “Something that combines a lab book with stock keeping features and an easy search function for DNA sequences, proteins and enzymes. Basically, a program that contains EVERYTHING.”

Most used	Most needed	Most wanted
1. SnapGene	1. SnapGene	Advanced visual presentation options in SnapGene
2. Microsoft Office	2. Microsoft Office	
3. Arduino		

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1. What software are you using in iGEM this year?

This year we are using Python and C.

2. What software have you used in previous competitions?

In our previous competitions we had been using Matlab.

3. What kind of software do you need most? Which features are you looking forward to?

We think that it is important to have software that is user friendly to the people that are not familiar with programming. It is also important that the software is free and open license because there are teams and people around the world willing to contribute to science, but that lack the resources to buy good a software for what they need, in the case of the iGEM competition, a software to run the mathematical modelling of the circuit. These are the main reasons why we chose to work this year with Python.

On the other hand, running the simulations can take time and require a lot of computational power (specially the stochastic simulations). This is why in addition to Python, we will try to implement C this year.

ETH-Zürich

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1. What software are you using in iGEM this year?

This year our modeling people are using MATLAB and COMSOL for their simulations. Although we have not reached this stage yet, they are planning to do all of their statistical data analysis in R once the microfluidics chip is constructed and data is generated. All code is being maintained in a Git repository hosted on BitBucket for version control and equations and diagrams are being typeset in LaTeX. All web design is being performed using plain text editors, using w3schools.com as reference material.

Our logo (still to be finalized and released) and other graphics are being designed using Adobe Illustrator and Inkscape, an open-source alternative.

We are currently using SnapGene as a tool for primer design and plasmid organisation. It has been very helpful and we would like to thank SnapGene for sponsoring our team this year!

Finally, we are using Google Drive and Google Docs to organize and share our files in a common repository, and to create documents that can be accessed and edited simultaneously by all members.

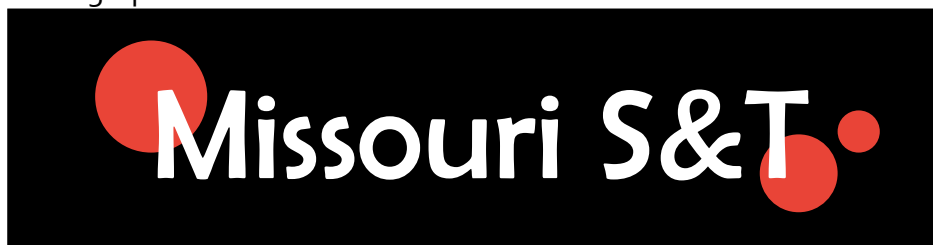
2. What software have you used in previous competitions?

Last year's team also used MATLAB and COMSOL for their modeling and SnapGene for primer design. For posters and videos, Adobe Illustrator, Premiere, and AfterEffects were used.

3. What kind of software do you need most? Which features are you looking forward to?

SnapGene is really important for us. We mainly want to assemble our plasmids using Gibson assembly and the functions that this program offers greatly facilitates our primer design.

MATLAB is essential for our modelling, as it allows us to simulate simple, yet accurate models and it produces nice graphs.



1. What software are you using in iGEM this year?

Finding useful software is something that my team has struggled with in past competitions. Therefore this piece will be fairly short. We've worked with various programs we already had and put a lot of time into our project design and testing because of that. I personally have used Microsoft Word and Excel extensively for sequence editing and manipulation. The character count feature in Word has been a very good time-saver for us. For online resources, we've used IDT's Codon Optimization and Oligo Analyzer tools for a large portion of our design work. In the project definition phase, we've also used the BLAST and nBLAST tools, as well as the BRENDA and KEGG databases for finding enzymes and pathways in nature.

2. What software have you used in previous competitions?

The types of software that could speed up the design of projects is a tool that designs DNA and protein sequences to manipulate GC content, secondary structure, reduce repeats, and swap compatible amino acids. Tools for characterization are necessary as well, but I'm not as experienced on what is helpful on that end.

I look forward to reading what other teams have found and used for their projects.

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NJU_CHINA

We need to use some bioinformatics softwares such as MEGA and prime primer. This year, we are looking forward to some softwares which can help us to edit DNA sequence easily.



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Paris Bettencourt

At iGEM Paris Bettencourt, our use of softwares is, I think, quite usual.

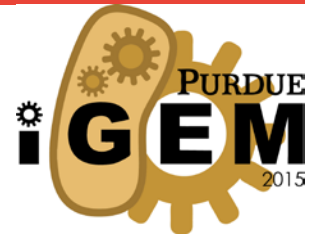
To organize ourselves and communicate we use a lot the services offered by Google. We are using Google Groups (a mailing list system) to communicate with all our team members, previous teams and advisors. For instant messaging, Google Hangouts is useful since it is available both on web browsers and smartphones. All our documents are synced and shared via Google Drive and Google Docs, which allow several people to work on the same document at the same time. We manage and distribute our tasks with Trello.

For the modelling part, we are using Matlab to develop, test and make simulations of our in silico work.

Geneious is our best friend for preparing all of our synthetic biology work. With it we edit our sequences, prepare our oligos, and create maps of our constructs. For the codon optimization we use jcat.de and the IDT tool.

To design our posters, flyers and wiki, we are using Adobe softwares: Photoshop, Illustrator and InDesign.

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1. What software are you using in iGEM this year?

To create our genetic constructs we used a free software called Serial Cloner. We also obtained licenses from Mathworks to use their Matlab software to model our systems. We also heavily rely on Google Drive and Dropbox to share files with each other. Another software we use is called Image Lab, which we use to view image formats of gels we run from a Bio-Rad imaging system. We also used Biobrick Seeker to search for biobricks related to our project.

2. What software have you used in previous competitions?

The past years used softwares similar to Serial Cloner, but we currently don't have any records of the software they used. They also used Photoshop CS5 to create graphic designs for the theme.

3. What kind of software do you need most? Which features are you looking forward to?

We are excited to see different softwares evolve. We are anxious to see software, in the future, that is able to design our genetic constructs automatically and access databases with ease. We are also excited to see an accurate protein folding software be developed in the near future.



Our experience and tips about software

By SJTU-BioX-Shanghai

In every branch of engineering, the practical implementation of a new, complex product is normally preceded by an accurate computational procedure. So it's necessary and helpful to develop computer-aided design software for the silico implementation of synthetic gene networks. Nowadays features of tools for the analysis of biochemical networks and the design of electric circuits have been combined to develop new software for synthetic biology.[1]

Reference :

[1] Methods in Molecular Biology : Synthetic Gene Networks

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SJTU-BioX

We haven't used any software which is specifically designed for synthetic biology because we hardly design complicated gene circuits or networks. The simple system can be easily designed and implemented by heart, so it isn't a practical way to spend many time to learn a new software.

However we use some software which are widely used in biology research like Vector NTI, to construct the vector and determine the temperature in PCR. And some programming language like matlab and python for modeling. This year we still construct a straightforward gene circuit.

Although we haven't used too many software, we can imagine what kind of software has the potential to us. I'd like a user-friendly database with quick search and part comparison function. There are many database contain standard parts and devices yet, but without a user-friendly interface, I find it hard to get the information I want. I think a project management platform designed for lab team, especially for an igem team is also attractive to me, for I get into trouble with the integration of the whole project, and my teammate can't get the overall process on real time.

I hope there will be more functional software for synthetic biology to enhance our ability to design more complex biologic system and run a better lab.



We mainly use softwares like Primer Premier and Snappene as assistive tools in our experiments, as for modeling, only Matlab. As we are mostly focus on experiments, only basic processes, like sequence editing, primer designing, gene map building, etc., requires softwares, and Snappene can almost meet all our needs with its powerful and versatile functionality. As a matter of fact, we don't anticipate too much about softwares, yet considering that a more advanced and user-friendly database port is the future direction.

SYSU_China

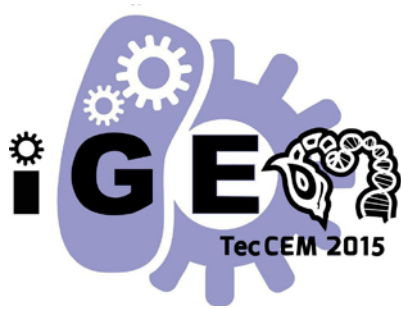
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We used Autodock, SnapGene, matlab. Now we are using GeneRunner, NTI, SPSS, matlab, origin. We hope we can have a software which can quickly query module.

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1.- What software are you using in iGEM this year?

The iGEM TecCEM 2015 Collegiate team is working with DNA origami technique. Due to the nature of our project, we needed to perform several preparatory analysis using bioinformatic tools. These included a software to model the DNA nanoparticle structure and sequence, one to analyse its thermal stability and fluctuation profile, and one to perform an ion-nanoparticle docking in order to determine both the affinity of the selected aptamer and its ability to bind and capture the ion of interest. Having analysed all the clusters of results provided by these softwares, we designed the biobricks that will be developed during the Wetlab work. After having developed these biobricks and produced the DNA nanoparticles, we will characterise their features by several means, and we plan to address their efficiency rates and activity with software tools that allow the treatment of experimental data and its usage for equation modelling. We plan to present at the Giant Jamboree with much more details, so stay tuned and meet you in Boston!

2.- What software have you used in previous competitions?

iGEM TecCEM has only participated once before this year's competition. Last year's project consisted in developing a new metabolic pathway capable of degrading 7-ketocholesterol in the human body in order to address atherosclerosis. This metabolic pathway included three enzymes, two of them hypothetic, which jointly would ideally be able to perform the degradation. Therefore, this project required software that appropriately fitted its objectives: protein structure simulation and modelling, bioinformatic tools that could simulate genetic engineering protocols, and a simulation of the activity of the coupled enzymes. The list of the used software includes:

- i-TASSER server for protein structure simulation

- PyMOL for protein alignment and comparison

- SerialCloner for genetic engineering simulation

- Mathematica for the equation modelling of the pathway

3.- What kind of softwares do you need the most? Which features are you looking forward to?

Mostly, the software that was crucial for our project is the DNA Origami designer which was the first step towards iGEM. We have seeked for and learnt about many features ranging from converting and creating PDB files for bioinformatic analysis and determining a fluctuation pattern, to the appropriate metalloid docking with organic molecules software. Having already done that, the features we look forward to are those that can allows us to simulate the behaviour of a biological circuit in order to model equations that can describe with high confidence our process of production and assembly of the DNA nanoparticles. Notwithstanding, another feature that we require is the ability of characterise mathematically our nanoparticles into giving insight to their activity and efficiency rates. This will hopefully, if time allows, be compared to other remediation strategies in order to determine its cost-benefit.

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Toulouse



[Titre]

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Here is a short recap of the softwares we are using in iGEM Toulouse.

As for in silico biology, the tool we use the most is Serial Cloner to design aligos, synthetic genes, and all we need to make our constructions. We also go on <http://genedesign.jbei.org/> for gene optimizations in E. coli. Plus, we use OptFlux for our metabolic modelisations and Matlab for the others kinds of modelisation (culture, growth, sustainability, reactor design, etc).



[teacherBee]



[geekBee]

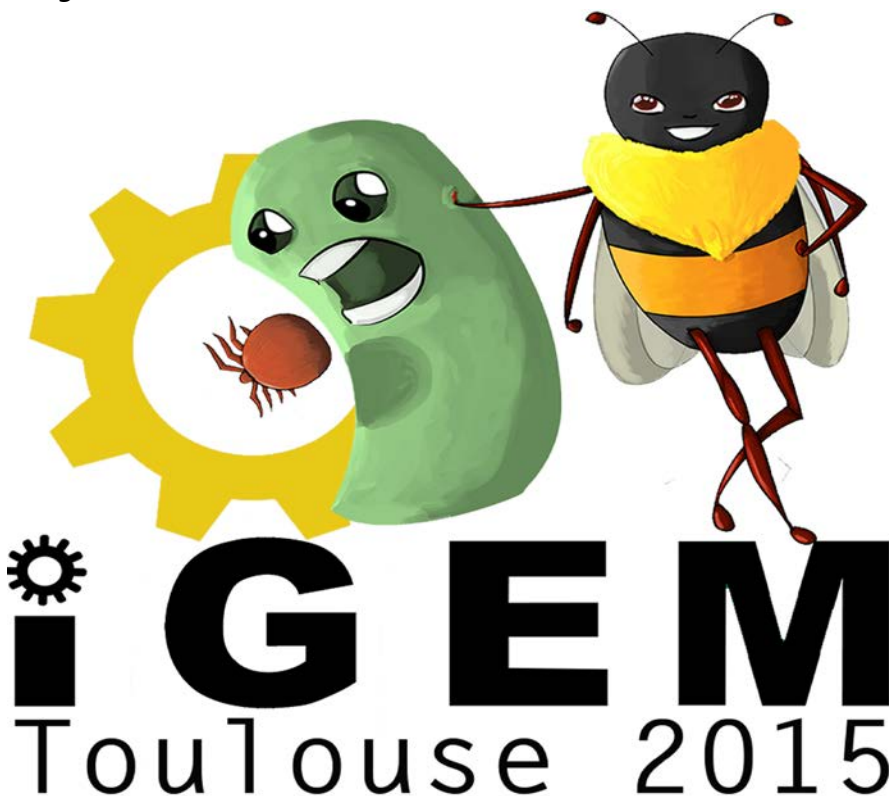
Though, our duties are not limited to labwork. Indeed, the art designer of our Team also used TheGimp and Krita with graphic pad to draw our logo and all the pictures that are related to it; that will be included in our future wiki and presentation for Boston. We will also use Sony Vegas Pro for our fundraising campaign video, quite soon.

For our experiments, we wouldn't need more softwares, but depending on the case some others might be required in the future competitions. We were thinking that a tool using all the iGEM database about biobricks to directly perform constructions would be very welcome, for example.



[Team - Toulouse]

[Logo - Toulouse]



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For our iGEM-project, we use a wide range of software packages this year. From our studies – Biomedical engineering and Medical Technology & Engineering – we are already familiar with many of these packages. One of the software packages with which we had no prior experience and which has already turned out to be vital for our project is SnapGene®. This software package can be used to design cloning experiments and model them in silico. Moreover, it offers a very convenient and intuitive experience which is as far as we know quite unmatched by other programs. Fortunately for us, SnapGene has offered teams including us licenses as a form of sponsorship. If you haven't tried it yet, you should definitely try it out!

In addition to using SnapGene for the design of our experiments, we use GeneRunner® and NUPACK. GeneRunner® is a really powerful tool to analyze primers and DNA sequences in general. We use it mainly to screen for hairpins and homodimers within our primers and overlaps. NUPACK can be used for similar purposes, but it offers tools to screen multiple DNA sequences at once. The main advantage of NUPACK is thus that you can also screen for heterodimers, rather than only homodimers.

Two final software programs which we have used, albeit not intensely, are QGRS Mapper and Primer3. Both are open source, web-only programs. The former can be used to screen for G-quadruplexes in primers and DNA sequences and we have used it to screen for G-quadruplexes within the overlaps of our gBlocks®. The latter is a program which can generate the best available primers which can be used to sequence your constructs. We haven't used Primer3 all that much since we had to design primers for certain fixed places, but if you need general primers for sequencing only, Primer3 is really the way to go.

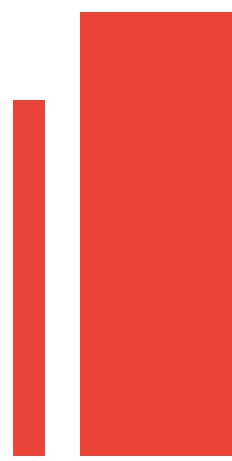
Of course, an iGEM project consists of more than just lab work. An essential part of our iGEM project this year is compiling a cloning guide. We make this cloning guide in Adobe Indesign which is really the ideal software program for compiling such a guide. Even though our university provides licenses for this software program, we did not have very much experience with it. The software program has a somewhat steep learning curve, but once you get a little familiar with it, it is truly amazing. Next to Adobe Indesign, we also use some of the other Adobe programs such as Photoshop and Illustrator. We use these programs mainly for the design of images and editing of photos which we will feature both on our wiki page as well as in our cloning guide.

A third important part of iGEM is of course modeling. A few weeks ago, our modeling efforts somewhat hit a wall as we really had to focus on the lab, cloning guide, sponsoring and other important aspects of our project. So far, we have made use of MathWorks® Matlab. Fortunately, we have much experience with this program as it is the workhorse modeling program from our studies. It is also quite straightforward and rather intuitive once you get into it. MathWorks is also a Partner Sponsor of the iGEM Competition this year, which means that it provides iGEM teams with licenses for Matlab. If you haven't got a modeling program yet, you should definitely check it out.

Many programs can be used to automate coding of webpages. One of these programs is Adobe Dreamweaver. We, however, do not use such a program and our wiki is coded entirely by hand. A program which is really intuitive and makes it particularly easy to find mistakes in your code is NotePad++, an open-source program in which we code.

Many of these programs were also used in previous years, in particular SnapGene, Matlab and the Adobe software package. We really look forward to hearing which software packages other teams use!

Program	Use
SnapGene	Design of primers, analyzing plasmids and in silico modeling of experiments
GeneRunner	Analysis of primers and overlaps. We use it to screen for hairpins and dimers
NUPACK	Analysis of hairpins and dimers, including heterodimers. Really powerful tool, although we did not use it that much.
Primer3	Open-source web-tool which can be used to automate primer design. Yields very good primers, but sometimes you need primers at fixed locations for which this tool cannot be used.
QGRS Mapper	Web-tool which can be used to scan for G-quadruplexes. We did not use it extensively, since we did not have problems with G-quadruplexes.
Adobe Indesign, Illustrator&Photoshop	Really powerful tools for the design of magazines/guides and images respectively. We use this for our cloning guide
MathWorks Matlab	Our go-to tool for modeling purposes.
NotePad++	Eases the design of webpages in general, and is really useful for troubleshooting problems with webpages. We use it to design our wiki.





1. What software are you using in iGEM this year?

In order to do the modeling part, or engineers are using MatLab due to its versatility and its computational power to solve difficult problems with a lot of variables.

LaTeX is also used in order to create several documents that will be used in conferences of given to businesses while looking for financing.

Also, the web Genome Compiler is very useful as it can be used for creating plasmids and digest them, it is very useful for "in silico" labwork.

The package from Microsoft is also used; Excel and Word mainly.

In order to design 3D structures, SolidWorks is used.

Specific software from our machines, as fmDim from LIAGRO dimmer

2. What software have you used in previous competitions?

The same as in this competition, maybe this year we have used more than in previous years (SolidWorks) because they didn't create a device as this year.

3. What kind of software do you need most? Which features are you looking forward to?

The one we are using the most is the one from our machines because if not, our experiments would lack of sense as we need specific wavelenghts and intensities.

The other that we use the most is the one that allows us to create plasmids and digestions.

The most important feature is accuracy, if it wasn't accurate, it wouldn't be helpful at all, also we look for the possibility to save a lot of time, if the program is very slow or it slows the computer down too much, it is discarded.



Facebook: www.facebook.com/ValenciaUPViGEM2015

Twitter: <https://twitter.com/UPVigem>

Google: <https://plus.google.com/u/2/110318939646477138807/posts>

Wiki: http://2015.igem.org/Team:Valencia_UPV

Email: Valencia.upv.igem@gmail.com

1. What software are you using in iGEM this year?

Microsoft Office

MATLAB

2. What software have you used in previous competitions?

Microsoft Office


Adobe Illustrator – for a lab manual

3. What kind of software do you need most? Which features are you looking forward to?

Data modeling software- our team is very unexperienced in this world. We are excited to use MATLAB this year and explore it's capabilities. Software to make website design easier would also help us- the aesthetic part of web design has not been our team's strong-suit in the past.

Facebook: <http://www.facebook.com/WLCiGEM>

Email: sierra.tackett@mail.wlc.edu

The logo for WLC-Milwaukee is presented within a white rectangular box. This box is centered within a larger red rectangular frame that features a diagonal line pattern. The text 'WLC-' is positioned on the top line, and 'Milwaukee' is on the bottom line, both in a bold, red, sans-serif font.

WLC-
Milwaukee

**PRO
JECT**

By: EPFL 2015 iGEM &
Valencia UPV Team

WET



**iGEM₂₀₁₅
team**

EPFL

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Twitter: @EPFL_iGEM
Instagram: @igem2015epfl

Biologic Orthogonal GRNAimplemented Circuit

This summer, the EPFL iGEM team strives to pave the way for simpler implementation of digital circuits in vivo. Using the newly discovered dCas9 as a synthetic transcription factor, we aim to design biocompatible transistorlike elements. Our ultimate goal is to make cells smarter by assembling these transistors into logic gates that are both chainable and parallelizable in a



Team-EPFL

homogenous logic framework.

Thinking binary

Boolean Logic is the bedrock of the digital revolution. Developed by George Boole in the mid-19th century, it is based on a simple set of values: 0 ("FALSE") or 1 ("TRUE"). Modern computers represent all forms of information using strings of the same 0s and 1s (also named "Bits"). The processing of bits is handled by logical transistors which can be seen as electronically controllable switches. Elementary logic operations are performed using cleverly assembled transistors. Such assemblies are named "logic gates". Gates are the bricks with which complex behaviour is produced.

Biological computers

Since the early 2000's¹, multiple synthetic biological gates have been built, revolutionizing our ability to dictate the way organisms react to stimuli. Their applications range from intelligent biosensors to cellular therapeutics with improved in vivo targeting and curing.

Unfortunately, the development of programmable cells has been hampered by difficulties in the multiplication and chaining of logic elements². This has hindered the complexification of biocircuits as well as the automation and flexibility of their design.

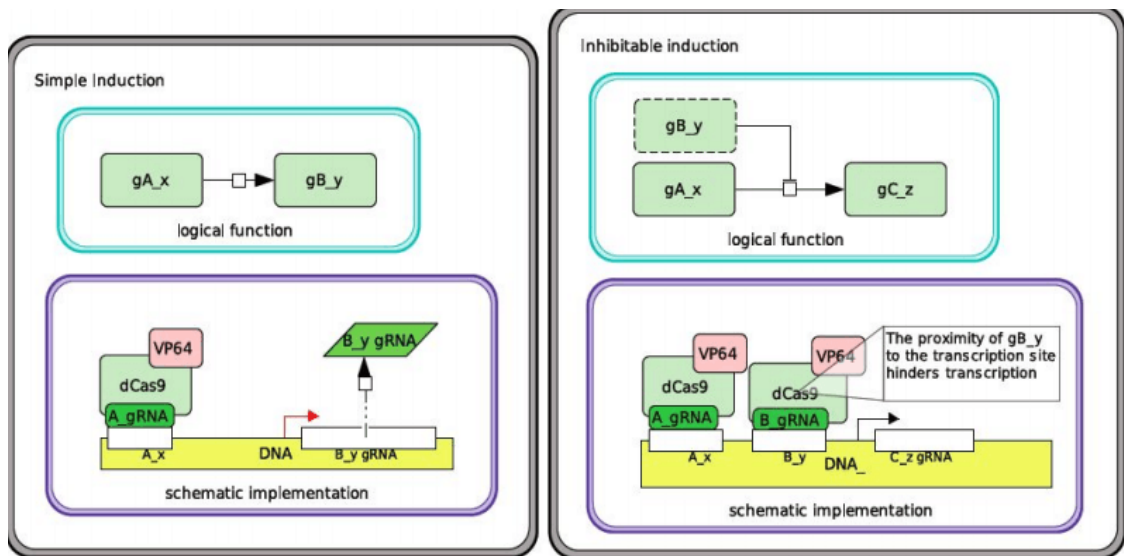
To overcome these limitations, an ideal in vivo logic element should be modular, reusable, and orthogonal i.e. avoiding unwanted crosstalk with its host organism as well as other elements of the engineered circuit.



Cas9 Logic Gates

Cas9 (CRISPR associated protein 9) is an RNAguided DNA endonuclease that targets and cleave any DNA sequence complementary to its guide RNA (gRNA)³ Our project will be based upon a derivative of this technology : catalytically "dead" Cas9 (dCas9) that lack the ability to cleave DNA. When fused to a RNA polymerase (RNAP) recruiting element (e.g. the omega subunit of RNAP in E. Coli or VP64 in eukaryotes), chimeric dCas9 can act as a programmable transcription activator⁴. In addition, activating dCas9 may also act as a DNA transcription inhibitor: depending on its gRNA-determined binding site, it has been shown in yeasts to sterically hinder RNAP recruitment to promoter sequences.

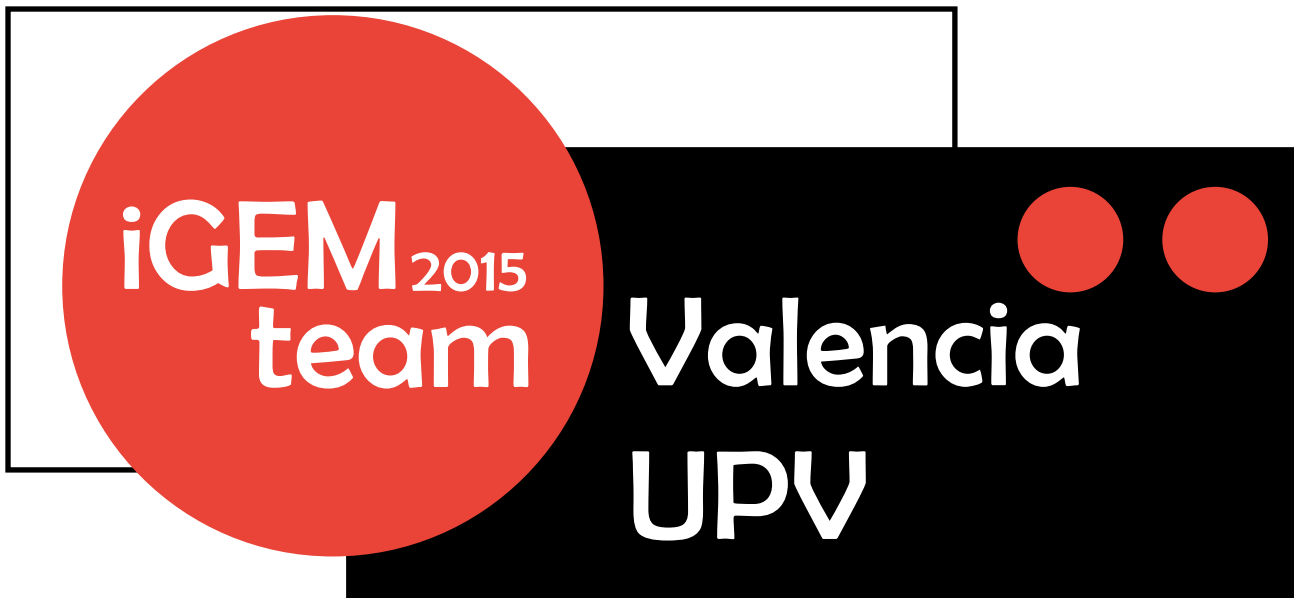
Exploiting dCas9/VP64's ambivalence, we propose the creation of gRNA-controlled switchlike elements analogous to transistors. The state of the switch



The two states of a gRNA-controlled transistor.

would be solely dependent on the position of dCas9 relative to the promoter. The content of the gRNA-targeted sequences might therefore be designed such that each transistor is orthogonal to other logic elements. Using gRNA to make what could be seen as "biological wires", we also hope to achieve chainability of the transistors and thus complexification of biocircuits.

1. Gardner, TS. "Construction of a genetic toggle switch in : Escherichia coli ..." 2000. < <http://www.nature.com/articles/35002131> >
2. Wang, B. "Engineering modular and orthogonal genetic logic gates for ..." 2011. < <http://www.nature.com/articles/ncomms1516> >
3. Cong, L. "Multiplex Genome Engineering Using CRISPR/Cas Systems." 2013. < <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3795411/> >
4. Bikard, D. "Programmable repression and activation of bacterial gene ..." 2013. < <http://nar.oxfordjournals.org/content/early/2013/06/12/nar.gkt520.long>



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AladDNA

It makes your wishes come true!

The idea of this project is the product of tones of brainstorming hours, so, first of all I would like to explain what the problem we want to solve is.

The Problem

Producing materials in all countries involves the creation of huge factories, enormous quantities of raw material and high costs for transporting the entire production. This is a big problem, especially for non-accessible areas or regions where it is impossible to create a factory, as space stations.

The idea

So is there any object that produces utilities from raw material? Maybe a kind of Magic Lamp? That is what we want to create in Valencia_UPV! Miniaturization of a factory to its minimum expression thanks to genetic engineering.

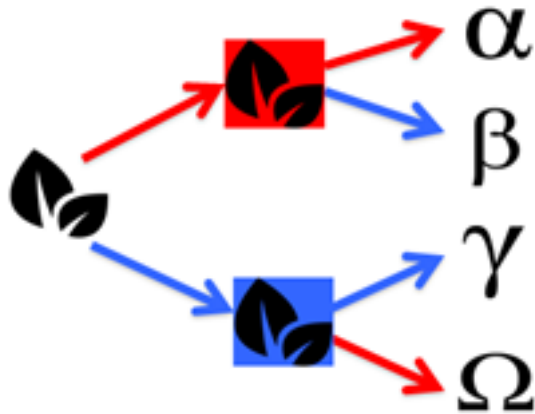
The solution

In order to create lots of different product from a single media, we have designed a biological circuit that allows plant to change their metabolic pathway thanks to light stimulus. It is a two-steps optogenetically controlled cascade where the first level can be activated with red light or blue light. When it is activated with red light, the blue light pathway is deactivated and vice-versa... But why stopping there?



The second part of the cascade involves another combination of red and blue light switches. This allows creating a kind of binary code for the cell where series of light pulses are traduced as combination of 0 and 1.

With this technology we can avoid using chemicals for changing the metabolic pathway and produce nearly anything we want in the cell, what is more, this can be virtually expanded to infinite, allowing the creation of several different compounds just with one machine and



two stimulus.

The chassis for the experiment are plants, but why plants? They need light to grow, so maybe they aren't the best organism for optogenetics, aren't they?

In their primary growth steps, light is not needed, and, what is more, seeds are very resistant to unfavorable environments, so this allows us the creation of a gadget that keeps the seeds in its interior and which can be usable in many different environments, from the desert

to the Space. Just pressing a button, the gadget can be programmed to stimulate the plant with the correct sequence of light and with the enough intensity and time thanks to LEDs technology.

Modeling is very important in our experiment. Protein production in living organisms involve a lot of variables that must be controlled in order to not produce other compounds apart from the one selected.

That is why we trust so much in our engineers. They are spending hours and hours working with equations, kinetic constants and sophisticated software in order to make everything work properly, allowing the creation of a small and compact dispositive.

In order to obtain results, we are trying to produce some small proteins such as interferon alpha, a rotavirus vaccine, a cholera vaccine and lactoferrin, compounds that can be useful in underdeveloped countries, but keep in mind that the range of possibilities is enormous.

And that's it! Mix a little bit of biology with another bit of engineering sauce and add the magic touch to create AladDNA, the GENEious that will make your wishes come true!

Written by:

Daniel Pellicer

Member of Valencia UPV Team in 2015



**Human
Practices**

**Collaboration
&
Questions**



Collaboration Opportunities

Let's work together

Facebook:

<https://www.facebook.com/bbk.igem>

Twitter:

<https://twitter.com/bbkigem>

Wiki:

<http://2015.igem.org/Team:Birkbeck>

BBK
iGEM
2015

iGEM₂₀₁₅
team

Birkbeck

Local London Labs

Our experiments are the bread and butter of iGEM. The breadth and depth of PCR, transformation, culturing, characterisation and other wet lab techniques require substantial resources, materials, equipment and supervision. We welcome all London-based iGEM teams to collaborate with us in carrying out experiments and sharing findings.

Recreation

With the core work now underway, we are all extremely busy, worried, stressed, caught up in all the elements of competing in iGEM, and would welcome the chance to unwind and relax with fellow participants from other teams! Whether it's organising a barbecue or a synthetic biology pub quiz, let's chill out iGEM style after hours.

Fundraising

Collaborate with Birkbeck iGEM 2015 by taking part in, sharing and donating to our Giant Jamboree fund here gofundme.com/zq5h6s. Other ways of helping include organising joint fundraising events and coming up with ideas on effective fundraising from various sources.

Wiki design and Art

Developing a successful wiki takes a diverse range of skills including programming, editing and design. As a strong team of science-minded members, we've found the perfect collaboration

opportunity in having an art-minded person come up with some cool ideas for our wiki, T-shirts, etc. Do you know someone who might help? Are you that person? If so, please get in touch!

[Picture - Birkbeck]



A black circle containing the text "iGEM 2015 team" in white. The "iGEM" is in a large, bold, sans-serif font, "2015" is smaller and to the right, and "team" is below "iGEM".

iGEM₂₀₁₅
team

A red parallelogram containing the text "ETH-Zürich" in white, bold, sans-serif font.

ETH-Zürich

A solid red vertical bar.

Facebook: <https://www.facebook.com/iGEM.ETH.Zurich>

Twitter: https://twitter.com/ETH_iGEM

Email: igem2015@bsse.ethz.ch

Problems we have in the lab

Problem No. 1: Not nicely growing Jurkat cells

For some experiments we work with Jurkat cells. Cultivating mammalian cells is way more complicated than cultivating bacterial ones. So it comes that our Jurkat cells sometimes just do not grow or even die. What could be the reason? Do you have any ideas what we could improve, so they better grow?

Problem No. 2: Random GFP contamination in some constructs

We keep getting random GFP contamination in our constructs from time to time. Why could that be? What can we do so it does not happen again?

Problem No. 3: Losing small fragments when doing biobrick assembly

When we do Biobrick assemblies with small fragments we often lose them and on the gel it can not be seen if the digest worked or not. Does anyone have some tips how to avoid losing the fragments?

iGEM₂₀₁₅
team

TU
Eindhoven



Facebook:

<http://www.facebook.com/EindhoveniGEM>

Twitter:

via @Eindhoven_iGEM

Email:

igem2015@tue.nl

As team TU Eindhoven we are searching for different iGEM teams which are willing to collaborate with us. We have started to make a cloning guide for new iGEM teams to be able to make a clear choice on what cloning method to use. For this guide we are looking for different teams who are working with one of the following cloning methods:

- Classical Cloning
- Biobricking
- Rapid DNA prototyping
- 3A assembly
- Golden Gate Assembly
- Gateway Cloning technology
- TA cloning/ TOPO TA cloning
- In-Fusion
- Ligation independent cloning
- Di or Multi cistronic cloning

If your team is working with one of these cloning methods and is interested to collaborate with us, please e-mail us at igem@tue.nl. More information will be given to the collaborating teams.

A black circle containing the text "iGEM 2015 team" in white. The "iGEM" is in a large, bold, sans-serif font, "2015" is smaller and to the right, and "team" is in a slightly smaller font below it.

iGEM₂₀₁₅
team

A red parallelogram containing the text "WHU-China" in white, bold, sans-serif font.

WHU-China

Facebook: river Li

Email:rivero70405@gmail.com

Problems on our way

First thanks for inviting! This is our honour to share the problems we met in the pass few months in the News letter.

The process of preparing for iGEM would be a life changing experience for many of us and the problems we met during this are far more beyond Biology. The multidimensional problems, sure, are part of the fun but still the pain in the ass. By describing our problems and some solutions, we hope to reach some kind of consensus on other teams.

The problems are coming up on and on from normally these five parts: Experiment; Mathematic model; Website design; Team construction and Human practice.

1. Experiment

- Wether should we ask all the team members to stay in the University in the summer holiday or only those who got the chances to go to the giant jamboree?

Fortunately this year our team is really unitive so we do not have to deal with this question directly. However we think the answer maybe is yes because this huge competition needs teamwork and the jamboree is merely one part. Maybe this problem should be clearly delivered when recruiting.

- Wether should we change a person when the experiment is struck or change the methods or...?

Change a person is the easiest way but this surly will hurt the team. In fact we tended to re-do the experiment or ask for help from our advisors etc. , which means we try to work it out together first.

2. Mathematic model

- Should we looking for people that have some relative knowledge about biology while are capable of building a mathematic model—this is really hard?

- If not, but, how can this pure mathematic builder interact with other members?

- And where can we find some information and resource for mathematic model building?



3. Website design

- How to divide the job of art design group and website building group?

Now our art designers who come from COFS are working out whole website outlook plan and the website builders are realising it. What if we could not recruit new members with good sense of design while the website builders from other college could not catch the main idea of the whole project either?

- How to update the building work with the builders come from other college, should we push them everyday?

While, this question is truly awkward.

4. Team construction

- Are there any restrictions of grades, ages, member numbers that we should consider seriously?

- Whether should we construct our team like a student society with clear divisions to manage different jobs or just like a team where team leaders are responsible for solving almost all the problems?

Currently we do not have a clear division of labor, which indeed cause some chaos and deficiency. On the other hand, these multitasks situation keeps most team members really active and close to the game.

5. Human practice

- Besides attending exchange meetings, do we have any other form of activity that may more interesting and creative?

- Whether should we follow the instruction in the iGEM official website or come up with our own ideas of HP activities?

Human practice may be the most difficult part for us and, we believe, many other teams. If we can have any colourful HP project and get a fine result, our presentation in the jamboree would be much more richer and impressing.

These are the main problems we have met in the past couples of months and we are trying to solve them everyday. Hopefully we can find the cure soon. We also hope that some widely happened problems could get some official attention.

Thanks for reading!

Feed Back

Thanks for your support



Feedback

1. Is this issue useful for your team?

- A. Yes. It may help.
- B. No. I cannot see any important reference value to my own team, because each situation differs.
- C. Maybe a little.

2. How many passages are suitable for each issue?

- A. Not more than 5.
- B. 6-8
- C. 9-12
- D. 13-15
- E. 15-20

3. How often should we publish Newsletter?

- A. Weekly.
- B. Biweekly. (The same as last year)
- C. Triweekly.
- D. Monthly.

4. Is it necessary to add new content besides project & update?

- A. Yes. (Run to 5)
- B. No (Run to 6)

5. What contents can be added in Newsletter (multiple-choice)?

- A. Discussion on bioethics.
- B. Experts' interviews.
- C. Summary information for Biobricks.
- D. Wiki technology.
- E. Art & Design.
- F. Others _____ (Please let us know your idea)

6. Are there any problems you have encountered? Would you like to write them down on Newsletter so that other readers can help you?

7. Any suggestions after reading this issue? Help us to make the Newsletter better!

Thank you for your support.

Please complete the feedback form and send it to us: igemxmu@gmail.com

