User Guide

SJTU-Software 2015

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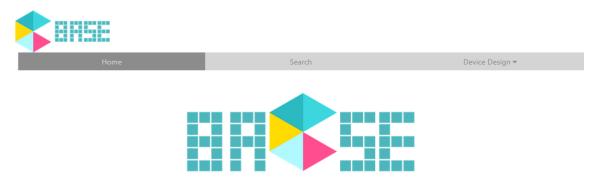
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1 What is BASE

BASE is a web-based application developed by 2015 iGEM team SJTU-Software to help users select appropriate biobricks. The full name of BASE is *Biobrick Auxiliary Selection Explorer*.

BASE has two main functions: biobrick **search** and **device design**. And there are three subordinate functions in the device design function: **construct**, **evaluate**, and **upload**. BASE has its own database and a set of well-developed scoring algorithms. The information in the database is extracted from the source code of the websites of the biobricks in the iGEM part registry. The scoring system is based on factors selected from the database. The weights of the factors are optimized with several methods.

With BASE, you can pick good biobricks out of others much more easily. When you open the website of BASE, the interface will be like this:



BASE: Biobrick Auxiliary Selection Explorer

Many existing biobricks are not well documented, which make it challenging to use them. Here we present a web-based tool BASE (Biobrick Auxiliary Selection Explorer) to search, evaluate and visualize biobricks at part, devise and system levels. At part-level, similar to our work last year, biobrick parts are scored according to their current status, user comments and reviews, times of citation and etc.

At device level, features, such as the order of parts and the co-existence frequency of two parts in a device, are added into the scoring system.

At system-level, the regulation relationship between devices is added to the scoring system.

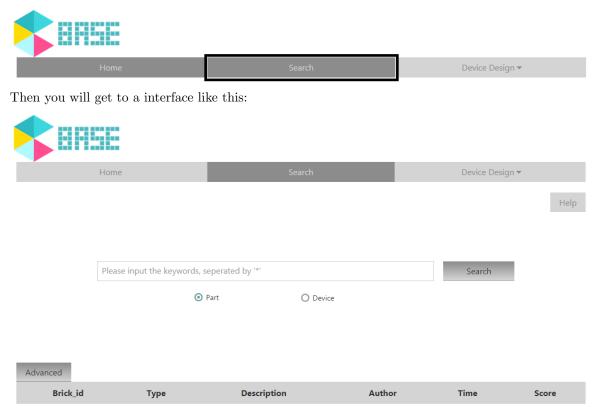
At each level, the biobricks can be searched, evaluated and ranked according to their scores. A visualization function is also provided.

In addition, the score can also be calculated according to a user-defined configuration, and an automatic adjusting system is also provided to incorporate users' selection preference.

2 Search Function

The *search* function is just like a normal search engine. The difference is that BASE provides you with information of the bricks and the features that you are interested in.

To begin to use the search function, you can click the "Search" button on the navigation bar in the home interface.



You can click the circle in front of the words – "Part" and "Device" (Shown in Figure ??). Part means one single biobrick without subparts while Device means bricks that are composed of parts. You can also get the explanation simply by moving your mouse onto the words.



Figure 1: Part and Device selection

Then you may input the keyword for search into the bar frame. You can get a list of results under the factor names when you click the "Search" button, shown in Figure ??.

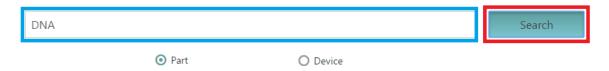


Figure 2: Search function, in this case, *DNA* is used as the keyword.

The result will be like this:

Advanced					Total: 7
Brick_id	Туре	Description	Author	Time	Score
BBa_K143001	DNA	5? Integration Sequence for the amyE locus of B. subtilis	Chris Hirst	2008/8/27	81.23
BBa_K143002	DNA	3? Integration Sequence for the amyE locus of B. subtilis	Chris Hirst	2008/8/28	81.19
BBa_B0040	DNA	Spacer.1 (generic)	Vinay S. Mahajan, Brian Chow, Peter Carr	2003/1/31	77.53
BBa_J61001	DNA	[R6K] Origin of replication	John Anderson	2006/7/31	73.70
BBa_J44000	DNA	hixC binding site for Salmonella typhimurium Hin recombinase	Missouri Western and Davidson Groups, Todd Eckdahl	2006/6/6	71.19
BBa_I13450	DNA	Removes BioBrick End	jkm	2005/5/25	67.13
BBa_J61046	DNA	[Lox] site for recombination	John Anderson	2007/2/20	58.76

The background color varies according to the score of the biobrick. It shows to what degree we recommend the biobrick. Blue-green appears when the score is higher than 80, which mean greatly recommended. Bricks with scores within 70 and 80 will get the yellow background, which means moderately recommended. Grey means recommended while red means the average level. And we differentiate these two according to whether the score is greater than 60.

You can select biobricks from the list. The total number of the results is shown at the top-right corner. If you need more information, still, there are two ways. If you click the ID of the biobrick, which is shown in the first column, you will get a new web page which is the website for the biobrick in the iGEM registry. You can get the specific information there. You can also click the score which is shown in the last column. And if you do that, you would get a popup box about the detail scores the biobrick gets with all the factors, like this:

Score Detail								
Part_status: 7.50/7.50	Sample_Status: 0/6.80	Part_Results: 11.90/11.90						
Star_rating: 7.50/7.50	Uses: 15.79/13.70	DNA_Status: 6.70/6.70						
Qualitative_experience: 3.50/3.50	Group_favorite: 0/2.70	Del: 5.50/5.50						
Confirmed_times: 0.52/10.00	Number_comments: 10.50/10.50	Ave_rating: 13.70/13.70						
	OK							

The number in the front shows the score that the biobrick gets, and the number behind shows the total score for the factor.

If you are not satisfied with the built-in weight, or if you want to show biobricks whose scores are relatively low, you can click the "Advanced" button, which is located at the top-left corner of the factor names, shown as below.



Then you will get a popup box like this:

Weight					
Part_status	7.5	Sample_Status	6.8		
Part_Results	11.9	Star_rating	7.5		
Uses	13.7	DNA_Status	6.7		
Qualitative_experience	3.5	Group_favorite	2.7		
Del	5.5	Confirmed_times	10		
Number_comments	10.5	Ave_rating	13.7		
The lower bounds of score					
Score	45				

At the top of the box, you can adjust the weights of the twelve factors. The built-in weights are optimized and add up to 100, but you do not need to care about the summation. You can input any nonnegative number into the blanks, and the score of each factor will be automatically calculated according to the weights to ensure the total score is 100.

At the bottom of the box, you can change the lower bound of the score. The built-in bound is 45. You can adjust the number to fit special needs. But if you set the lower bound to 0 and input a very ambiguous keyword, the waiting time may be very long, and the website may crash, since there are too many results to show on the interface.

If you need to input more than one keyword, you need to separate those words with "*", like this:



Advanced					Total: 58
Brick_id	Туре	Description	Author	Time	Score
BBa_B0034	RBS	RBS (Elowitz 1999) defines RBS efficiency	Vinay S Mahajan, Voichita D. Marinescu, Brian Chow, Alexander	2003/1/31	83.11
BBa_R0040	Regulatory	TetR repressible promoter	June Rhee, Connie Tao, Ty Thomson, Louis Waldman	2003/1/31	66.80
BBa_R0010	Regulatory	promoter (lacI regulated)	registry	2003/1/31	66.43

There are also some tips if you click the "Help" button.

			SEARCH HE	ELP				
This part provides you v b	vith information about the b iobrick in this blank to start y	iobrick at the lev our search.The	vel of part or device. keywords can only b	. You can enter one or m be the brick ID ,type,or so	ore keyword (ome words in	(separated by '*' the description.	related to your target)	
	Please input the keyw	oras, seperat	ed by **			Search		
		Part	○ De	vice				
Click radio button 'Par	t' or 'Device' before searchir	ig to choose wh	ich kind of biobrick biobrick:	you need (part or device).You can get	these information	on about your target	
	Brick_id Ty	pe	Description	Author	Time	Score		
		arch scope. Rem	ember to click butto	on 'Sure' to save your cha	anges.			
	Part_status	7.5		Sample_Status	6.8			
	Part_Results	11.9		Star_rating	7.5			
	Uses	13.7		DNA_Status	6.7			
	Qualitative_experience	3.5		Group_favorite	2.7			
	Del	5.5		Confirmed_times	10			
Number_comments 10.5 Ave_rating 13.7								
The lower bounds of score								
Score 45								
Sure								
			OK					

3 Device Design Function

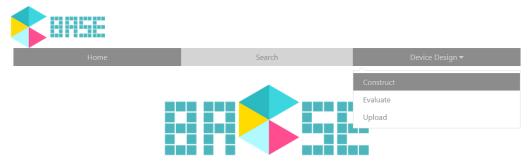
The device design function is a composite function, composed of three functions. We have made it a linkage function, that is, users can use the three functions continuously, and do not need to enter the input three times. Still, users can use only one or two of the three functions.

The device design function helps users build up a complete device and upload it to BASE's database. The three functions will be presented in the next three sections.

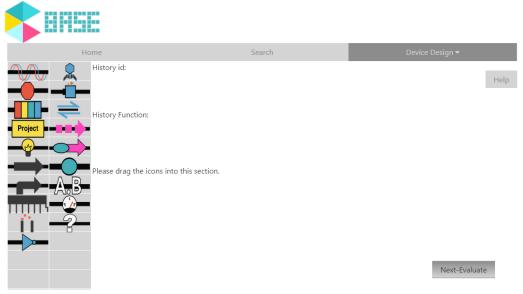
3.1 Construct Function

The *construct* function is a visualization and recommendation function.

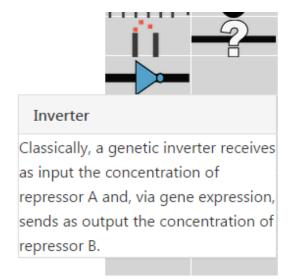
To start to use this function, you need to click the "Device Design" button and select the "construct" button.



After that, you will get the interface like this:



There are 19 different icons placed on the left side of the interface. Those represent 19 different types that a part may belongs to. When you move your mouse onto the icons, a brief introduction of the type will be displayed. An example is shown below.



These icons can be dragged to the right-hand side of the interface to build a device.

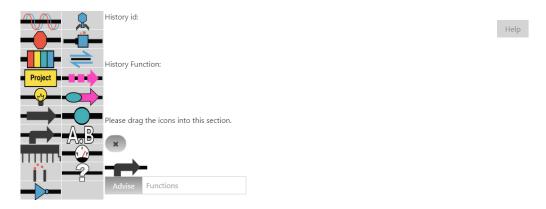


Figure 3: In this case, *Regulatory* is dragged into the right interface as the first part.

For example, you can drag a *Regulatory* into the interface (Figure ??). You can input your keywords into the frame after the "Advice" button. Or you can also input nothing. If you click the "Advice" button, there will be a popup box showing five recommended parts ordered by their scores to choose from.



And you can also directly input the ID of the part you want. What you need to do is to select the little the circle in front of the word "other" (Figure ??).

Then there will be a new frame. You can input any brick ID into the frame. Then you need to click on the "Check" button on the right side since BASE has to check whether there is a part that has the same ID and type you have dragged in. When you have selected one from the five, or the appointed ID have passed the check, the confirm button would appear (Figure ??).

When you click the "Sure" button, the ID will be recorded, and cannot be altered, though you can delete it. The ID and the function are displayed, shown in Figure ??:



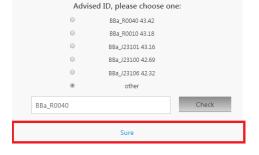


Figure 4: User can also choose "other" and input a biobrick to check.

Figure 5: After input a biobrick, press "Sure" button to return to the "construct" process.

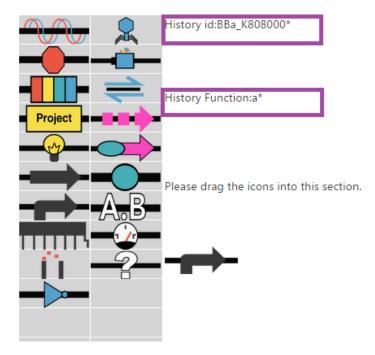


Figure 6: The ID and function of the selected biobrick are displayed and recorded.

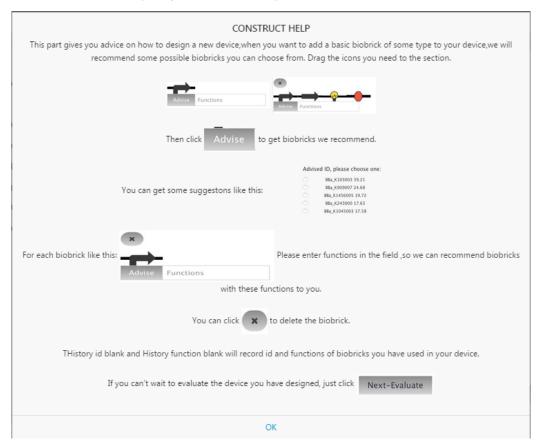
You can choose the ID right after you drag an icon. Or you can drag several icons into the interface, and then begin to choose ID for all these parts. However, there is another thing worthy of mentioning in this function. the score not only calculates the parts' own score, but also considers the interactions between parts. That is, the score you see in the box is affected by the part IDs that you have already chosen.

If you want to delete a part, you can click the " \mathbf{x} " button. The *History ID* and *History Function* records will also be deleted. But one thing needs to be careful: if you delete a part that is not the last one in the device, the parts after it will also be deleted, since the part IDs you chose are affected by the one you delete.

When you finish building the device, you can have a screenshot and finish the work. Or you can click the "Next-Evaluate" button to go to the next function: "evaluate".



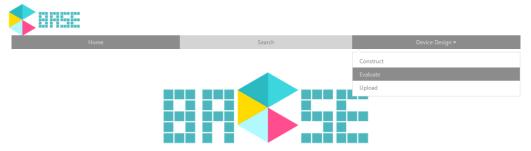
There are also some tips if you click the "Help" button.



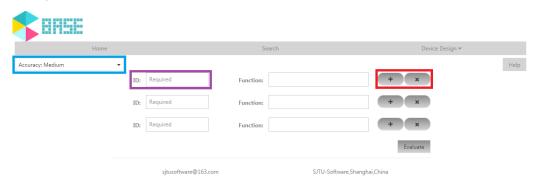
3.2 Evaluate Function

The evaluate function scores the devices that user creates and provides advice. In this part, the main part and the principle of the scoring are the function of the device, that is, the description and score of the coding parts.

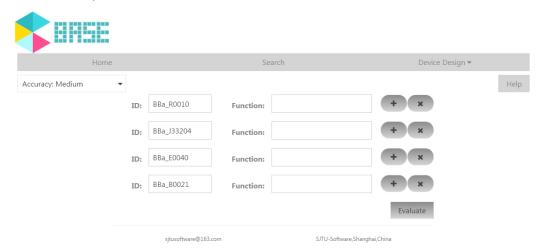
There are two ways getting to this function: either getting to the interface from the *construct* interface, or selecting the "Evaluate" button after clicking the "Device Design" button.



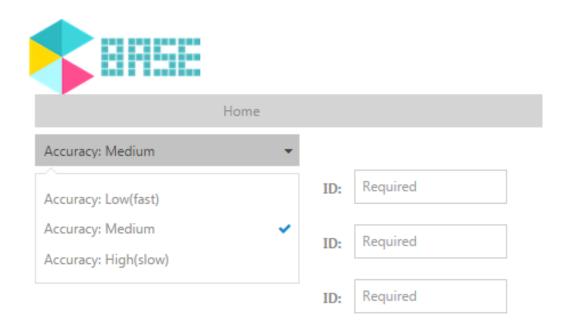
Then you will see the interface like this:



By clicking the "+" button, you can add a row to the bottom of the current row. By clicking the " \mathbf{x} " button, you can delete the current row. If you choose the former one, you do not have to input anything again. Or you need to input the parts' ID and the function you expect the parts to perform(the IDs are required but the functions are not).

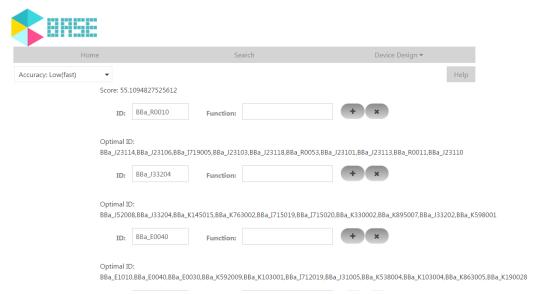


Then you need to choose the accuracy. There are three levels – low, medium, and high. The built-in accuracy is medium.

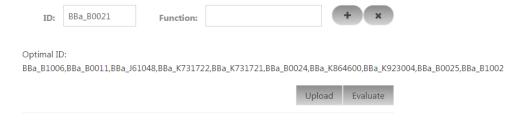


Higher level requires more time but provides more accurate result. And if you place many(more than 5) parts in one device, even the low precision may cost dozens of seconds.

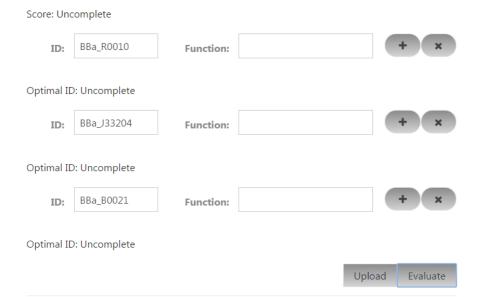
After selecting the accuracy, you can click the "evaluate" button. It may take some time to calculate, so please DO NOT leave the page. You will finally get a score for the whole device and the top 10 recommended parts will be shown in a row.



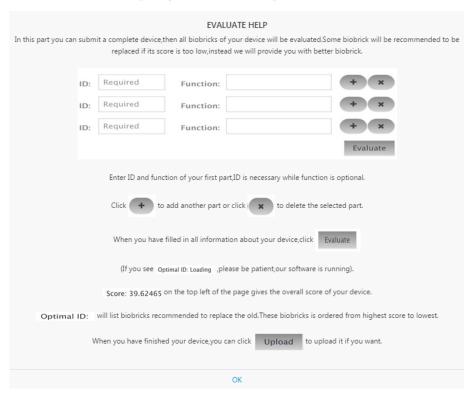
The part you use may also be one of the ten parts. If you want to revise your device, you need to input the ID that you want and click the "evaluate" again.



We add the judgment of completeness and order into BASE. That is, if your device lack the necessary type of part, or the order of the parts is in a mess, no score will be given, but some words, like this:



When you finish the evaluation, you can click the "Upload" button, reaching the final function. There are also some tips if you click the "Help" button.



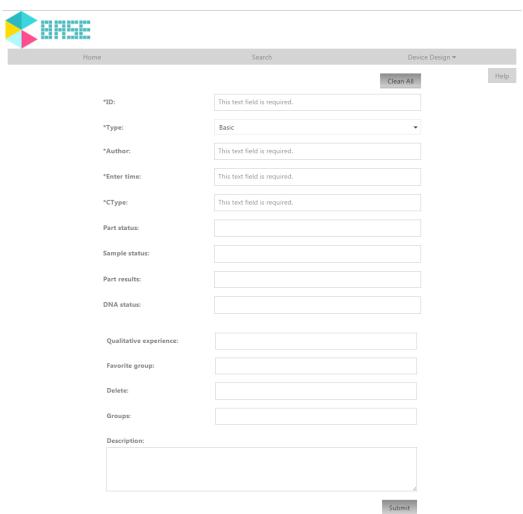
3.3 Upload Function

Users can upload their devices into BASEs database with the upload function.

Like the previous functions, you also have two ways to use this function, via the former function or by clicking the button.



The interface will be like this:



The frame with a "*" is required. If you get here via the former function, some of the frames will be automatically filled in, including type, subpart and description. Of course, you can still change these factors. When you click the "Submit" button, your device will be delivered to BASEs database.

If you click the "Clean all" button, all input information will be removed.

There are also some tips if you click the "Help" button.

