

BASE Version Control

SJTU-Software 2015

*This document specifies all the version upgrades of the **BASE** project.*

1. judge

- v1.0
Judge whether the biobrick in the database or not according to its ID.
- v2.0
Judge whether the biobrick of a certain type in the database or not according to its ID.

2. baseadvice

- v1.0
Find several bricks with higher scores on the basis of the type of biobrick and its description.
- v2.0
Use a score limit to filter the candidate parts with low score.
- v3.0
Use new default score to rank the candidate parts;
Return the result by printing the biobricks and their score.
- v4.0
The candidate parts in the existing parts group will not be recommended.

3. gscore

- v1.0
Use a few features to score the biobrick;
The weights of features are the same.
- v2.0
Add more features to score the biobrick;
The default weights of features are trained to be optimal.
- v3.0
The default weights of features are optimal;
Allow users to reset the weights to score the biobrick.

4. basearch

- v1.0
Search the database on the basis of the biobrick ID, type, and description;
Return a few features of biobrick.
- v2.0
Call *gscore* to score the candidate biobricks and rank them.
- v3.0
Allow users to reset the weights to score the biobrick.

- v4.0
Use a score limit given by users to filter the candidate biobricks with low score;
Return the score of each feature of the biobrick.

5. `evaluate_score`

- v1.0
Calculate the score of the device that depends on the score of each part.
- v2.0
Calculate the score of the device that depends on the score of each part and the interactional score of each two parts.
- v3.0
Calculate the score of the device that depends on the score of each part and the interactional score of each two parts, and the type of one part must be coding.

6. `evaluate`

- v1.0
Evaluate the best ten biobricks of each part users input and the biobrick we evaluate will make the score of the device higher if replacing the original biobrick.
- v2.0
Before evaluation, we will judge the completeness of the device.
- v3.0
Before evaluation, we will judge if the order of the parts in the device is correct.
- v4.0
The device will be judged complete if there is an *Inverter* or *Generator*.

7. `upload`

- v1.0
Upload the biobrick with a few features.
- v2.0
Upload the biobrick with more features;
Set some features a default value.

8. **The web development**

- v1.0
Finish the basic framework and implement all the main functions.
- v1.1
Add enter key function and warning when leaving the webpage.
- V1.2
Allow users to select weight themselves.
- V2.0
Modify the logic among the webpages and support the data transfer between functions.
- V2.1
Add the lower bound of the score, add home page, and show the total row number.
- v2.2
Finish *readme* file.
- V2.3
Fix the existing bugs.

9. The database development

- V1.0
There are 4,000+ biobricks.
- V2.0
By reconstructing the database table, we have about 14,000 biobricks. We give each biobrick a default score.
- V2.1
There are 28637 biobricks
- V3.0
With the new database table, our Scoring function and Advice function are faster.

BASE Software Test

SJTU-Software 2015

*This document specifies the function and module tests of the **BASE** project.*

1. judge

A function to find out whether the biobrick of a certain type is in the database or not, and returns result by printing “Yes” or “No”.

Call function *judge.pl* to judge, the result is shown in Table 1.

Table 1: Test result of judge function

Command	Expectation	Result
perl judge.pl BBa_B0034 RBS	Yes	Yes
perl judge.pl BBa_B0034 Regulatory RBS	No	No
perl judge.pl BBa_R0040 Regulatory	Yes	Yes
perl judge.pl BBa_Z Regulatory	No	No

2. baseadvice

- perl advice.v4.pl “-” RBS “”
 - Expectation
The function should return the *RBS* biobricks and rank them by scores.
 - Result
BBa_B0034 | 54.02
BBa_B0032 | 40.06
BBa_B0030 | 40.01
...
BBa_K783048 | 12.86
BBa_K783047 | 12.86
BBa_J34803 | 12.81
BBa_J34801 | 12.81
BBa_J70591 | 12.80
- perl advice.v4.pl BBa_B0034 Coding “Lux”
 - Expectation
The function should return the *Coding* biobricks about *Lux* and rank them by scores.
 - Result
BBa_C0062 | 28.75
BBa_K594001 | 24.68
BBa_K082006 | 22.96
BBa_K091109 | 13.70
BBa_K581013 | 13.61
BBa_K1230000 | 13.61
BBa_K199125 | 13.59
BBa_K199143 | 13.58
BBa_K199142 | 13.58

BBa_K1202002 | 13.58

...

- perl advice_v4.pl BBa_B0034*BBa_C0062 terminator “”
 - Expectation
The function should return the *terminator* biobricks and rank them by scores
 - Result
 - BBa_B0011 | 37.76
 - BBa_B0021 | 37.56
 - BBa_B0025 | 32.87
 - BBa_B1006 | 28.32
 - BBa_B1007 | 27.95
 - BBa_B1003 | 27.94
 - BBa_B1010 | 27.94
 - BBa_B1005 | 27.94
 - BBa_K731722 | 24.77
 - BBa_K731721 | 24.69
 - ...

3. gscore

A function to score the biobrick based on the features of biobrick and the weight of features, and returns the score of biobrick and scores of features.

4. basearch

A function to search the biobrick according to the name, type or description of the biobricks, and returns the biobrick and its feature. The biobricks are ranked by the score in the descending order.

Use *hcount_v1.pl* to call the function basearch

- perl hcount_v1.pl RBS brick 10*10*5*5*10*5*10*10*5*5*10*5 50
 - Expectation
The function should return the biobrick parts about *RBS* with score > 50 and rank them by scores.
 - Result
 - BBa_B0034 | RBS | RBS (Elowitz 1999) – defines RBS efficiency | Vinay S Mahajan, Voichita D. Marinescu, Brian Chow, Alexander | 2003/1/31 | 66.78 10.00 | 0 | 5.00 | 5.00 | 11.52 | 5.00 | 10.00 | 0 | 5.00 | 0.26 | 10.00 | 5.00
 - BBa_J33204 | Reporter | xylE reporter gene with rbs | Chris French | 2006/10/17 | 57.19 10.00 | 0 | 5.00 | 5.00 | 0.02 | 5.00 | 10.00 | 10.00 | 5.00 | 0.17 | 2.00 | 5.00
 - BBa_K346004 | Translational_Unit | RBS(B0034)_MBP(lead metal binding peptide engineered from PbrR)+Terminator(B0015) | Junyi Jiao | 2010/10/14 | 51.11 10.00 | 0 | 5.00 | 0 | 0.01 | 5.00 | 10.00 | 10.00 | 5.00 | 0.10 | 1.00 | 5.00
 - BBa_K863005 | Coding | ecol laccase from E. coli with T7 promoter, RBS and His-tag | Isabel Huber | 2012/9/18 | 51.07 10.00 | 0 | 5.00 | 0 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.07 | 1.00 | 5.00
 - BBa_J44001 | RBS | Reverse RBS (RBS_{rev}) – corresponds to BBa_B0030 | Todd Eckdahl | 2006/8/2 | 50.24 10.00 | 0 | 5.00 | 5.00 | 0.06 | 5.00 | 10.00 | 10.00 | 5.00 | 0.19 | 0.00 | 0
 - BBa_B0030 | RBS | RBS.1 (strong) – modified from R. Weiss | Vinay S Mahajan, Voichita D. Marinescu, Brian Chow, Alexander D | 2003/1/31 | 50.06 10.00 | 0 | 5.00 | 5.00 | 2.42 | 5.00 | 10.00 | 0 | 5.00 | 0.31 | 3.00 | 4.33
- perl hcount_v1.pl RBS brick 5*5*10*5*5*10*5*5*10*10*15*5 50
 - Expectation
The function should return the biobrick parts about *RBS* with score > 50 and rank them by scores

- Result
 - BBa_B0034 | RBS | RBS (Elowitz 1999) – defines RBS efficiency | Vinay S Mahajan, Voichita D. Marinescu, Brian Chow, Alexander | 2003/1/31 | 66.78 10.00 | 0 | 5.00 | 5.00 | 11.52 | 5.00 | 10.00 | 0 | 5.00 | 0.26 | 10.00 | 5.00
 - BBa_J33204 | Reporter | xylE reporter gene with rbs | Chris French | 2006/10/17 | 57.19 10.00 | 0 | 5.00 | 5.00 | 0.02 | 5.00 | 10.00 | 10.00 | 5.00 | 0.17 | 2.00 | 5.00
 - BBa_K346004 | Translational_Unit | RBS(B0034)_MBP(lead metal binding peptide engineered from PbrR)+Terminator(B0015) | Junyi Jiao | 2010/10/14 | 51.11 10.00 | 0 | 5.00 | 0 | 0.01 | 5.00 | 10.00 | 10.00 | 5.00 | 0.10 | 1.00 | 5.00
 - BBa_K863005 | Coding | ecol laccase from E. coli with T7 promoter, RBS and His-tag | Isabel Huber | 2012/9/18 | 51.07 10.00 | 0 | 5.00 | 0 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.07 | 1.00 | 5.00
 - BBa_J44001 | RBS | Reverse RBS (RBS_{rev}) – corresponds to BBa_B0030 | Todd Eckdahl | 2006/8/2 | 50.24 10.00 | 0 | 5.00 | 5.00 | 0.06 | 5.00 | 10.00 | 10.00 | 5.00 | 0.19 | 0.00 | 0
 - BBa_B0030 | RBS | RBS.1 (strong) – modified from R. Weiss | Vinay S Mahajan, Voichita D. Marinescu, Brian Chow, Alexander D | 2003/1/31 | 50.06 10.00 | 0 | 5.00 | 5.00 | 2.42 | 5.00 | 10.00 | 0 | 5.00 | 0.31 | 3.00 | 4.33

- perl hcount_v1.pl Generator devic 10*10*5*5*10*5*10*10*5*5*10*5 55

- Expectation
 - The function should return the biobrick devices about *Generator* with score > 55 and ranking by scores.
- Result
 - BBa_E0840 | Reporter | GFP generator | Jennifer Braff | 2004/10/18 | 58.48
10.00 | 0 | 5.00 | 5.00 | 0.53 | 5.00 | 10.00 | 10.00 | 5.00 | 0.28 | 3.00 | 4.67
 - BBa_K145201 | Generator | INPUT TetR generator | Jonas Demeulemeester | 2008/8/20 | 56.17
10.00 | 0 | 5.00 | 5.00 | 0.02 | 5.00 | 10.00 | 10.00 | 5.00 | 0.15 | 1.00 | 5.00
 - BBa_K143082 | Generator | Pveg-spoVG RFP expression construct | Chris Hirst | 2008/10/27 | 56.15
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.15 | 1.00 | 5.00
 - BBa_K143079 | Generator | Pveg-spoVG GFP expression construct | Chris Hirst | 2008/10/27 | 56.15
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.15 | 1.00 | 5.00
 - BBa_K084007 | Signalling | Lac repressible lasI generator (No LVA) | Masahiro Tominaga, Yoshimi Iyama, Kohei Kawasaki | 2008/9/18 | 56.14
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.14 | 1.00 | 5.00
 - BBa_K084012 | Signalling | Lac repressible 3OC6HSL generator (No LVA) | Yoshimi Iyama, Kohei Kawasaki, Masahiro Tominaga | 2008/9/22 | 56.09
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.08 | 1.00 | 5.00
 - BBa_K084008 | Signalling | Lac repressible RhlI generator (No LVA) | Masahiro Tominaga, Yoshimi Iyama, Kohei Kawasaki | 2008/9/18 | 56.08
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.08 | 1.00 | 5.00
 - BBa_K081022 | Composite | Plambda regulated luxR generator and Plux | Lorenzo Pasotti, Paolo Magni | 2008/10/19 | 56.08
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.08 | 1.00 | 5.00
 - BBa_J45319 | Generator | PchA & PchB enzyme generator | Andr?Green II | 2006/10/28 | 55.16
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.16 | 1.00 | 4.00
 - BBa_K081008 | Translational_Unit | luxI protein generator (TERM-) | Lorenzo Pasotti, Paolo Magni | 2008/10/18 | 55.16
10.00 | 0 | 5.00 | 5.00 | 0.02 | 5.00 | 10.00 | 10.00 | 5.00 | 0.14 | 1.00 | 4.00

- perl hcount_v1.pl Generator devic 10*10*5*5*10*5*10*10*5*5*10*5 80

- Expectation

- Nothing. The weight is the same as above, but the score limit is 80. There is no brick with score > 80.
- Result
 - nothing
- perl hcount_v1.pl Generator*RBS*Lux devic 10*10*5*5*10*5*10*10*5*5*10*5 55
 - Expectation
 - The function should return the biobrick devices about *Generator*, *RBS*, or *Lux*, with score > 55 and are ranked by scores.
 - Result
 - BBa_E0840 | Reporter | GFP generator | Jennifer Braff | 2004/10/18 | 58.48
10.00 | 0 | 5.00 | 5.00 | 0.53 | 5.00 | 10.00 | 10.00 | 5.00 | 0.28 | 3.00 | 4.67
 - BBa_K145201 | Generator | INPUT TetR generator | Jonas Demeulemeester | 2008/8/20 | 56.17
10.00 | 0 | 5.00 | 5.00 | 0.02 | 5.00 | 10.00 | 10.00 | 5.00 | 0.15 | 1.00 | 5.00
 - BBa_K143082 | Generator | Pveg-spoVG RFP expression construct | Chris Hirst | 2008/10/27 | 56.15
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.15 | 1.00 | 5.00
 - BBa_K143079 | Generator | Pveg-spoVG GFP expression construct | Chris Hirst | 2008/10/27 | 56.15
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.15 | 1.00 | 5.00
 - BBa_K084007 | Signalling | Lac repressible lasI generator (No LVA) | Masahiro Tominaga, Yoshimi Iyama, Kohei Kawasaki | 2008/9/18 | 56.14
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.14 | 1.00 | 5.00
 - BBa_K084012 | Signalling | Lac repressible 3OC6HSL generator (No LVA) | Yoshimi Iyama, Kohei Kawasaki, Masahiro Tominaga | 2008/9/22 | 56.09
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.08 | 1.00 | 5.00
 - BBa_K084008 | Signalling | Lac repressible RhlI generator (No LVA) | Masahiro Tominaga, Yoshimi Iyama, Kohei Kawasaki | 2008/9/18 | 56.08
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.08 | 1.00 | 5.00
 - BBa_K081022 | Composite | Plambda regulated luxR generator and Plux | Lorenzo Pasotti, Paolo Magni | 2008/10/19 | 56.08
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.08 | 1.00 | 5.00
 - BBa_J45319 | Generator | PchA & PchB enzyme generator | Andr?Green II | 2006/10/28 | 55.16
10.00 | 0 | 5.00 | 5.00 | 0.00 | 5.00 | 10.00 | 10.00 | 5.00 | 0.16 | 1.00 | 4.00
 - BBa_K081008 | Translational_Unit | luxI protein generator (TERM-) | Lorenzo Pasotti, Paolo Magni | 2008/10/18 | 55.16
10.00 | 0 | 5.00 | 5.00 | 0.02 | 5.00 | 10.00 | 10.00 | 5.00 | 0.14 | 1.00 | 4.00

5. evaluate

- Input
 - The first parameter: the biobrick ID of these parts within a device, the biobrick IDs are split by “,”
 - The second parameter: the keyword of these parts within a device, the biobrick IDs are split by “,”, and split by “+” if there are more than two keywords for a part.
 - The third parameter: precision of the evaluation, the default precision is 20 for low level, 40 for middle level, 80 for high level.
- Output
 - In the first line, it judges the completion, 0 for incomplete and 1 for complete(the completion means if there are Regulatory, Coding and Terminator part)
 - In the second line, it judges the order, 0 for unordered and 1 for ordered(the order means if the first part is Regulatory, the last part is Terminator and the coding part is between Regulatory and Terminator)

- In the third line, it outputs the score of the device.
 - The following lines show the biobrick ID the user inputs and evaluate the best ten parts for each part according to their types and keywords.
- Example 1 : Evaluate the complete and ordered device with low accuracy and no keyword.
 - Command


```
perl score.pl BBa_R0010,BBa_J33204,BBa_E0040,BBa_B0021 ,, 20
```
 - Expectation


```
1(mean complete)
1(mean ordered)
The score of the device
The biobrick we evaluate
```
 - Result


```
1
1
55.11
BBa_R0010
BBa_J23114, BBa_J23106, BBa_I719005, BBa_J23103, BBa_J23118, BBa_R0053, BBa_J23101,
BBa_J23113, BBa_R0011, BBa_J23110
BBa_J33204
BBa_J52008, BBa_J33204, BBa_K145015, BBa_K763002, BBa_I715019, BBa_I715020, BBa_K330002,
BBa_K895007, BBa_J33202, BBa_K598001
BBa_E0040
BBa_E1010, BBa_E0040, BBa_E0030, BBa_K592009, BBa_K103001, BBa_I712019, BBa_J31005, BBa_K538004,
BBa_K103004, BBa_K863005, BBa_K190028
BBa_B0021
BBa_B1006, BBa_B0011, BBa_J61048, BBa_K731722, BBa_K731721, BBa_B0024, BBa_K864600,
BBa_K923004, BBa_B0025, BBa_B1002
```
 - Example 2 : Evaluate the complete and ordered devices with high accuracy and no keyword
 - Command


```
perl score.pl BBa_R0010,BBa_J33204,BBa_E0040,BBa_B0021 ,, 80
```
 - Expectation


```
1(mean complete)
1(mean ordered)
The score of the device
The biobrick we evaluate which may be different from the low accuracy
```
 - Result


```
1
1
55.11
BBa_R0010
BBa_K398326, BBa_K091100, BBa_J23114, BBa_K206000, BBa_K143012, BBa_J23106, BBa_I719005,
BBa_J23103, BBa_J23118, BBa_J23115
BBa_J33204
BBa_J52008, BBa_J33204, BBa_J54103, BBa_K145015, BBa_K763002, BBa_I715019, BBa_I715020,
BBa_E0032, BBa_E0022, BBa_K330002
BBa_E0040
BBa_E1010, BBa_E0040, BBa_E0030, BBa_K592009, BBa_K103001, BBa_I712019, BBa_J31005,
BBa_K538004, BBa_K103004, BBa_K863005, BBa_K190028
BBa_B0021
BBa_B1006, BBa_B0011, BBa_J61048, BBa_K731722, BBa_K731721, BBa_B0024, BBa_K864600,
BBa_K923004, BBa_B0025, BBa_B0010
```
 - Example 3 : Evaluate the complete and ordered devices with low accuracy and some keywords

- Command
perl score.pl BBa_R0010, BBa_J33204, BBa_E0040, BBa_B0021 lacI+regulated, Reporter, Coding, Terminator 20
- Expectation
1(mean complete)
1(mean ordered)
The score of the device
The biobrick we evaluate
- Result
1
1
55.11
BBa_R0010
BBa_K731500, BBa_K731300, BBa_R0011, BBa_R0010, BBa_K101001, BBa_K091112, BBa_K091110, BBa_K091111, BBa_J33204
BBa_J33204, BBa_K330002, BBa_K812030, BBa_K1555000, BBa_K1555001, BBa_K775004, BBa_K821001, BBa_K766003, BBa_K1020001, BBa_K1555002
BBa_E0040
BBa_K118003, BBa_K118002, BBa_K118015, BBa_I732005, BBa_K1072001, BBa_K118000, BBa_K118022, BBa_K118023, BBa_K118001, BBa_K118008, BBa_C0024
BBa_B0021
BBa_B1006, BBa_J61048, BBa_K731722, BBa_K731721, BBa_B0024, BBa_K864600, BBa_K923004, BBa_B0025, BBa_B1002, BBa_K1051008
- Example 4 : Evaluate the complete and unordered devices with low accuracy and some keywords
 - Command
perl score.pl BBa_B0021, BBa_R0010, BBa_J33204, BBa_E0040 Terminator, Regulatory, Reporter, Coding 20
 - Expectation
1(mean complete)
0(mean not ordered)
 - Result
1
0
- Example 5 : Evaluate the incomplete and unordered devices with low accuracy
 - Command
perl score.pl BBa_R0010, BBa_E0040 Regulatory, Coding 20
 - Expectation
0(mean not complete)
0(mean not ordered)
 - Result
0
0
- Example 6 : Evaluate the complete and ordered devices with low accuracy and the type of one of the biobricks is *Inverter* or *Generator*.
 - Command
perl score.pl BBa_I13409, BBa_B0021 , Terminator 20
 - Expectation
1(mean complete)
1(mean ordered)
The score of the device
The biobrick we evaluate

- Result
 - 1
 - 1
 - 18.64
 - BBa_I13409
 - BBa_K1385000, BBa_K1385001, BBa_K377704, BBa_I13409, BBa_K1362991, BBa_M1398
 - BBa_B0021
 - BBa_B0025, BBa_B1006, BBa_B1007, BBa_B1003, BBa_B1005, BBa_K731722, BBa_K731721, BBa_B0024, BBa_J61048, BBa_B1002

- Example 7 : Evaluate the complete and unordered devices with low accuracy and the type of one of the biobricks is *Inverter* or *Generator*.

- Command
 - perl score.pl BBa_E0040, BBa_I13409 Coding, Inverter 20
- Expectation
 - 1(mean complete)
 - 0(mean not ordered)
- Result
 - 1
 - 0

6. upload

A function to upload the basic information of the new biobrick to the database.

Use *upload.pl* to call the function *upload*.

- perl upload.pl BBa_check*check*check*check*check*check*check*check*check*check*check*check* check*check brick

- Expectation
 - The information of BBa_check will be added into database table *brick*.
- Result

```
mysql> select * from brick where bri_id = "BBa_check";
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
+-----+
| Bri_id    | Author | Enter_time | Btype | Part_status | Sample_status | Part_r
results | Star_rating | Uses | DNA_status | Qualitative_experience | Group_favori
te | Del   | Groups | Confirmed_times | Number_comments | Ave_rating | Des   | S
core |
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
+-----+
| BBa_check | check  | check      | check | check      | check          | check
| check | check | 0 | 0 | check      | check          | check
| check | check |   |   | 0 |          | 0 | -1.000 | check |
0.00 |
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
+-----+
1 row in set (0.01 sec)
```

- perl upload.pl BBa_check*check*check*check*check*check*check*check*check*check*check*check* check*check devic

- Expectation
 - The information of BBa_check will be added into database table *combine*.

- Result

```
mysql> select * from combine where com_id = "BBa_check";
+-----+-----+-----+-----+-----+-----+-----+
+-----+-----+-----+-----+-----+-----+-----+
+-----+-----+-----+-----+-----+-----+-----+
+-----+
| Com_id    | Author | Enter_time | Ctype | Part_status | Sample_status | Part_r
results | Star_rating | Uses | DNA_status | Qualitative_experience | Group_favori
te | Del    | Groups | Confirmed_times | Number_comments | Ave_rating | Des    | S
core |
+-----+-----+-----+-----+-----+-----+-----+
+-----+-----+-----+-----+-----+-----+-----+
+-----+
| BBa_check | check  | check      | check | check      | check      | check
|          |        | 0 | 0 | check      | check      | check
| check | check |          | 0 |          | 0 | -1.000 | check |
0.00 |
+-----+-----+-----+-----+-----+-----+-----+
+-----+-----+-----+-----+-----+-----+-----+
+-----+
1 row in set (0.00 sec)
```