UNIVERSITY OF LUXEMBOURG
Educational Measurement and
Applied Cognitive Science (EMACS)

PUBLIC RESEARCH CENTRE HENRI TUDOR

Genetics Lab

A Computer-Based Microworld to Assess Complex Problem Solving

User's guide to apply, configure and adapt the Genetics Lab

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IMPORTANT: The user agrees that any reports or published results obtained with the software will acknowledge its use by citing the following reference:

Sonnleitner, P., Brunner, M., Greiff, S., Funke, J., Keller, U., Martin, R., Hazotte, C., Mayer, H., & Latour, T. (2012). The Genetics Lab: Acceptance and psychometric characteristics of a computer-based microworld assessing complex problem solving. *Psychological Test and Assessment Modeling*, *54*, 54–72.

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Content

Preface

This user's guide should provide you with information on how to apply, configure and adapt the Genetics Lab. The Genetics Lab is a computer-based, psychometric sound microworld to assess complex problem solving behavior. It was developed within a cooperation between the University of Luxembourg and the Centre de Recherche public Henri Tudor. This cooperation was supported by the National Research Fund Luxembourg (FNR/C08/LM/06).

Note that this user's guide contains no information concerning the theoretical background, the development procedure and psychometric characteristics of the Genetics Lab's performance scores. Related information can be found in Sonnleitner et al. (2012a, 2012b). In this guide, we tried to cover all the technical questions which might arise when using the Genetics Lab despite being aware that this won't be feasible. Nevertheless, we hope that this guide should enable you to correctly install the application, apply it in various research settings and finally, gather reliable data with it.

Part 1 explains in detail how to install the Genetics Lab and how to extract performance scores from the stored data. On basis of this information you should be able to use and apply the Genetics Lab as it was used for research at the University of Luxembourg.

Part 2 shows you how you can modify the Genetics Lab and adapt it to your needs. For example, it is possible to increase or decrease the number of items, to change the semantic embedding or the pictures used in the microworld. Thus, the Genetics Lab can be adapted to various research needs. Note, however, that the psychometric quality of the Genetics Lab was only explored for the original version.

We hope that this user's guide will ease the application of the Genetics Lab and thus foster its use in research and educational contexts.

A special thank goes to Ingo Schandeler for creating the many creatures inhabiting the Genetics Lab and to Eric Francois and Markus Scherer for their technical support and expertise.

April 2012, the authors

References:

Sonnleitner, P., Brunner, M., Greiff, S., Funke, J., Keller, U., Martin, R., Hazotte, C., u. a. (2012a). The Genetics Lab: Acceptance and Psychometric Characteristics of a Computer-Based Microworld Assessing Complex Problem Solving. *Psychological Test and Assessment Modeling*, *54*(1), 54–72.

Sonnleitner, P., Brunner, M., Keller, U., Hazotte, C., Mayer, H., Latour, T., & Martin, R. (2012b). Genetics Lab: Theoretical background and psychometric evaluation (Research Report). Luxembourg: University of Luxembourg.

Part I – Using the Genetics Lab

1.1. Installation of the Genetics Lab

Please follow the steps in order to set up the Genetics Lab test application.

1) Unzip the Package with 7zip. Please use the version 9.2. or newer of 7zip as problems occurred with older versions.

2) Copy the folder „Genetics_Lab" to the directory C:\

3) In order to start the test there are 3 possibilities:

    - run_local_GL (you first need to start the server (server_start.bat – contained in the same folder) to run this version locally on your machine, data is stored in the localhost-folder of your Flashplayer)
    - run_local_GL_wo_local server (starts the GL without local server)
    - run_remote_GL (uses the online version of the GL, data is stored in a database which has to be set up first; only if online testing is planned this feature is interesting)

4) There is an icon file "scientist.ico" that can be used as icon for the application. Create a shortcut of the batch-file you want to use (e.g. run_local_GL) and then define this icon.

5) On the start screen (language selection) click on the right mouse button and set the local storage of your Flash-settings to „unlimited" (otherwise, you will be asked to confirm the storage process during the test)

6) Start the instructions by clicking on the flag of your choice and follow the instructions on the screen

7) To start the test, type in "start" (the password to enter the lab)

8) After the test has ended, press Alt + F4 to close the window and open the directory in which the data are stored

Please note, all other Firefox-applications have to be closed before starting the test. It is strongly recommended to make at least one test run before applying the GL in real test settings and to check for unexpected messages of the Firefox-browser!

1.2. Data storage

During test execution a log (or “trace”) is created that contains detailed information on the test takers’ interaction with the Genetics Lab. For an overview of the logged events, please refer to the document “*Events_list_for_the_Genetics_Lab_v0.1*” that is part of the Genetic Lab’s documentation. An R script for processing the event logs is described in the next section.

The event logs can be stored in two ways:

- Using the “local shared objects” functionality offered by Adobe Flash. Files are stored locally on the computer used for test execution and must be manually collected after testing.

- Using a remote MySQL database on a central server that receives results from clients running the Genetics Lab software. The procedure for setting up such a database is not part of this manual. Please contact the authors if you need more information on this subject.

The local shared object files are written to subdirectories of the computer user’s profile or home directory. Table X lists the typical locations of this directory for various operating systems. Note, this folder opens automatically if the application is ended using Alt + F4.

Operating system	**SOL file directory**
Windows XP	~\Macromedia\Flash Player\#SharedObjects
Linux-based operating systems	~/.macromedia/Flash_Player/#SharedObjects

The files have the extension “.sol”. They are binary files from which an XML representation can be extracted. While the test is running, a partial .sol file is written every 10. If the test is terminated properly (i.e. if the test taker finishes all items), a complete .sol file containing all recorded events is written in addition to the partial .sol files. The filenames of the .sol files are composed as follows (square brackets indicate variable parts):

COGSIM_Genetics_Lab_[date]_[time]_rnd[random user id][part indicator].sol

For information on the random user id, see chapter 2.2.1.. The “part indicator” is only added to the filename if the file is a partial .sol file; it is omitted for the complete .sol files generated at the end of test execution.

Here is an example for the name of a partial .sol file:

COGSIM_Genetics_Lab_20110201_07h50m10s275_rnd452238212899839408_p21.sol

The corresponding complete .sol file has an almost identical file name, excluding the part indicator at the end:

COGSIM_Genetics_Lab_20110201_07h50m10s275_rnd452238212899839408.sol

The XML files that can be assembled from the .sol files each contain a single element, “taoEvents”, which has all elements recorded during a test execution as its child elements.

1.3. Data analysis

The event logs created by the Genetics Lab contain very detailed information that has to be aggregated in order to be analyzed further. In this chapter, we briefly introduce an R script (Genetics lab scoring algorithm.R) that was written for this purpose and part of the documentation. The script reads .sol files, converts them to XML files and stores aggregated results in R and CSV formats which can then be used for further analysis.

IMPORTANT: The delivered script was developed and tested with the original version of the Genetics Lab only. Any modifications may lead to a failure of the script!

The user agrees that any reports or published results obtained with this Software will acknowledge its use by citing the following reference:

Keller, U. & Sonnleitner, P. (2012). Genetics lab scoring algorithm. University of Luxembourg.

1.3.1. Applying the provided script

The script uses the freely available statistics environment R, which can be obtained online for various platforms (including Windows, Mac OS X, and Linux) at the R website (http://www.r-project.org/). Please refer to this website for information on how to install R on your system.

In addition to R itself, the script needs a number of R add-on packages to run (gsubfn , gtools, plyr, sfsmisc, and XML). It will try to install these packages if they are not yet installed. On Mac OS X, the script also needs X11 to run. At the time of writing, X11 is included in Mac OS X (10.7 “Lion”), but this may not be true for future versions. Should X11 be missing from future versions of OS X, the XQuartz project provides a replacement (http://xquartz.macosforge.org).

The script can be started in the following ways:

- On Windows: Start R, then drag the script file “cogsim.R” from Windows Explorer into the R window. The script should then run automatically.
- On Mac OS X: Start R, select “Source script” from the “File” menu, and select the script file.
- On Linux: the script can be run directly once it has been made executable. Note that it might be advisable to install the required packages from the package manager of your distribution if possible.

By default, the script will interactively ask for an input directory (where the .sol files are located) and an output directory (where the various output files will be placed). However, you can also hard-code the input and output paths in the script. To do so, open the script in a text editor and follow the instructions in the script. Note that the input directory is searched recursively, so the .sol files may be located in subdirectories of the input directory.

It may take several minutes to process a large number of results. After the script has run, the output directory will contain the following files:

- A folder 'xml' that contains the XML files generated from .sol files. Its directory structure mimics that of your input directory.
- A file 'cogsim_results.csv' that contains the most important results in a spreadsheet format. (see section 1.3.2.)
- A file 'cogsim_results_small.csv', a short version of the above with only total results. (see section 1.3.2.)
- A file 'cogsim_results.RData', an R file containing two objects:
    - 'csdf': The same basic results as in the CSV file
    - 'cslist': A nested list with all the details

1.3.2. Description of the resulting scores

On basis of the resulting .sol-files, the included R-script computes several variables as well as performance scores. The following table gives you an overview of the resulting variables including a short description of them.

variable name	variable label	description
user_id		Individual and random user ID
date		Date of test session

ex.rel*		Refers to the user's causal diagram of the exercise item during the instruction phase. This variable scores the relational knowledge the user has about the item.
ex.sta*		Refers to the user's causal diagram of the exercise item during the instruction phase. This variable scores the knowledge the user has about the strengths of the existing connections of this item.
ex.glob*		Refers to the user's causal diagram of the exercise item during the instruction phase. This variable scores both, the relational knowledge as well as the knowledge about the connection strengths. Relational knowledge is emphasized with a weight of .75, strength knowledge with .25.
n_events		Number of events produced by the user (every click of the user for example is stored as event)
time_tkn		Time, the user has interacted with the Genetics Lab.
instrct_		Shows if instructions were completed
n.items		Number of items the user has finished
mssng.tm		Items, the user has not worked on due to time out
language		Language, the user has chosen and in which the Genetics Lab was presented
tst.drtn		Duration of the test
d.ins		Duration of the instructions
dur_e_x		Time the user has spent exploring the item/ items
dur_c_x		Time the user has spent achieving the target values
SC01_x	sc.stars.expl	Number of stars which were presented to the user as feedback about his exploration performance (see section 2.5.1.1.)
SC02_x	sc.stars.ctrl	Number of stars which were presented to the user as feedback about his control performance (see section 2.5.1.1.)
SC03_x*	sc.gdk.rel*	Relational knowledge the user has gained about the item/ items
SC04_x*	sc.gdk.stä*	Knowledge the user has gained about the strength of the item's/ items' relations
SC05_x*	sc.gdk.global*	Combination of the relational knowledge and knowledge about the strength of these relations (see also ex.glob)
SC11_x	sc.sysex.mean	Number of "informative" states the user has realized during exploration phase. A step is informative if all changes in the

		output variables can be traced back to one input variable.
SC12_x	sc.sysex.sum	Proportion of realized informative states in relation to all possible informative steps.
SC13_x	sc.sysex.rel	Proportion of informative steps related to the total number of steps taken during exploring an item.
SC21_x	sc.null.expl	Number of items for which the causal diagram/ database has been left empty. Can be used as control variable to identify users not properly working on the test.
SC22_x	sc.null.ctrl	Number of items during which the user has made no change during control phase. Can be used as control variable to identify users not properly working on the test.
SC41_x	sc.help.test.n.	Number of times the user has used the help function
SC48_x	sc.n.steps	Number of steps/ days the user has used to explore an item
SC49_x**	sc.optim	Number of “optimal” steps per item/ over all items. A step is optimal if it maximally decreases the distance to the target values during control phase.

*These scores refer to the so called “Güte des Kausaldiagramms”- performance scores introduced by Müller (Funke, 1993; Müller, 1993) and are based on the causal diagram the user depicts to demonstrate his knowledge about an item. Relational knowledge as well as knowledge about the strength of the relations are scored separately and then using different weights, combined to an overall knowledge score. For further information please engage the following sources:

Funke, J. (1993). Microworlds based on linear equation systems: A new approach to complex problem solving and experimental results. Elsevier Science Publishers.

Müller, H. (1993). Komplexes Problemlösen: Reliabilität und Wissen [Complex Problem Solving: Reliability and knowlegde]. Bonn, Germany: Holos.

sc.gdk.rel: (Güte des Relationswissens [Quality of relational knowledge])

$$sc.gdk.rel = (1- p_{Rel}) * (C_{Rel}/ C_{Max}) – (p_{Rel}) * (E_{Rel}/E_{Max})$$

with p_{Rel} = guessing probability (usually set to .5, relation exists or not)
C_{Rel} = number of correctly depicted relations
E_{Rel} = number of errors (falsely depicted non-existent relations)
C_{Max} = maximal number of correctly depicted relations
E_{Max} = maximal number of errors (falsely depicted non-existent relations)

sc.gdk.stä: (Güte des Stärkewissens [Quality of knowledge about the strength of relations])

$$\text{sc.gdk.stä} = (1- p_{\text{Stä}}) * (C_{\text{Stä}}/ C_{\text{Max}}) – (p_{\text{Stä}}) * (E_{\text{Stä}}/E_{\text{Max}})$$

with
$p_{\text{Stä}}$ = guessing probability (attention: depending on the number of available strengths, see section xx)
$C_{\text{Stä}}$ = number of correctly depicted strengths
$E_{\text{Stä}}$ = number of errors (falsely depicted strengths)
C_{Max} = maximal number of correctly depicted strengths
E_{Max} = maximal number of errors (falsely depicted strengths)

sc.gdk.global: (Güte des Kausaldiagramms [quality of the causal diagram])

$$\text{sc.gdk.global} = \text{weight}_1 * \text{GdK}_{\text{Rel}} + \text{weight}_2 * \text{GdK}_{\text{Stä}}$$

with
weight_1 = weight of relational knowledge (sc.gdk.rel); typically set to .75
weight_2 = weight of strength knowledge (sc.gdk.stä); typically set to .25

Note that the weights used are typically used in the CPS literature and place an emphasis on relational knowledge.

Table of theoretical minima and maxima of sc.gdk.rel, sc.gdk.stä, sc.gdk.global

	sc.gdK.rel (sc03)		**sc.gdK.stä (sc04)**		**sc.gdK.global (sc05)**	
Item	**Min**	**Max**	**Min**	**Max**	**Min**	**Max**
1	-0.5	0.5	-0.5	0.5	-0.5	0.5
2	-0.5	0.5	-0.5	0.5	-0.5	0.5
3	-0.5	0.5	-0.5	0.5	-0.5	0.5
4	-0.5	0.5	-0.5	0.5	-0.5	0.5
5	-0.5	0.5	-0.5	0.5	-0.5	0.5
6	-0.5	0.5	-0.25	0.75	-0.4375	0.5625
7	-0.5	0.5	-0.25	0.75	-0.4375	0.5625
8	-0.5	0.5	-0.25	0.75	-0.4375	0.5625
9	-0.5	0.5	-0.25	0.75	-0.4375	0.5625
10	-0.5	0.5	-0.25	0.75	-0.4375	0.5625
11	-0.5	0.5	-0.25	0.75	-0.4375	0.5625
12	-0.5	0.5	-0.25	0.75	-0.4375	0.5625
Total	**-0.5**	**0.5**	**-0.35417**	**0.6458333**	**-0.46354**	**0.536458**

** Please see also:

Sonnleitner, P., Brunner, M., Keller, U., Hazotte, C., Mayer, H., Latour, T., & Martin, R. (2012). Genetics Lab: Theoretical background and psychometric evaluation (Research Report). Luxembourg: University of Luxembourg.

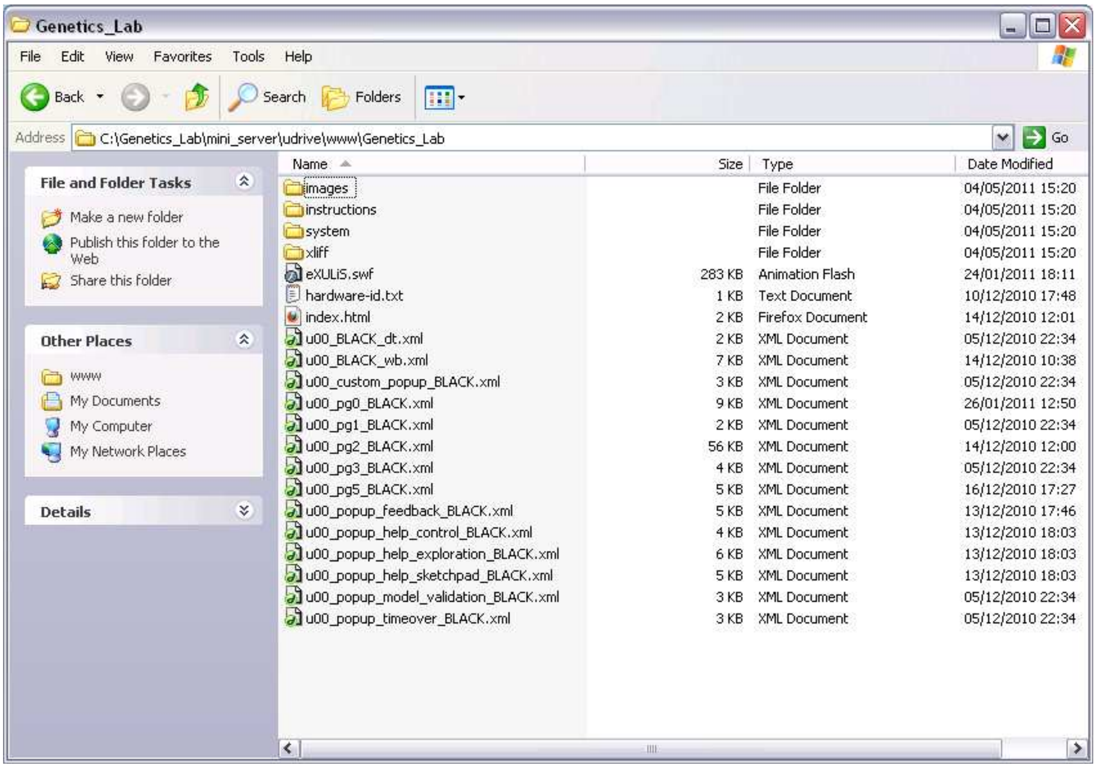
Part II – Modifying the Genetics Lab

This section explains how to modify the Genetics Lab. Every aspect of the Genetics Lab (Text of Instructions, Item rationales, Layout, etc.) is defined in related files which can be found in the main folder of the application. Below, it is described how to proceed in order to modify a certain feature. To give you an overview, where to find the specific files, at first the structure of the main folder of the application is explained.

2.1. Structure of the main folder

The main folder contains all relevant files of the Genetics Lab and is structured itself in several sub-folders. Below, each sub-folder and all files belonging to this folder are explained. The main folder can be found after the correct installation of the Genetics Lab at the following path:

`Genetics_Lab\mini_server\udrive\www\Genetics_Lab`



Address C:\Genetics_Lab\mini_server\udrive\www\Genetics_Lab

Name	Size	Type	Date Modified
images		File Folder	04/05/2011 15:20
instructions		File Folder	04/05/2011 15:20
system		File Folder	04/05/2011 15:20
xliff		File Folder	04/05/2011 15:20
eXULiS.swf	283 KB	Animation Flash	24/01/2011 18:11
hardware-id.txt	1 KB	Text Document	10/12/2010 17:48
index.html	2 KB	Firefox Document	14/12/2010 12:01
u00_BLACK_dt.xml	2 KB	XML Document	05/12/2010 22:34
u00_BLACK_wb.xml	7 KB	XML Document	14/12/2010 10:38
u00_custom_popup_BLACK.xml	3 KB	XML Document	05/12/2010 22:34
u00_pg0_BLACK.xml	9 KB	XML Document	26/01/2011 12:50
u00_pg1_BLACK.xml	2 KB	XML Document	05/12/2010 22:34
u00_pg2_BLACK.xml	56 KB	XML Document	14/12/2010 12:00
u00_pg3_BLACK.xml	4 KB	XML Document	05/12/2010 22:34
u00_pg5_BLACK.xml	5 KB	XML Document	16/12/2010 17:27
u00_popup_feedback_BLACK.xml	5 KB	XML Document	13/12/2010 17:46
u00_popup_help_control_BLACK.xml	4 KB	XML Document	13/12/2010 18:03
u00_popup_help_exploration_BLACK.xml	6 KB	XML Document	13/12/2010 18:03
u00_popup_help_sketchpad_BLACK.xml	5 KB	XML Document	13/12/2010 18:03
u00_popup_model_validation_BLACK.xml	3 KB	XML Document	05/12/2010 22:34
u00_popup_timeover_BLACK.xml	3 KB	XML Document	05/12/2010 22:34

Figure 1: Screenshot of the main folder

2.1.1. The images folder

This folder and its subfolders contain all pictures which are used in the Genetics Lab. If you want to use new images or modify the existing ones, you have to drop the new or modified ones in this folder. The method to alter the code in order to use the new images in the application will be explained in sections 2.3.2., 2.4.2.6., 2.7.3. & 2.8.2.1.3.

2.1.2. The instructions folder

This folder contains all animations (in every supported language) which are used during the instructions. The animations were created with the tool Adobe Captivate (http://www.adobe.com/products/captivate.html). In order to change the animations or include new ones you have to use this application and drop the new animations in this folder.

2.1.3. The system folder

This folder contains one of the most critical files in which elementary parts of the Genetics Lab are defined: the configuration file, labeled as ***GL-system-v4.xml***. In this file, the overall test time limit, time limit per item and all other aspects of items occurring during the instruction phase (in exercises) or during the test itself are defined. In later sections, it will be explained how to modify this file in order to modify the Genetics Lab.

2.1.4. XLIFF

This folder contains two types of files for each provided language:

1) ***u00_common_BLACK_xx-XX.xliff files***

In these files (xx-XX must be changed to any target language), every textual and localized content which appears in the Genetics Lab (instructions and test) is defined. The following sections will demonstrate how to modify these files, ***we will only refer to the English versions*** of these files (u00_common_BLACK_en-EN.xliff and variables_en-EN.xliff).

2) variables_xx-XX.xliff files

These files are used for the names of the creatures and the names of the input and output variables. We will explain how to change them in the section 3.4.2.

2.1.5. The exulis.swf file

The Genetics Lab application is an eXULiS-powered Flash application. While most of the application logic is embedded to the exulis.swf file, some elements such as the user interface and content such as texts are externalized. This allows any non-developer to change and eventually tweak some parts of the application without any change required in the code. The application is launched like a simple HTML page, using the object and embedded tags to ensure compatibility with most browsers.

2.1.6. Some xml files: the BLACK files

The main folder also contains some BLACK files in which the structural components and the layout of the Genetics Lab are defined. Modifying these files will be explained in the following sections. A BLACK (Business, Layout, Action, Content, Knowledge) file is a format based on XML. This file type is used to separate the description of the interface of media content to which they relate and the specific treatments to apply (location, triggering a trace). To keep it simple, the BLACK file is a XML-based format that provides dedicated sections to manage:

- the description of most parts of visible components (layout and user interface)
- localized contents (for instance, provide a multi-lingual feature)
- a separation between content and layout is encouraged, using xpath query XML standard and XML-based xliff format

Its extension stays as .xml but by convention, such file is suffixed by "_BLACK.xml". The most used sections are the Layout and Content sections. The Business section is still used in some cases to indicate the path to some translation files. The Layout section describes all components that are part of the interface, hidden or visible at a given time.

2.1.7. The hardware-id.txt file

This file is intended to set a specific hardware id when using the local version (with or without local server). Thus, the identification of the PC on which the data were produced and, furthermore the user itself, is possible (see section 2.2.1). The remote version, stored on a web server, would give the same (hardware) id for all remote tests, so that for the remote version this file should be removed from the root of the Genetics Lab folder. For the remote version, the hardware id is passed as an external parameter when the starting index.php page is called.

2.1.8. The index.html / index.php page

This page is the starting page to launch the Genetics Lab Flash application.

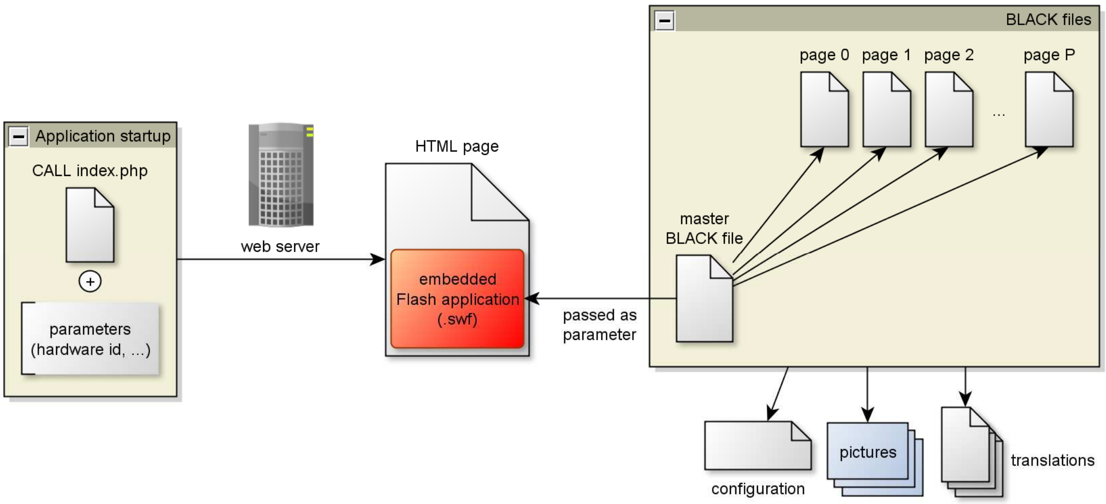


Figure 2: Schematic view of the application launcher with target parameters

The Genetics Lab application is launched by calling the index.php startup page with the hardware id parameter specific to the computer the test taker works on (see 3.1.7). Such call is done from the command batch file (.bat). As a response, the server sends back the HTML page that contains an embedded link to the Flash application that is called with some extra parameters. The most significant of these parameters is the master BLACK page that links to the subset of BLACK pages. The content section of each BLACK file may contain links to content such as pictures, textual data (translations) shown during the execution of the Genetic Lab. The configuration file is also loaded from an external function call.

2.2. Modifying the sequence of the Genetics Lab

This section will explain how to modify the sequence of the Genetics Lab (see the file ***Genetics Lab_item rationales, semantic embedding, and sequence*** for an overview of the item sequence). In order to make changes, you have to modify the related files. For each change we will give you the file name and the id that matches the tag[1] you want to change.

Each file which contains content has the same structure, for example:

```
[…]
<trans-unit id="u00p5_lang_de">
        <source xml:lang="de">Bitte wähle eine Sprache aus!</source>
        <target xml:lang="en">Bitte wähle eine Sprache aus!</target>
        <note xml:lang="en">u00p5_lang_de</note>
</trans-unit>
```

You can see a tag called <trans-unit> (= translation unit). Each language has its own trans-unit tag.

- “id” is the name of the part.

Within this tag you can see 3 other tags : <source>, <target> and <note>:

- <source>: in this line, the text reference is proposed. In our file, our reference language is German.
- <target>: the text in brown on this line will appear on the screen. So if you have any change to do, make them at this place!
- <note>: if you want to add any comments. They don’t appear on the screen. In our example, the tag “note” contains the id of the text.

2.2.1. User-ID and Hardware-ID storage

These identifiers (user id and hardware id) are distinct and complementary. The user id is randomly generated for each test taker and keeps the user anonymous. The hardware id is set to identify the hardware the test is passed on, and it can help to detect any hardware-related issue. Both identifiers are stored as one event triggered and stored to the traces for a further exploitation.

The user id cannot be set as it is randomly generated and changes at each turn so that it is a unique number. In the contrary, the hardware id has to be set

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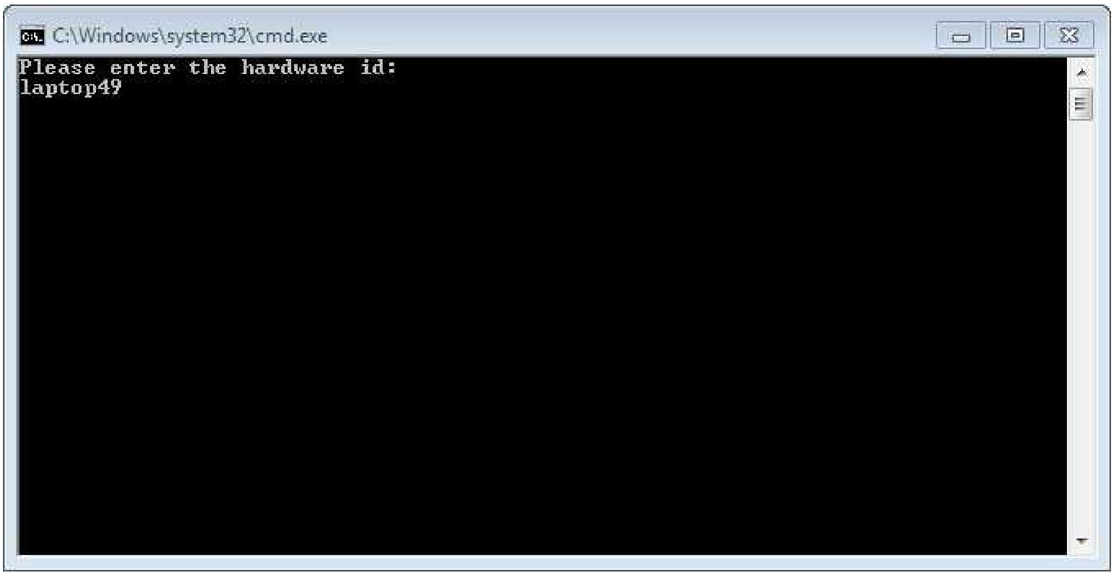
[1] A tag is an index term assigned to a piece of information

(typically by the test administrator) after the Genetics Lab package is installed and before the real test session is launched.

When using the local version of the GL, you can manually change the hardware id by modifying the file “hardware-id” in the folder *C:\Genetics_Lab\mini_server\udrive\www\Genetics_Lab.* Whatever id you type in will be stored as hardware-id of this test session and enables you to identify users. Don’t forget to change the hw-id before a new user starts the GL.

When using the remote version of the GL, the hardware id can be set after running the batch command file ‘run_remote_Genetics_Lab.bat’. The hardware id is asked prior to launching the application:



```
Please enter the hardware id:
laptop49
```

Here the test administrator can set the hardware id (‘laptop49’ in the example above) then click enter. When the application starts, the same hardware id will be displayed.

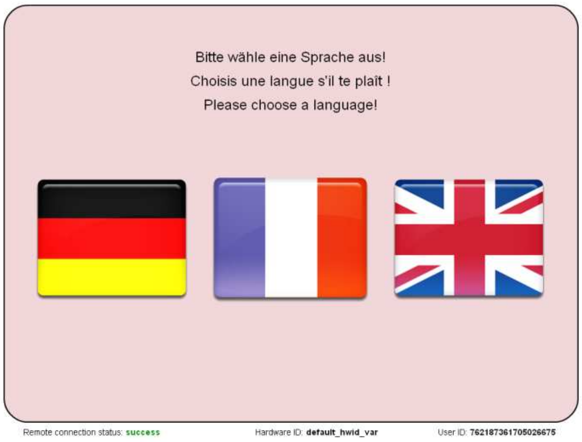
This hardware id can also be set manually in the same batch file, so that it will look like this:

```
@echo off
cls
rem echo Please enter the hardware id:
rem SET /P hid=
SET hid=myhardwareid
echo Launch of the Genetics Lab...
FirefoxPortable\FirefoxPortable.exe
"http://cogsim.tao.lu/Genetics_Lab/index.php?hwid=%hid%"
echo Open the shared objects folder to get the local traces...
%SystemRoot%\explorer.exe              %APPDATA%\Macromedia\Flash
Player\#SharedObjects
```

The hardware id set above in bold red is ‘myhardwareid’. When the hardware id is set manually, the lines 3 and 4 can be ignored by adding the ‘rem’ keyword, or by removing these two lines. On line 5, the ‘rem SET hid=’ should be uncommented by removing the same ‘rem’ keyword.

2.2.2. Start screen – Choosing the test language

On the first screen, the user can decide in which language he wants to take the test. After this choice, the language **cannot** be changed anymore. Depending on the chosen language, the corresponding texts from the XLIFF-files (see section 2.1.4. above) are loaded. This choice is also stored in the traces files.



Bitte wähle eine Sprache aus!
Choisis une langue s'il te plaît !
Please choose a language!

Remote connection status: **success** Hardware ID: **default_hwid_var** User ID: **762187361705026675**

Figure 3: Start screen: Select your language

You can modify this screen in several ways:

1) If you want to change or modify the flags, you have to put the new version(s) in this folder:
   Genetics_Lab\mini_server\udrive\www\Genetics_Lab\images\flags
   It is recommended to keep the size of the images which is 262x208 pixels.

2) To change the text which is presented on this screen, you have to alter the following file which is located in the XLIFF folder (see section 3.1.4 above):
   u00_common_BLACK_en-EN.xliff

You can open the file with a text editor such as Notepad. We recommend a free one such as PSPad[2].

In this file you have to find the following sequence:

---

[2] http://www.pspad.com/

```
[…]
<trans-unit id="u00p5_lang_de">
        <source xml:lang="de">Bitte wähle eine Sprache aus!</source>
        <target xml:lang="en">Bitte wähle eine Sprache aus!</target>
        <note xml:lang="en">u00p5_lang_de</note>
</trans-unit>
<trans-unit id="u00p5_lang_en">
        <source xml:lang="de">Bitte wähle eine Sprache aus!</source>
        <target xml:lang="en">Please choose a language!</target>
        <note xml:lang="en">u00p5_lang_en</note>
</trans-unit>
<trans-unit id="u00p5_lang_fr">
        <source xml:lang="de">Bitte wähle eine Sprache aus!</source>
        <target xml:lang="en">Choisis une langue s'il te plaît !</target>
        <note xml:lang="en">u00p5_lang_fr</note>
</trans-unit>
```

You can see 3 tags called <trans-unit> (= translation unit). Each language has its own trans-unit tag.

- "id" is the name of the part.

As above, within this tag you can see 3 other tags : <source>, <target> and <note>:

- <source>: in this line, the text reference is proposed. In our file, our reference language is German.

- <target>: the text in brown on this line will appear on the screen. So if you have any change to do, make them at this place!

- <note>: if you want to add any comments. They don't appear on the screen. In our example, the tag "note" contains the id of the text.

"xml:lang" notice only the language of the text which will appear after in the line of the tag. "xml:lang="de"": text in German, "xml:lang="en"": text in English

2.2.3. End screen

Thank you very much for working in our lab!

We hope you enjoyed investigating the various creatures.

Please stay seated and raise your hand to let the test administrator know you're finished.

Figure 4: Last screen

All the texts are localized in the xliff file ‘u00_common_BLACK_xx_XX.xliff’ located in the folder

Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff.

Be careful, select the file in the language you need (EN for English, FR for French or DE for German, or any language you need or created). *In this user guide, we will always refer to the English version!*

As mentioned before (in the section 2.2.2.), the text you can change is in brown and between the tag: “<target xml:lang="en"><![CDATA[XXXXXX]]></target>”

1) If you want to change the picture of the scientist (scientist.png), you have to put the new version(s) in this folder:
Genetics_Lab\mini_server\udrive\www\Genetics_Lab\images
It is recommended to keep the size of the images which is 255x453 pixels.

2) To change the text which is presented on this screen, you have to alter the following file which is located in the XLIFF folder (see section 3.1.4. above): u00_common_BLACK_en-EN.xliff

File	**Id**	**Line**[3]
u00_common_BLACK_en-EN.xliff[4]	final_message_lbl	729

```
[…]
<trans-unit id=" final_message_lbl ">
      <source xml:lang="de">
Vielen Dank für die Mitarbeit in unserem Labor!
Wir hoffen, du hattest Spaß beim Erkunden und Erforschen der verschiedenen
Lebewesen.
Bitte bleibe nun noch auf deinem Platz, und gib den Testleitern ein Zeichen, dass du
fertig bist. </source>
      <target xml:lang="en">
Thank you very much for working in our lab!
We hope you enjoyed investigating the various creatures.
Please stay seated and raise your hand to let the test administrator know you're finished.
</target>
      <note xml:lang="en"> final_message_lbl </note>
</trans-unit>
[…]
```

Hint: to quickly find something in your file, press Ctrl+F and write the sentence or id you are looking for!

2.2.4. Overall time limit

The current overall time limit (starting with the first item) for working on the Genetics Lab is 35 minutes or 2100 seconds. To change this limit you have to alter the tag <test time_limit="**2100**" /> which can be found at the beginning of the file "***GL-system-v4.xml***" in the "***system***" - folder (see section 2.1.3 above). Just enter the new time limit in seconds within the brackets and save the file.

2.2.5. Number of presented items

In general, there is no limit to the number of items. In case you want to add additional items just copy and paste one of the existing scenarios (beginning with <scenario …> and ending with </scenario>) in the file "***GL-system-v4.xml***" and

---

[3] The line number given of each tag is used only as a landmark. You can see this number in some tools that allows you to easily locate the tag you're looking for

[4] Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff

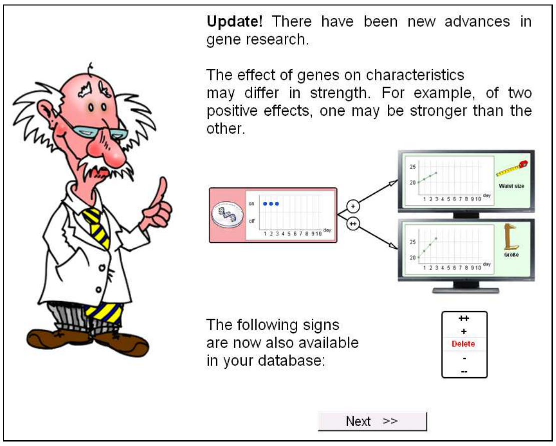
then alter the characteristics in order to create a new item. The number of items shown in the header will be automatically adjusted.

In case you want to decrease the number of items, just delete some scenarios (each beginning with <scenario …> and ending with </scenario>) and adapt the remaining ones. Again, the number of items shown in the header will be automatically adjusted.

Be careful! Don’t forget to also adjust the text of the instructions!

2.2.6. In-between instructions

In the original version of the Genetics Lab, there are two so-called in-between instructions. The first is presented after item 5 and explains and introduces additional connectivity strengths and how to draw them in the causal diagram/ data base:



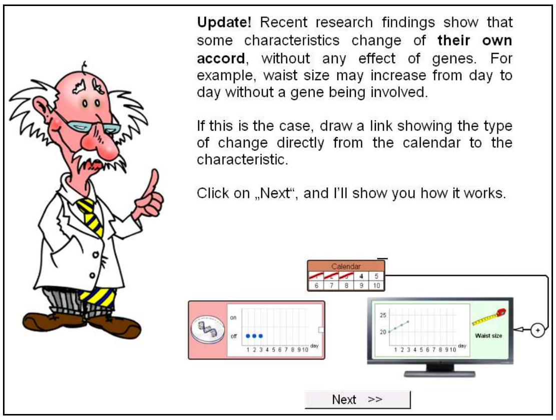
Update! There have been new advances in gene research.

The effect of genes on characteristics may differ in strength. For example, of two positive effects, one may be stronger than the other.

The following signs are now also available in your database:

Figure 5: 1st in-between instruction

The second is presented after item 7 and explains and introduces the influence of time or so-called eigendynamic:



Update! Recent research findings show that some characteristics change of **their own accord**, without any effect of genes. For example, waist size may increase from day to day without a gene being involved.

If this is the case, draw a link showing the type of change directly from the calendar to the characteristic.

Click on „Next“, and I'll show you how it works.

Figure 6: 2nd in-between item

The following tag allows changing the order and place of these instructions and shows the default settings:

```
<in_between_instructions connectivity_5_values="5" time_influence="7" />
```

By changing the number(s) between the quotation marks you can define after which items the in-between instructions should occur. As said above, in the default settings a 5-values connector is introduced after the 5th item and replaces the 3-values connector starting the 6th item; time is introduced after the 7th item and may affect the outcome starting the 8th item.

If you do not need in-between instructions at all, just delete this line.

Important to note is that the use of the connectivity selector with 5 values is linked to the occurrence of the related in-between instruction. Before this instruction is presented, the connectivity selector in the data base only contains 3 different strengths.

2.2.7. Pausing of the timer during the use of the help function

During the instructions and the test the overall time limit is paused when the user clicks on the “help-button”. The overall timer starts again as soon as the help-function is closed. If you want to disable this feature so that the timer never stops, you have to delete two expressions in two different files:

- First :

File	id	Line
u00_popup_help_exploration_BLACK.xml	u00_popup3_txt0	35

[…]
<button id="u00_popup3_txt0" left="275" top="597" width="153" height="37"
label="xpath:////text[@id='ok2_lbl']"
oncommand="as://customFeedTrace(HELP_CLOSE);as://setBlockerBox(blocker_box,false);as://closeWindow(popup_model_validation);~~as://resumeTimer();as://resumeTestTimer();~~"
image="xpath:////image[@id='u00_popup3_img2_im']"
imagePress="xpath:////image[@id='u00_popup3_img4_im']"
imageRollOver="xpath:////image[@id='u00_popup3_img3_im']"
imageRollOut="xpath:////image[@id='u00_popup3_img2_im']"
imageChecked="xpath:////image[@id='u00_popup3_img4_im']" style="fontSize: 18;
fontFamily: Arial; border: none"/>
[…]

- Second :

File	id	Line
u00_pg2_BLACK.xml	u00_page2_help_button	410

[…]
<button id="u00_page2_help_button" visible="false" left="949" top="69"
oncommand="~~as://pauseTimer();~~as://getHelp();"
image="xpath:////image[@id='u00p2_img21_im']" style="font-size: 20px; font-family:
Arial" imagePress="xpath:////image[@id='u00p2_img21_im']"
imageRollOver="xpath:////image[@id='u00p2_img21_im']"
imageRollOut="xpath:////image[@id='u00p2_img21_im']"
imageChecked="xpath:////image[@id='u00p2_img21_im']" />
[…]

2.2.8. Causal diagram during control phase

During the control phase, the user can switch to the database in order to see the records he made during the exploration phase. The user's records can however be replaced by the true underlying model of the item. In order to change this attribute you have to find the following file:

File	id	Line
GL-system-v4	Control_phase model	15

And change the attribute of the tag <control_phase model> to “true”:

```
<control_phase model="user" />
    - <!--  model: user(default)/true -->
```

Beware to adapt the instructions accordingly!

2.3. Modifying the instructions

This section explains how to modify the instructions, including its texts, animations and pictures used in the instructions throughout the Genetics Lab.

2.3.1. Text

The text of the instructions (except the so-called in-between instructions) which can be changed is presented in the upper side of the screen with a pink background.

All the texts which are used for the instructions are from the localized xliff file ‘***u00_common_BLACK_xx_XX.xliff***’ located in the folder `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff`
Each tag including such a text is a ***trans-unit*** tag with an id starting with ‘instructions_header_’. As mentioned above, the text you can change is in brown and between the tag: “<target xml:lang="en"><![CDATA[XXXXXX]]></target>”

Be careful to select the file in the language which you need to modify (EN for English, FR for French or DE for German, or any language you need or created). This document will always refer to the English version.

This table gives an overview which tag refers to which page (element) of the instructions:

Element	**id**	**Line**[5]
Introduction 1	u00p0_txt3_txt	17
Introduction 2	u00p6_txt1_txt	662
Introduction 3	u00p0_txt3c_txt	34
Instruction 1	instructions_header_1_lbl	374
Instruction 2	instructions_header_2_lbl	389
Instruction 3	instructions_header_4_lbl	403
Instruction 4	instructions_header_5_lbl	414
Instruction 5	instructions_header_6_lbl	422
Instruction 6	instructions_header_7_lbl	444
Instruction 7	instructions_header_8_lbl	455
Instruction 8	instructions_header_9_lbl	466
Instruction 9	instructions_header_11_lbl	477
Instruction 10	instructions_header_12_lbl	494

---

[5] The line numbers serve as a rough guide

Instruction 11	instructions_header_13_lbl	502
Instruction 12	instructions_header_14_lbl	515
Instruction 13	instructions_header_15_lbl	525
Instruction 14	instructions_header_16_lbl	536
Instruction 15	instructions_header_20_lbl	572
Instruction 16	instructions_header_21_lbl	577
Instruction 17	instructions_header_22_lbl	590
Instruction 18	instructions_header_23_lbl	601
Instruction 19	instructions_header_24_lbl	613
End instruction 1	end_instructions_starter_lbl_1	83
End instruction 2 + password	end_instructions_starter_lbl_2	121

The text of the in-between instructions can be changed in the following way. To change the text of the first in-between instruction (different connectivity strengths), modify the following element:

File	**id**	**Line**
u00_common_BLACK_en-EN.xliff[6]	end_instructions_inbetween 2_lbl	150

To change the text of the second in-between instruction (influence of time or eigendynamic), modify the following element:

File	**id**	**Line**
u00_common_BLACK_en-EN.xliff[7]	end_instructions_inbetween 1_lbl	138

2.3.2. Pictures

All the pictures of the Genetics lab are stored in the same folder: `\www\COGSIM\Genetics_Lab\images` In this folder you can find the following folder and files:

- “buttons”
- “flags”
- “genetic_lab”: pictures for the items
- “help”
- “instructions”
- “introduction”

---

[6] `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff`

[7] `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff`

To change the pictures which are used for the in-between instructions, you have to modify or replace the pictures ***conn_strengths_example_xx-XX.png*** and ***five_values_selector_xx-XX.png*** which are located in the file “instructions” and were created with demomaker.

2.3.3. Animations

If you want to change or modify the animations which are presented throughout the instructions, you can do this by making your own animations. To record a new animation it is also possible to create new items and to use them for recording. The ***demomaker*** attribute allows the test user to switch between different scenarios and to then record animations with these scenarios. To record the animations we used and recommend the tool Adobe Captivate (http://www.adobe.com/products/captivate.html).

To switch to demomaker you have to open the file `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\system\GL-system-v4.xml` and alter the following line:

```
[...]
<instructions_mode demomaker="false" /> <!-- demomaker: false(default)/true -->
[...]
```

If you set the demomaker value to “true”, you can see your demo item instead of the instructions when you start the Genetics Lab application. If “false”, the instructions are presented. By default, this parameter is left as false, and the instructions are played normally which show the recorded animations.

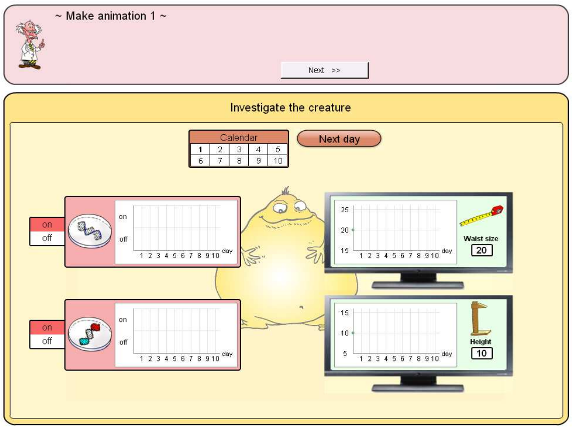


Figure 7: animation 1

In case you want to change the items which are used in the demomaker, you have to modify the following file:

`Genetics_Lab\mini_server\udrive\www\Genetics_Lab\system\GL-system-v4.xml`
How to modify the items is discussed in section 2.4., please see this section.

If you finally have created some new animations, you have to put it in this folder: `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\instructions` in order to use it.

Each animation should have a size of 940x520 pixels and a .swf[8] format.

The order of embedded animations in the flow of instructions cannot be changed by the user. See the developers guide for the process to change the order of animations.

2.3.4. Exercises

How to modify the exercises will be explained in chapter “2.4.2. Structure of an item”.

2.3.5. Pop-Ups

During the exercises of the instructions as well as at certain phases of the test, there are several pop-ups reminding the user of certain tasks or explaining several features. The texts of these pop-ups can be changed in this folder:
`Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff\u00_common_BLACK_en-EN.xliff`

This table shows what each pop-up is about and where it can be find:

	Element	**id**	**Line**
Pop up 1	Restart	instructions_header_6b_lbl	437
	OK	ok_lbl	328
Pop up 2	Go to the database	instructions_header_18_lbl	554
	OK	ok_lbl	328
Pop up 3	Exploration time over (top banner)	u00pu2_title	338
	Time over	instructions_header_19_lbl	561
	OK	ok_lbl	328
Pop up 4	Confirmation of your model (top banner)	u00pu1_title	317
	Model confirmation	validation_msg_lbl	322
	OK	ok_lbl	328
	Model confirmation	validation_msg_lbl	322

---

[8] **SWF** is a file format for multimedia, vector graphics and ActionScript in the Adobe Flash environment.

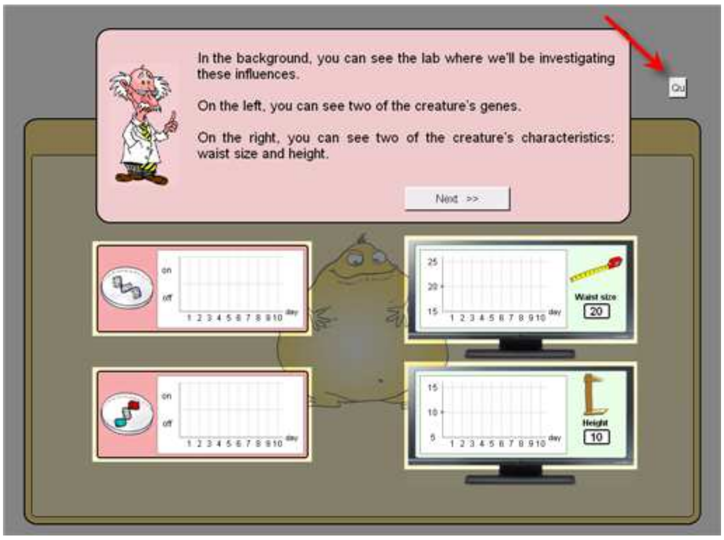
2.3.6. Skipping the instructions

For demonstration purposes or trials it might be useful to skip the instructions at the beginning of the Genetics Lab. To get a quit-button at the beginning of the instructions which allows such a skipping you have to open the following file:

`Genetics_Lab\mini_server\udrive\www\Genetics_Lab\u00_pg2_BLACK.xml`

Then find the id "***u00_page2_skip_instr***" (line 465) and set the tag "***visible***" to:
- false: quit-button not visible
- true: quit-button is visible

```
[…]
<button id="u00_page2_skip_instr" visible="false"
oncommand="as://prepareLoginScreen();as://hide(unit00page2);as://show(unit00default0);"
left="950" top="100" width="25" height="30"
label="xpath:////text[@id='u00p2_instructions_quit_lbl']" style="fontSize:14; fontFamily: Arial;
border: none" />
[…]
```



In the background, you can see the lab where we'll be investigating these influences.

On the left, you can see two of the creature's genes.

On the right, you can see two of the creature's characteristics: waist size and height.

Figure 8: Quit-button at the beginning of the instructions

2.3.7. Password screen prior to test start

In the default version of the Genetics Lab, the user has to type in the password "start" at the end of the instructions in order to start the test. This feature was implemented to allow a simultaneous start of the users in group administrations. All users have to wait until the test administrator gives the password.

In order to modify the way the password is displayed, you have to open the file: `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\u00_pg0_BLACK.xml`

Then find the id "**u00_default_txt8**" (line 23):

```
[…]
<textbox id="u00_default_txt8" visible="false" value="" left="475" top="567"
width="170" height="28" style="font-size: 20px; font-family: Arial; background-color:
#ffffff; border-style: solid; border-width: 2px; border-color: #c0c0c0; textAlign:center"
type="nopassword" maxlength="8" restrict="a-zA-Z0-9" multiline="false"/>
[…]
```

If you write the password between the quotation marks "" of ***value***, like shown here, the password is filled in automatically during the test:

```
[…]
<textbox id="u00_default_txt8" visible="false" value="start" left="475" top="567"
width="170" height="28" style="font-size: 20px; font-family: Arial; background-color:
#ffffff; border-style: solid; border-width: 2px; border-color: #c0c0c0; textAlign:center"
type="nopassword" maxlength="8" restrict="a-zA-Z0-9" multiline="false"/>
[…]
```

If you want the password to be invisible while it is typed in (every letter is then represented with “*, you have to replace "nopassword" by "password" (in green below):

```
[…]
<textbox id="u00_default_txt8" visible="false" value="start" left="475" top="567"
width="170" height="28" style="font-size: 20px; font-family: Arial; background-color:
#ffffff; border-style: solid; border-width: 2px; border-color: #c0c0c0; textAlign:center"
type="password" maxlength="8" restrict="a-zA-Z0-9" multiline="false"/>
[…]
```

For example, if you insert the password, "start", into the value="" and change the type "nopassword" into, "password", the password is automatically filled in and you can only see: *****

How can I change the password to another word?

The password can be changed in the configuration file (“***GL-system-v4.xml***” in the “***system***” – folder; see section 2.1.3 above), by providing the md5 hash outcome of the password. Any password should not stay in a clear format.

```
<test time_limit="2100"
md5_password=”ea2b2676c28c0db26d39331a336c6b92”/>
```

To get the md5 hash of the password to be defined, you can use an online tool like: http://md5-hash-online.waraxe.us. For instance, the md5 hash outcome of ‘start’ is ‘ea2b2676c28c0db26d39331a336c6b92’. Set the md5_password attribute accordingly. If this attribute is missing or left blank, it means that the default password is an empty string.
At runtime, the application will check if the md5 hash provided in the configuration file matches with the md5 hash of the password the user types in when requested.

2.4. Modifying the items

This section explains how to modify each aspect of the items of the Genetics Lab. Please see the file ***Genetics Lab_item rationales, semantic embedding, and sequence*** for further information on the items of the original version of the Genetics Lab.

2.4.1. Start screen and names of variables

The names of the creatures as well as the variables are stored in specific files, located in the ‘xliff’ folder. The name of these translation files is ‘***variables_xx-XX.xliff’***[9]. They contain all translated creatures and variable names for any label defined in the configuration file.

Each item is classified by <!-- item -->. The trans-unit tag also allows to modify the start screen. For example item 1:

Comment which allows finding items in the file

```
[…]
  <!-- item 1 -->
    <trans-unit id="drachus_longus">
      <source xml:lang="de">Drachus longus</source>
      <target xml:lang="en"><![CDATA[Dragus longus]]></target>
      <note xml:lang="en">drachus_longus</note>
    </trans-unit>
[…]
```

Hint: The relevant parts to change are texts colored in brown.

---

[9] `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff`

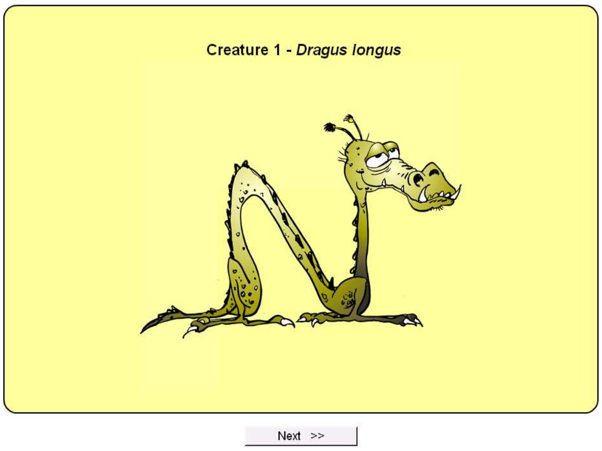


Figure 9: Start screen of item 1

2.4.1.1. How can I change the name of the variables?

In order to change the names of the variables you have to alter the corresponding tags in the same file (‘***variables_xx-XX.xliff’)****:***

```
<!-- variable names -->
   <!-- item 1 -->
```

2.4.1.2. How to change the pictures?

Each picture representing a creature shown when introducing a new item is located here:
Genetics_Lab\mini_server\udrive\www\Genetics_Lab\images\genetic_lab
If you want to change these pictures, please respect the size of: 500x500 pixels maximum. Update the file name accordingly in the configuration file (“***GL-system-v4.xml***” in the “***system***” – folder; see section 2.1.3 above) by changing the following tag within the related scenario:

```
<foreground image="drachus_longus.png"/>
```

2.4.2. Structure of an item

An item is basically a single problem-solving scenario with a set of exogenous and endogenous variables that are eventually connected by linear equations. It is also bounded by time or a restricted number of steps, as well as the numeric values at the start and the target values at the end of the item. A complete structure is required to express all these characteristics.

One item is composed of different parameters:

- the required time for exploration (P1)
- the number of steps for each phase (P2)
- the underlying linear equation model (P3)
- the initial value for exogenous variables (P4)
- the starting value for endogenous variables (P5)
- the target values for endogenous variables (P6)
- the input variable and its position, name or label, picture (P7)
- the output variable and its position, name or label, picture (P8)

Let’s take item 1 as an example:

GL-system-v4.xml:

```
[…]
<!-- item 1 -->
<item>
        <time>0</time> <!-- time in seconds -->                    (P1)
        <exploration_phase steps="10"/>                            (P2)
        <control_phase steps="3"/>                                 (P2)
        <weight_matrix rows="5" columns="2">                       (P3)
                <!-- influence of A on OVs -->                     (P3a)
                <row number="0">
                        <column number="1">-1</column>
                </row>
                <!-- influence of B on OVs -->                     (P3b)
                <row number="1">
                        <column number="1">1</column>
                </row>
                <!-- influence of intercept T on OVs: none -->     (P3c)
                <!-- self-influence of OV X -->                    (P3d)
                <row number="3">
                        <column number="0">1</column>
                </row>
                <!-- self-influence of OV Y -->                    (P3e)
                <row number="4">
                        <column number="1">1</column>
                </row>
        </weight_matrix>
        <!-- initial state vector (ISV) -->
        <vector id="isv" size="4">
                <!-- initial IVs -->
                <entry index="0">1</entry>                         (P4)
                <entry index="1">1</entry>
                <!-- initial OVs -->
```

```
          <entry index="2">40</entry>                                  (P5)
          <entry index="3">30</entry>
     </vector>
     <!-- goal state vector (GOSV) -->
     <vector id="gosv" size="2">                                       (P6)
          <entry index="0">40</entry>
          <entry index="1">28</entry>
     </vector>
     <input_variables>                                                 (P7)
          <variable name="" label="" picture="helix_bry.png" posx="0.1"
posy="0.25"/>
          <variable name="" label="" picture="helix_rwb.png" posx="0.1" posy="0.6"/>
     </input_variables>
     <output_variables>                                                (P8)
          <variable name="Länge" label="length" posx="0.58" posy="0.25"/>
          <variable name="Rücken- krümmung" label="back_bend" posx="0.58"
posy="0.6"/>
     </output_variables>
</item>
[…]
```

2.4.2.1. Time limit for the exploration phase of each item (P1)

In case you want the user to explore a creature for a fixed amount of time, it is possible to set a time limit for the exploration phase of each item by doing the following: Open the file "***GL-system-v4.xml***" in the "***system***" - folder (see section 3.1.3 above) and find the tag <item>:

```
[…]
<item>
     <time>0</time> <!-- time in seconds -->
[…]
```

The default setting is no time limit for the exploration phase of each item. Therefore, you can see a "0" in the example above and for every item of the test. For example, if you want to set a time limit of 1 minute for the exploration phase of a specific item, you have to enter 60 instead of 0 (time is expressed in seconds) in the time-tag of the item.

2.4.2.2. Number of steps (P2)

The number of (possible) steps can be changed for exploration as well as for control phase. The tags referred to with P2 allow setting the number of allowed steps for each phase.

2.4.2.2.1. Exploration phase

Regarding the number of steps/ days in the exploration phase, it is configured to 10. If you want to change this number, you have only to change 10 to another number.

Change the number in quote

```
[…]
     <exploration_phase steps="10"/>
[…]
```

2.4.2.2.2. Control phase

Regarding the control phase, the user has 3 attempts to reach the target. You can change this number of 3 to another one.

Change the number in quote

```
[…]
     <control_phase steps="3"/>
[…]
```

2.4.2.3. Underlying linear equation model (P3)

The weight_matrix (P3 section) tag is the section dedicated to the design of the linear equation model underlying each item. Each influence of any exogenous variable is specified in the row section for any endogenous variable. As commented in the document, the row number defines which exogenous variable to consider. The column tags inside the row tag define the potential influence on the endogenous variables.

The rows and columns attributes in this item specify the dimensions of the matrix used for the representation of the following model:

F=f(t)	**X(t+1)**	**Y(t+1)**
A(t)	0	-1
B(t)	0	1
Time(t)	0	0
X(t)	1	0
Y(t)	0	1

In the provided example, we consider the exogenous variables A and B and the endogenous variables X and Y. The first entry (P3a) states that the first (as number 0) input variable has a (negative) influence (-1) on the second (as number 1) output variable. The second entry (P3b) states that the second input variable has a positive influence (+1) on the second output variable. In this example, the time (T) doesn't influence any endogenous variable (P3c) which means that there is no "eigendynamic" in the system.

The section P3d and P3e state that each endogenous variable influences itself with 1. This means that an endogenous variable keeps its current value for the next step (t+1); consequently, only the sum of influences from exogenous variables or the time (T) can make this value drop or raise.

The number of columns corresponds to the number *no* of output variables, while the number of rows corresponds to the number *ni* of input variables, the time variable (T) and the number of output variables *no*. Note that the number of rows *nr* could have been replaced by the number of outputs, so that *nr=ni+1+no*. Such attributes are mandatory because only existing influences have to be specified.

2.4.2.4. Values of the variables

The next thing to take care of is the initial state of all variables. The initial state vector (ISV) stores the initial values to use at the beginning of each phase for both input and output variables (P4 and P5 sections). It is defined as a vector tag with the 'isv' id. The goal state vector (GOSV) does exactly the same with the values to reach for control phase (P6 section). It is defined as a vector tag with the 'gosv' id.

2.4.2.4.1. Starting values of the variables (P4+P5)

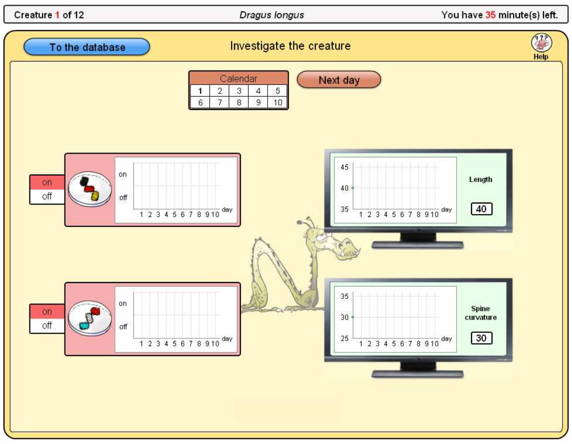
Both, input and output variables have starting values that can be changed. For input variables (P4), the default states are 'on' and 'off'. In the configuration file, the 'on' state corresponds to the numeric value 1 and the 'off' state corresponds to 0. For each output variable (P5), the numeric value is displayed as is. These values stay the same when starting exploration and control.

2.4.2.4.2. *Goal values of target variables (P6)*

As for the P5 section where the starting values are specified, the output values to reach are provided by using the same format.

2.4.2.6. *Pictures*

The characteristics of the variables itself can be modified: default name, translation, picture, position of the main user interface.



Creature 1 of 12 Dragus longus You have 35 minute(s) left.

Figure 10: definition of the input and output variables

2.4.2.6.1. *Input variables (P7)*

The input variables (P7) are displayed on the left side, in the pink rectangles. In this part, we define three things:

- You can give a name to each gene if you want. This name is only for the developer as a reference point. It is not visible. In our case, we did not give one.
- You can define a label for this element. This attribute will be visible in the Genetics lab and placed below the picture. You have only to put the name between the quotes. In our case, we did not give one.
- We define the picture which is in the file: www\COGSIM\Genetics_Lab\images\genetic_lab.
  Each picture is stored in the file of the item concerned.
- The last part concerns the position of the picture in the rectangle. You have to change the axes of x and y between the quotes.

```
[…]
        <input_variables>
               <variable name="" label="" picture="helix_bry.png" posx="0.1" posy="0.25"/>
               <variable name="" label="" picture="helix_rwb.png" posx="0.1" posy="0.6"/>
        </input_variables>
[…]
```

File for the picture

Position of x to change

2.4.2.6.2. Output variables (P8)

The output variables (P8) are displayed on the right side, in the green rectangles. Again, three things can be defined:

- You can give a name to each characteristic. This name is only for the developer as a reference point. It is not visible. In our case, it's in German.
- You can define a label for this element. This label has been defined in the files: www\Genetics_Lab\xliff\ variables_en-EN.xliff. You have only to put the id of the appropriate output variable between the quotes.
- the last part concerns the position of the picture in the rectangle. You have to change the axes of x and y between the quotes.

GL-system-v4.xml

```
[…]
        <output_variables>
                <variable name="Länge" label="length" posx="0.58" posy="0.25"/>
                <variable name="Rücken- krümmung" label="back_bend" posx="0.58"
posy="0.6"/>
        </output_variables>
[…]
```

Id which define the name of the output variable

variables_en-EN.xliff

```
[…]
        <trans-unit id="length">
        <source xml:lang="de">Länge</source>
        <target xml:lang="en">Length</target>
        <note xml:lang="en">length</note>
       </trans-unit>
      <trans-unit id="back_bend">
        <source xml:lang="de">Rücken-krümmung</source>
        <target xml:lang="en">Spine curvature</target>
        <note xml:lang="en">back_bend</note>
      </trans-unit>
 […]
```

2.5. Modifying the feedback

After each item as well as after the whole test, feedback concerning the user's exploration and control performance is provided. Note that the underlying algorithm which produces this feedback can not be changed because it is hard-coded (see the GL developer's guide). However, in the following this algorithm is explained.

2.5.1.1. Item feedback

After each item, the test taker gets feedback about his performance on the item. The user gets feedback about his performance in the exploration phase and as well about the performance in the control phase. The feedback is provided on one modal pop up window. The performance of each phase is illustrated by a number of stars. The better the user performed the more stars he will get out of 5 reachable stars. An example is given by the following picture:

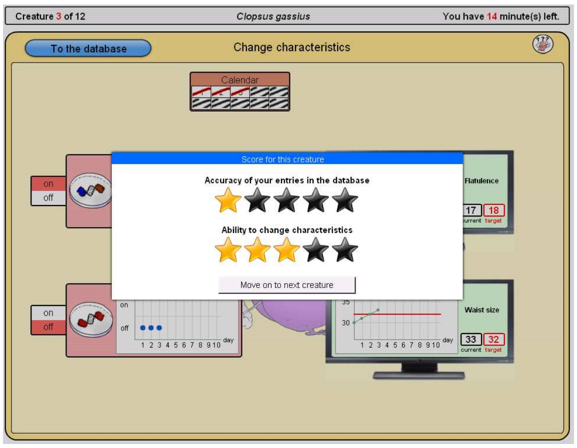


Figure 11: Pop up Feed back

Feedback about the user's exploration performance:

Feedback about the exploration performance is based on the causal diagram, the user draws in his database during exploration phase. This causal diagram is compared to the correct one. The more similar these two diagrams are, the higher the user scores. How many stars the user gets is calculated in the following way:

The User's causal diagram is scored by a rule:

- Correct connection with correct weight: 2 points
- Correct connection, incorrect weight: 1 point
- Incorrect connection (false sign, e.g. positive connection instead of a negative one): (- 1) point
- Wrong connection (connection drawn although a connection doesn't exist): (-2) points
- No connection drawn although a connection exists: (- 2) points

The sum of the points (= score) is used to calculate the number of stars:

- Negative scores correspond to 0 stars
- Score of 0 correspond to 1 star
- Positive scores are rescaled to 2-5 stars (with rounding):
  (5/ max. score) * achieved number of points = number of stars

Example:
System with 2 connections:
Max. Score = 4 points = 5 stars
3 points = (5/4) * 3 = 4 stars
2 points = (5/4) * 2 = 3 stars
1 point = (5/4) * 1 = 1 star

Feedback about the user's control performance:

Feedback about the test taker's control performance is based on how close the user stirred the system to the target values of the output variables during the control phase. Again, the closer the test taker gets to the target values, the better he performs and therefore the more stars he gets. Calculation of the number of the stars is done in the following way:

Be careful: the score only uses variables which can be controlled!

For each controlled output variable, a score is calculated, the variable score (VS):

$VS = 1 - \left| (\text{target} - \text{current}) / (\text{target} - \text{start}) \right|$

Therefore several possibilities arise:

- the user has reached all the target values, there is no difference => (1-0) = 1
- difference stayed the same => (1-1) = 0
- difference has shrunk => (1- <1) = positive value < 1
- difference has grown => (1 - >1) = negative value (in this case, the VS should be set to 0)

<u>Number of stars:</u>

Mean of the VS (MVS) = $(VS_{n1} + VS_{n2} + VS_{n3})/ n$
MVS * 5 => number of stars (rounded)

Example:
$VS_1 : 1 - \left|(30 - 32)/ (30 - 27)\right| = 1- \left|(-2/3)\right| = 1- (2/3) = 0,333$
$VS_2 : 1 - \left|(45 - 44)/ (45 - 40)\right| = 1- \left|(1/5)\right| = 1- (1/5) = 0,8$
MVS = (0,333 + 0,8)/ 2 = 0,5665
Number of stars = 0,5665 * 5 = 2,8325 ≈ 3 stars

2.5.1.2. Overall feedback

The final number of stars is the mean of all the items the test taker passed.

2.5.2. Hiding the feedback

The feedback scores are displayed in two cases: Right after each item (item feedback) or at the end of the whole test (global feedback). For the second case there are two possibilities. Either the user has finished all items (12 in the original version) or the global time to complete the test is over (see section 2.2.4.)

In the current version, it is not possible to hide the feedback. This, however, is a planned change of a future version.

2.5.3. Changing the feedback text

2.5.3.1. Item feedback

The text provided for the item feedback ("Accuracy of your entries in the database"/ "Ability to change characteristics") can be changed in the following file: `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff\u00_common_BLACK_en-EN.xliff`

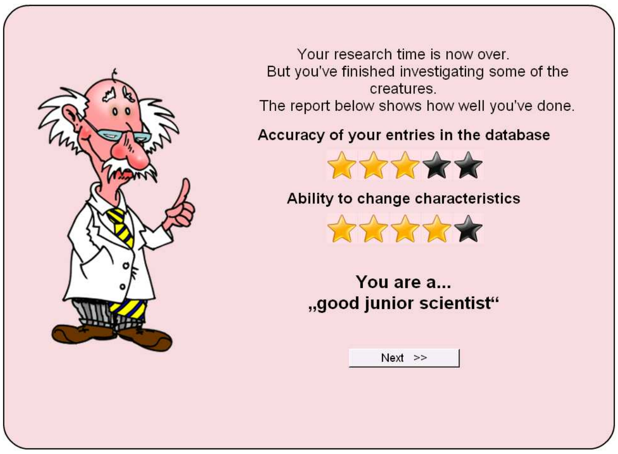
Text	**File**	**id**	**Line**
Accuracy of your entries in the database	u00_common_BLACK_en-EN.xliff[10]	u00p3_txt2	719
Ability to change characteristics		u00p3_txt3	724

---

[10] `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff`

2.5.3.2. Global feedback

As indicated above, there are two possibilities for the global feedback to appear: either the user has completed all items or the overall test time is over. Thus, there are also two different global feedback screens which can be modified:



Your research time is now over.
But you've finished investigating some of the creatures.
The report below shows how well you've done.

Accuracy of your entries in the database

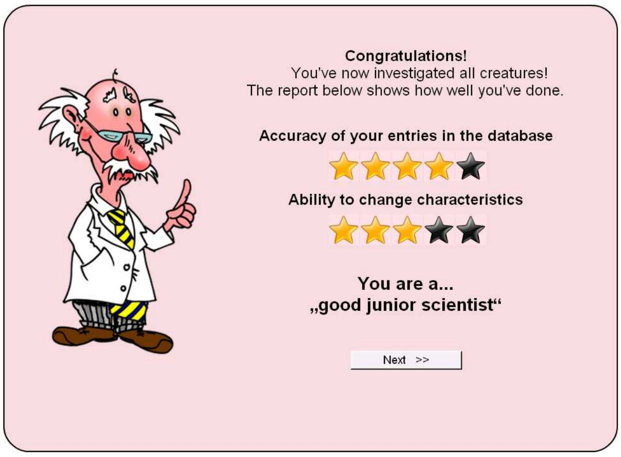
★★★☆☆

Ability to change characteristics

★★★★☆

You are a...
„good junior scientist“

Figure 13: Test time is over



Congratulations!
You've now investigated all creatures!
The report below shows how well you've done.

Accuracy of your entries in the database

★★★★☆

Ability to change characteristics

★★★☆☆

You are a...
„good junior scientist“

Figure 12: Test finished before time is over

The text of both versions can be changed in the same file as the item feedback.

Text	**File**	**id**	**Line**
Your research time is… (Figure 13)	u00_common_BLACK_en-EN.xliff[11]	final_score_aborted_lbl	710
Congratulations! You've now… (Figure 12)		final_score_lbl	701
Accuracy of your entries in the database		u00p3_txt2	719
Ability to change characteristics		u00p3_txt3	724
You are a…		you_are_a_lbl	916

---

[11] `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff`

The global feedback is conceived in a funny way and provides an overall "label" on the user's performance. Depending on the mean performance on both scales) one out of six different labels is presented. These labels can, of course, be changed.

Text	File	id	Line
Rookie	u00_common_BLACK_en-EN.xliff[12]	final_assessment_level_0	881
Beginner		final_assessment_level_1	886
Student		final_assessment_level_2	891
good junior scientist		final_assessment_level_3	896
great scientist		final_assessment_level_4	901
Nobel Prize winner		final_assessment_level_5	906

2.6. Modifying the pop-ups

During the test, there are several pop ups. All the related texts can be changed in the following folder: `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff\u00_common_BLACK_en-EN.xliff`

	Element	id	Line
Pop up A	Confirmation of your model (top banner)	u00pu1_title	317
	Model confirmation	validation_msg_lbl	322
	OK	ok_lbl	328
Pop up B[13]	Score for this creature (top banner)	system_score_title	691
	Accuracy of your entries in the database	u00pu6_txt2	267
	Ability to change characteristics	u00pu6_txt3	272
	Move on to next creature (button)	u00pu6_txt5	277

Hint: to find quickly something in your file, make Ctrl+F and write the sentence or id you are looking for!

---

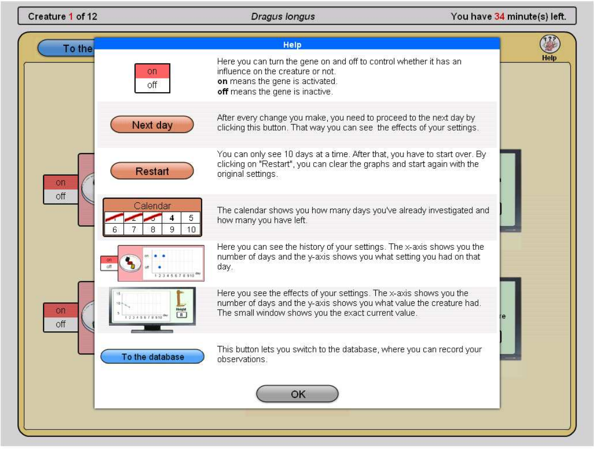
[12] `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff`

2.7. Modifying the help-function

In this part, we will explain how you can change the text and the pictures of the different help- pop ups. For each help- pop up, all the pictures are in the same folder and classified according to the phase:
`Genetics_Lab\mini_server\udrive\www\Genetics_Lab\images\help`

2.7.1. Text

Depending on the current phase, the help- pop up changes, only showing and explaining the symbols currently displayed on the screen. All texts can be found and changed in the following file:
`Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff\u00_common_BLACK_en-EN.xliff`



Here you can turn the gene on and off to control whether it has an influence on the creature or not.
on means the gene is activated.
off means the gene is inactive.

After every change you make, you need to proceed to the next day by clicking this button. That way you can see the effects of your settings.

You can only see 10 days at a time. After that, you have to start over. By clicking on "Restart", you can clear the graphs and start again with the original settings.

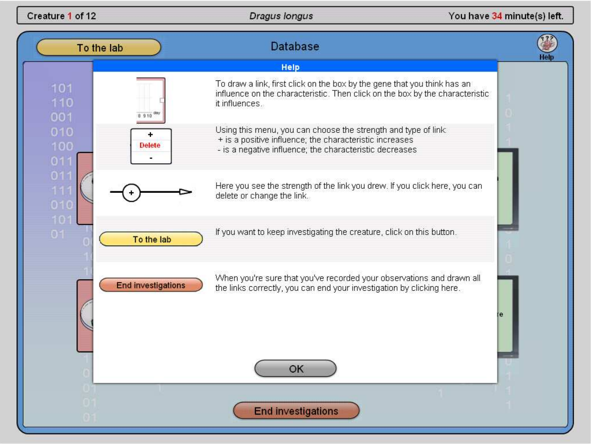
The calendar shows you how many days you've already investigated and how many you have left.

Here you can see the history of your settings. The x-axis shows you the number of days and the y-axis shows you what setting you had on that day.

Here you see the effects of your settings. The x-axis shows you the number of days and the y-axis shows you what value the creature had. The small window shows you the exact current value.

This button lets you switch to the database, where you can record your observations.

Figure 15: Pop up Exploration phase



To draw a link, first click on the box by the gene that you think has an influence on the characteristic. Then click on the box by the characteristic it influences.

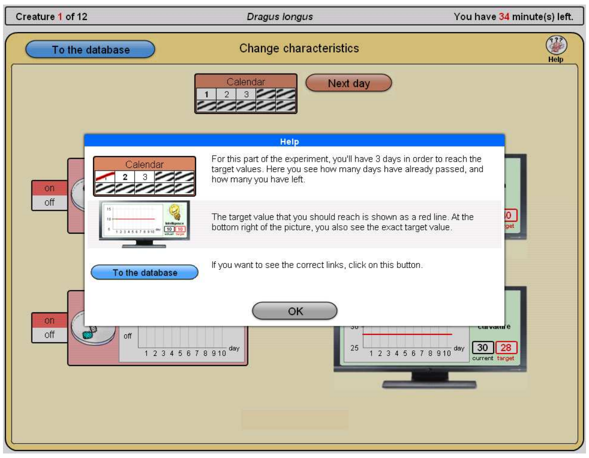
Using this menu, you can choose the strength and type of link:
\+ is a positive influence; the characteristic increases
\- is a negative influence; the characteristic decreases

Here you see the strength of the link you drew. If you click here, you can delete or change the link.

If you want to keep investigating the creature, click on this button.

When you're sure that you've recorded your observations and drawn all the links correctly, you can end your investigation by clicking here.

Figure 14: pop up database



For this part of the experiment, you'll have 3 days in order to reach the target values. Here you see how many days have already passed, and how many you have left.

The target value that you should reach is shown as a red line. At the bottom right of the picture, you also see the exact target value.

If you want to see the correct links, click on this button.

Figure 16: Pop up control phase

Overview of all text elements presented in the help pop up depending on the actual phase:

Help Pop up	Help (top banner)	u00pu3_title	343
	Exploration phase		
	Exploration phase – text1	help_exploration_desc1	757
	Exploration phase – text2	help_exploration_desc2	762
	Exploration phase – text3	help_exploration_desc3	768
	Exploration phase – text4	help_exploration_desc4	773
	Exploration phase – text5	help_exploration_desc5	780
	Exploration phase – text6	help_exploration_desc6	785
	Exploration phase – text7	help_exploration_desc7	790
	Database		
	Database phase – text1	help_sketchpad_desc1	797
	Database phase – text2 (3 strenghts)	help_sketchpad_desc2	802
	Database phase – text2b (5 strenghts)	help_sketchpad_desc2b	807
	Database phase – text3	help_sketchpad_desc3	812
	Database phase – text4	help_sketchpad_desc4	819
	Database phase – text5	help_sketchpad_desc5	824
	Database phase – text6	help_sketchpad_desc6	831
	Control phase		
	Control phase – text1	help_control_desc1	837
	Control phase – text2	help_control_desc2	842
	Control phase – text3	help_control_desc3	849

2.7.2. Buttons

You can also change the picture of the Help button which is in the upper right corner of the exploration and control phases.

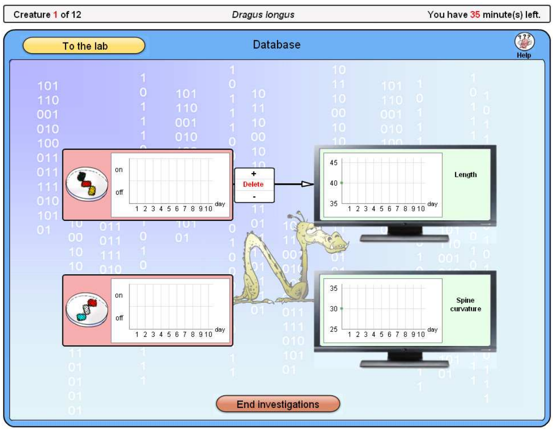


Figure 17: Database

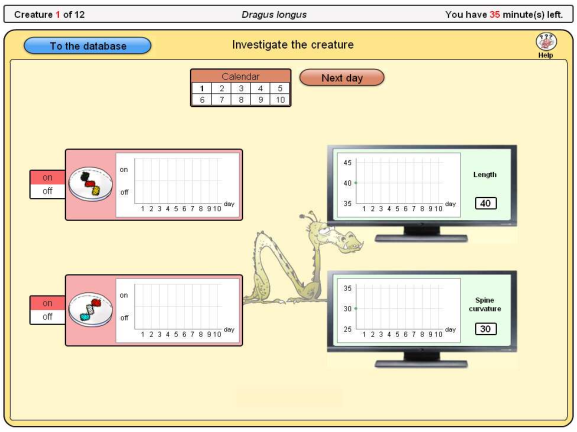
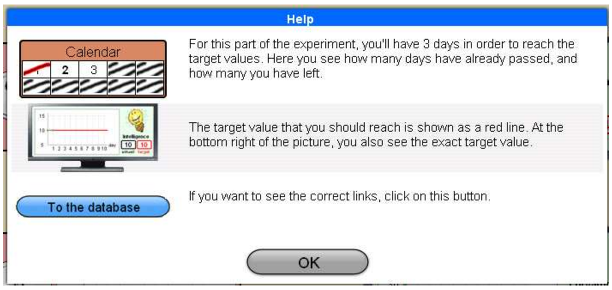


Figure 18: Lab

The picture of this button has a size of 36x33 pixels and is stored here: `Genetics_Lab\mini_server\udrive\www \Genetics_Lab\images`

The text within the button "Ok" in each help pop up can be changed as well in the same file:



For this part of the experiment, you'll have 3 days in order to reach the target values. Here you see how many days have already passed, and how many you have left.

The target value that you should reach is shown as a red line. At the bottom right of the picture, you also see the exact target value.

If you want to see the correct links, click on this button.

Text	File	id	Line
OK	u00_common_BLACK_en-EN.xliff[14]	ok2_lbl	359

---

[14] `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\xliff`

2.7.3. Pictures

All the pictures are in the folder `www\Genetics_Lab\images\help` which is divided into 3 others folders: control, exploration and sketchpad. There, they can be modified or replaced by new ones.

2.8. Modifying the layout

It is also possible to modify the general layout of the Genetics Lab including background colours, texts, etc. . In the following this is shown for each of the separate phases.

2.8.1. Layout during instructions

2.8.1.1. Background Color

To change the background colour, first open the file ‘u00_pg2_BLACK.xml’ in the following folder: Genetics_Lab\mini_server\udrive\www\Genetics_Lab. Then, you have to replace the current hex color information (#edcace) with the new one.

At the line 434, you will see this tag:

```
[…]
<svg:rect id="svg_upper_instructions_rect" x="-3" y="0" rx="20" ry="20" width="964"
height="140" style="fill:#edcace;stroke:black;stroke-width:2;opacity:0.75"/>
[…]
```

2.8.2. Layout of items

2.8.2.1. Exploration phase/ Control phase – Lab window

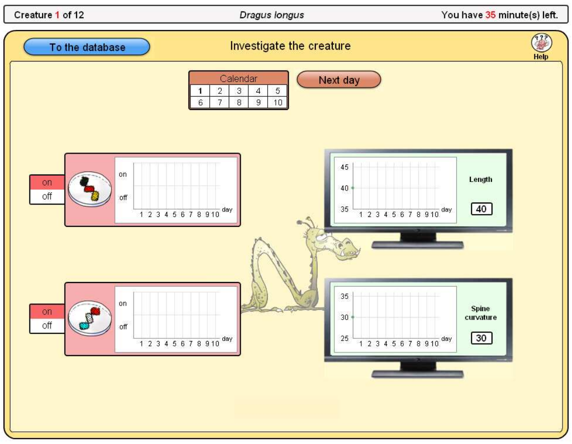


Figure 19: Lab

2.8.2.1.1. Text

The fixed text which occurs in the lab window (Investigate the creature, etc., see Figure 19) can be found and changed according to the following overview.

Element	File	id	Line
Top banner			
Creature … of…	u00_common_BLACK_en-EN.xliff	creature_lbl	911
Name Monster	variables_en-EN.xliff *		
You have …	u00_common_BLACK_en-EN.xliff	minutes_left_part1_lbl	936
minute(s) left		minutes_left_part2_lbl	941
Main banner			
Button “To the database”	u00_common_BLACK_en-EN.xliff	u00p2_txt8_txt	247
Investigate the creature		exploration_interface_ucfirst_lbl	202
Calendar		calendar_lbl	876
Next day		u00p2_next_step_lbl	262
On/Off (left side)		active_lbl inactive_lbl	856 861
On/Off (in the graph)		active_short_lbl inactive_short_lbl	866 871

Day (in the graph)		day_lbl	227
Name of characteristics (output)	variables_en-EN.xliff *		
Help	u00_common_BLACK_en-EN.xliff	u00pu3_title	343
Restart		u00p2_restart_lbl	257

*The variable names are stored in specific files, located at the ‘xliff’ folder. The name of these translation files is ‘variables_xx-XX.xliff’. They contain all translated variable names for any label defined in the configuration file (see 2.4.1.).

2.8.2.1.2. Pictures

Concerning the pictures for the genes and the characteristics (input and output), everything is classified in the folder of the item (see also section 2.4.1.2). For example: all the pictures for the item 7 are located here: Genetics_Lab\mini_server\udrive\www\Genetics_Lab\images\genetic_lab\item7

2.8.2.1.3. Buttons

You can change the picture for the button “To the database” in the folder `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\images\buttons.` You will find every button in a distinct colour. Note that for one button, there are always two pictures:

- blue_btn_state1.png: the button is in normal state
- blue_btn_state2.png: the button was clicked

2.8.2.1.4. Background

You can change the color of the background, again by changing the hex color code: #ffdb72

File	**id**	**Line**
Page u00_pg2_BLACK.xml	svg_test_interface_rect	20

```
[…]
<svg:rect id="svg_test_interface_rect" x="0" y="0" rx="20" ry="20" width="964"
height="698" style="fill:#ffdb72;opacity:0.85"/>
[…]
```

2.8.2.2. Exploration phase – Database window

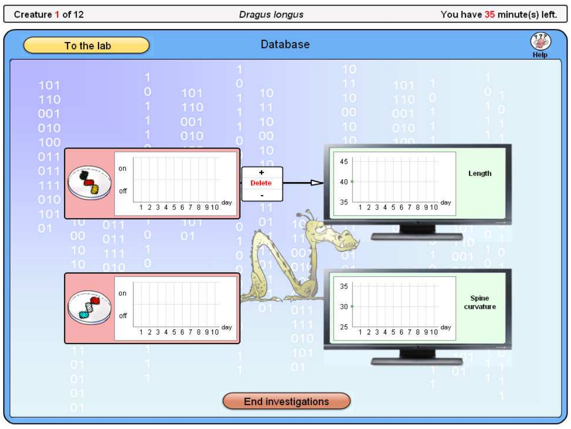


Figure 20: The database

Changing the elements of the database window strongly resembles the procedure for the Lab window. The text can be changed according to this overview:

Element	**File**	**id**	**Line**
Main Window			
Button “To the lab”	u00_common_BLACK_en-EN.xliff	u00p2_txt9_txt	252
Delete		remove_edge_lbl	921
Button “End investigations”		u00p2_txt4_txt	237
Database		u00p2_txt6_txt	242

2.8.2.2.1. Buttons

You can change the picture for the button “To the lab” and “End investigations” in the folder `Genetics_Lab\mini_server\udrive\www\Genetics_Lab\images\buttons`. You will find every button in a distinct colour. Note that for one button, there are always two pictures:

For the “To the lab” button:
- gold_btn_state1.png: the button is in normal state
- gold_btn_state2.png: the button was clicked

For the “End investigations” button:
- brown2_btn_state1.png: the button is in normal state
- brown2_btn_state2.png: the button was clicked

2.8.2.2.2. Background

You can change the colour of the background by changing the current hex color code (#519fed).

File	id	Line
Page u00_pg2_BLACK.xml	svg_sketchpad_interface_rect	28

```
[…]
<svg:rect id="svg_sketchpad_interface_rect" x="0" y="0" rx="20" ry="20" width="964"
height="698" style="fill:#519fed;opacity:0.85"/>
[…]
```

2.8.2.2.3. Background picture

In the current version, we are using a picture (paper_sheet.png) as background. You can find and modify it here:
`Genetics_Lab\mini_server\udrive\www\Genetics_Lab\images`