Psiz 4 All

Getting Started

Table of Contents:

1: Introduction

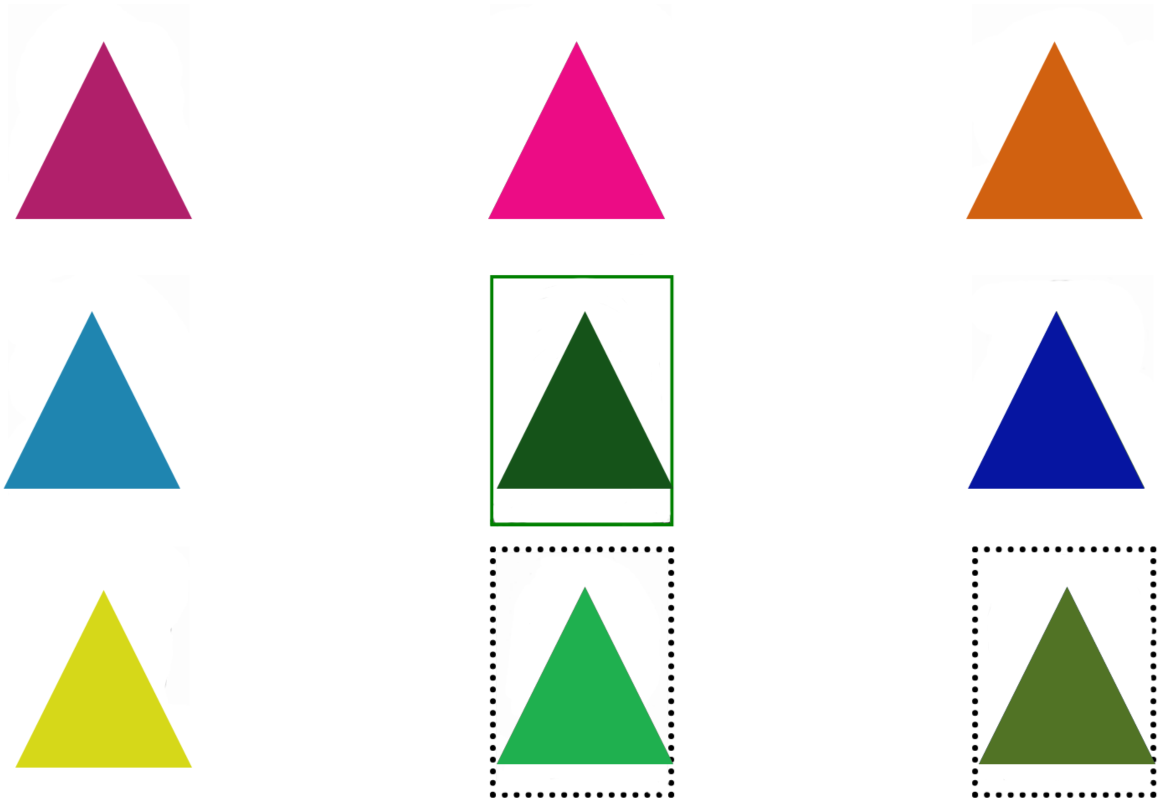
Hi! Welcome to the Psiz4All Getting Started document. This document is intended to serve as a guide to get you started using the Psiz4All platform.

But first what is the Psiz4All platform? Psiz4All is a tool originally developed for Dr. Jim Tanaka's Different Minds Lab (see more here) to help speed up the creation, running and analysis of Psiz experiments. The Platform itself is interacted by way of a GUI, instructions for which can be found here. Through the GUI you're able to design and create a Psiz experiment, complete analysis on data collected from said experiment and visualise the psychological embeddings created by Psiz from that data.

What is Psiz? I'm still working on the answer to that. Find out more about Psiz here.

What does a Psiz experiment look like? The basis for a Psiz experiment is ranking the similarity of reference images to a query image. The experiment consists of a number of trials of an X choose Y design where for each trial a participant sees a single query image at the centre of their screen and X reference images flanking that query and the participants goal is to select the Y most similar images to the query from amongst the references. The stimuli for the experiment are divided into discrete categories. For example, if you wanted to look at the perceived similarity participants had of people of different races you could have 3 categories of different races (Asian, Black, White).

Here is an example of what a Psiz trial might look like:



In this 8 choose 2 example the query image is the dark green triangle in the centre and the participant (me) has selected the 2 other green triangles as the most similar to that query.

2: Installation

This section details installing Psiz4All from scratch.

If you already have Psiz installed and you're installing Psiz4All again for a new experiment follow these steps however you may stop after step 6.

Step 1: Sign in to GitLab Pavlovia/ Create a GitLab account.

- This can likely be done for free through your academic institution.
- This can be done here: https://gitlab.pavlovia.org/

Step 2: Create a new empty repository by selecting new project from the dashboard

- I recommend naming this after the experiment Psiz4All will be used for.

Step 3: Clone that repository onto your computer

- You will need to install Git if you haven't already, this can be done here: https://git-scm.com/downloads
- Here is how to clone the repository if you're unsure:
  1. Open up the command prompt on your computer
  2. Navigate to the folder you want to have Psiz4All in
     a. For example if I wanted to clone the repository into a folder called Psiz4All in Documents I would enter: *cd Documents\Psiz4All*
  3. Copy the repository link from GitLab
     a. Click the blue Clone button in the repository and copy the HTTPS Link
  4. In the command prompt again enter the command:

     git clone [repository link here]

Step 4: Download the "dml_psiz" folder as a zip

- Found here: https://gitlab.pavlovia.org/nargument/dml_psiz

Step 5: Extract the “dml_psiz-master” folder & move it into your cloned repository

Step 6: In the dml_psiz-master folder create 2 new folders, 1 called data and one called converted_data

Step 7: Go into the required scripts folder and create a new folder called saved_data and a second new folder called plots

Step 8: Move all the files from dml_psiz-master out of that folder and into your repository, then delete the now empty dml_psiz-master folder

Step 9: Push the new files to your repository

- This can be done with the following commands in the command prompt:
- *cd [path to your repository]*
- *git add -A*
- *git commit -m* “Added Psiz4All files”
- *git push*
- These commands may take a little bit to run, that’s totally normal. You may also see a heap of warning messages after the git add command, don’t worry about those either.

Step 10: Install Miniforge

- This can be done here: https://github.com/conda-forge/miniforge
- Scroll down to Install and follow the instructions for your operating system, accept all default options as they appear.

Step 11: Open Miniforge prompt

Step 12: Create the psiz environment

- Do this by entering the following command into Miniforge:

```
conda create --name psiz python=3.9
```

- Enter y when prompted if you want to continue

Step 13: Enter your new psiz environment

- This can be done by entering the following command: *conda activate psiz*

Step 14: Clone the psiz files

- Enter the following command to clone the psiz files into the environment:

```
git clone https://github.com/nargument/psiz_demo_pc.git
```

Step 15: Enter the psiz_demo_pc folder in the Miniforge prompt

- This can be done with the following command: *chdir psiz_demo_pc*
- If that doesn’t work try: *cd psiz_demo_pc* instead

Step 16: Install Psiz

- Enter the following commands:
- pip install .
- pip install “numpy<2”
- pip install pyqt6
- pip install pandas
- This will once again likely take awhile

Step 17: Test Psiz installation

- To do this first enter the following directory: examples\rank
    - Or use this command: *chdir examples\rank*
- Run the following command: *Python mle_1g.py*

- If this runs without error Psiz has successfully been installed!

All Done! Psiz4All is now installed!

3: Launching Psiz 4 All

This section details how to launch the Psiz4All GUI once it has been installed.

How to launch Psiz4All

Step 1: Open a Miniforge prompt

Step 2: Enter the Psiz environment

- This can be done with the following command: `conda activate psiz`

Step 3: Navigate to your Psiz4All repository and then to required_scripts

- Using the chdir or cd command navigate the Miniforge prompt to the Psiz4All repository using the following command: `chdir [path to Psiz4All repository]\psiz4all \required_scripts`
- If my Psiz4All repository called Psiz4All was in my documents folder the command I would enter would be:

```
chdir Documents\Psiz4All\psiz4all \required_scripts
```

Step 4: Launch Psiz4All

- Do this with this command: `python experiment_gui.py`
- This might take a couple seconds the first time you launch it
- You will likely see a message from cudart in the terminal, you can ignore this.

4: How to Guide

This section details how to use and navigate the Psiz4All platform.

It includes a step by step guide to using the GUI, recommendations for running your own Psiz experiments and a functions list which explains in more depth what each aspect of the GUI does.

At any point you can also press the help button for a quick guide to navigating your current page.

Home Page:

Once you've launched the GUI (see section 3) you'll be met with the Home Page, this page provides quick aspects to all other aspects of the GUI.

To go to your desired page simply click the red Go button that corresponds to the page you wish to go to. What these pages contain and do is elaborated on below.

Page 1. Experiment Design:

This page is dedicated to designing your own Psiz experiment. It's split into 2 parts: 1. Stimuli Images & 2. Experiment Parameters.

Part 1: Create a List of Stimuli in the Experiment Code

Part 1 takes your stimuli images and adds them to the experiment script.

Before you do anything on this page you'll need to complete the following:

1. Add all your stimuli images to the pics folder, this can be found in dml_psiz-master/img
2. Name your stimuli in line with the following convention:
    a. Designate each category a letter

- b. Number all images in each category starting from 1
- c. Name each image the letter of its category and its unique number
- d. There are some example stimuli sets provided in the img folder to see exactly what this should look like

Once all your stimuli have been named and added to the pics folder head back to the GUI.

Click the Create Image List button to add your images to the experiment script. If this works you'll get a popup saying so.

Part 2: Set the Parameters for Your Experiment

Part 2 is where you'll design your Psiz experiment. First you'll specify all the parameters and then once you've done that click the Update Parameters Button to update the experiment script.

Here are what the parameters are and how you should set them:

Experiment Type: Also referred to as the Embedding is what each trial of the experiment will look like. The options are in the form X choose X, so 8c2 is 8 choose 2 which means in a given trial of the experiment the participant will see a central query image flanked by 8 reference images and of those references they must choose the 2 most similar to the query.

Same Category References: is the number of reference images that will be of the same category as the query image.

Restrictions:

- Must be an integer
- Cannot exceed the total number of reference images
- Cannot be greater than the number of images in a given category

Trials per Block: is how many trials a participant will complete between breaks. Sometimes Psiz experiments have hundreds of trials and as such can take awhile to complete so it's nice to give people a break every now and then.

Restrictions:

- Must be an integer
- Cannot be 0
- If you want no breaks set this to greater than the total number of trials

Repetitions: is how many times each image in the stimulus set will be presented as the query image. The default for this value is 1 however if your experiment has less than 50 stimuli I recommend increasing this to 2 or more.

Restrictions:

- Must be an integer
- Cannot be <1

Catch Trial Percentage: is the percentage of total trials that will be catch trials. Catch trials are trials where the query is present amongst the reference images so if a participant is paying attention they should always select the catch image as the most similar to the query.

Restrictions:

- Must be an integer
- Set to 0 if you don't want any catch trials
- Cannot be greater than 100 or less than 0

Online: is whether your experiment is to be run locally on your computer or hosted online through pavlovia. It is assumed most experiments will be run through pavlovia, the option to run locally is mainly present for demo purposes.

Fixed Trials: is whether your experiment will use fixed trials or random trials. The default selection here is no which means your experiment will use random trials.

Random Trial experiments randomly generate the reference images for each query image according to the parameters set above. Most experiments use random trials as they often provide sufficient coverage of the stimulus set however if you want more control/ you want to ensure specific query, reference pairings fixed trials are the way to do this.

Fixed Trial experiments require you to manually designate the reference images for each query (how to do this). This gives you more control over what participates will rank in each trial and allows you to guarantee which references will be ranked for each query.

Once you've set your parameters by clicking the Update Parameters button it's time to run your experiment!

(How to do this)

Page 2. Data Cleaning:

Now that you've run your experiment and have some data it's time to clean up the raw data files and prepare them for being run through Psiz.

Before you press that big red button on your screen you first have to move the raw data files into the correct folder. Go ahead and move all the raw data excel files into the folder you created called data and make sure there aren't any other files in there from other experiments.

When that's done specify which embedding your experiment used and click the large Clean Up Data button. You'll be prompted to name the converted date file that will be created here so do that but avoid using these characters when doing so: < > : " / \ | ? *

Now you're ready to move onto the next page!

Page 3. Analysis Scripts:

This page is dedicated to running Psiz on your experiment data and creating the embeddings.

There are 3 parts to this page, the first selects the mode to run Psiz in, the second actually runs Psiz and the third displays the convergence of the embeddings.

Part 1: Specify Psiz Parameters

There is only one choice here and that is to run Psiz on individual participants or on the group as a whole.

Group: is the default selection here which will compute a group embedding using the data from all your participants to compute a single embedding representative of the group as a whole.

Individual: will compute an embedding for every participant based solely on their data. This allows you to compare individuals rather than groups however because Psiz has less data to work with for each embedding this option takes significantly longer to run and depending on your experiment there may not be enough data to create an accurate embedding at all.

Part 2: Run Psiz

Once you've selected either individual or group embeddings you can proceed to part 2 and run Psiz by pressing the Run Psiz button. You will be prompted to select the file for Psiz to run on, enter the name of the file you wish to use and proceed. This file will likely be the one you just created during Data Cleaning and will be located in dml_psiz-master/converted_data.

This will likely take around 10 minutes! So be aware

It's also likely the GUI will say not responding while Psiz is running, don't trust this and let it run.

When Psiz is done you will be notified and the convergence for your embedding(s) will be printed in Part 3.

Page 4. Plot Embeddings:

Now that you’ve run Psiz and computed the embeddings for your data it’s time to visualise them.

This section is still in progress

Psiz4All Functions:

Home Page:

Go 1: Go to Page 1

Go 2: Go to Page 2

Go 3: Go to Page 3

Go 4: Go to Page 4

Page 1. Experiment Design

Create Image List: Loads stimuli from dml_psiz-master/img/pics to experiment script.

Reset Image List: Clears all stimuli from the experiment script.

Update Parameters: Loads specified parameters to the experiment script.

Reset Parameters: Resets experiment script parameters to their default values

Display Current Parameters: Displays the current experiment parameters on screen.

Clear Parameters: Clears all entries on screen, does not affect experiment script.

Page 2. Data Cleaning

Clean Up Data: Cleans up raw participant data files located in dml_psiz-master/data and compiles them into a single converted data file named by the user located in dml_psiz-master/converted_data

Page 3. Analysis Scripts

Run Psiz: Runs Psiz on a converted date file specified by the user. First it runs a parsing script which parses the data then it runs a modelling script which runs Psiz and computes the embedding.

Page 4. Plot Embeddings

Run Plotting Script: Runs the plotting script on the most recently computed embedding. Do Not use this when running Psiz on individual participants, plots for those are made during the previous step.

Show Plot: Displays the embedding plot on screen.

How to Run a Psiz Experiment

There are 2 ways to run a Psiz experiment through the Psiz4All Platform:

1. Through Pavlovia
2. Hosted Locally

1: How to Run an Experiment Through Pavlovia

Step 1: Go through and complete Page 1: Experiment Design in the GUI.

Step 2: In a Miniforge prompt navigate to your repository and enter the following commands:

- git add -A
- git commit -m “[Your commit message here]”
- git push

Step 3: Pilot or Run the experiment on Pavlovia

- To do this go here and sign in: https://pavlovia.org/
- Then go to your dashboard then experiments and you should see your Psiz experiment.
- Select you experiment and under status select Piloting (To test) or Running (To Run)

Step 4: Upon conclusion of data collection, return to the GUI and complete Page 2: Data Cleaning and continue from there

Step 5: Make another git push with your results

- This can be done through these commands again once you’ve navigated to your git repository in a Miniforge terminal:
- *git add -A*
- *git commit -m “[Your commit message here]”*
- *git push*

2: How to Run an Experiment Locally

Step 1: Go through and complete Page 1: Experiment Design in the GUI.

Step 2: Launch a standard command prompt

Step 3: Navigate to your repository

- *cd [Path to your repository]*

Step 4: Start hosting the experiment

- Enter this command to do this:
- *npm run experiment*
- You may have to install npm first, if so instructions will appear in the terminal

Step 5: In a Google Chrome tab got to http://localhost:8000/

Step 6: Complete your experiment

Step 7: When done return to the terminal and hit ctrl+c then confirm by entering y

How to Use Fixed Trials

To use fixed trials for your experiment follow these steps:

Step 1: Load your stimuli into the experiment via Page 1 of the GUI

Step 2: Open fixed_trials.csv located in required_scripts

- This excel file will look something like this depending on your stimuli:

Query	1st Ref	2nd Ref	3rd Ref	4th Ref	5th Ref	6th Ref	7th Ref	8th Ref
A1.png								
A2.png								
A3.png								

B1.png								
B2.png								
B3.png								

This Excel file is how you will create the fixed trials for your experiment.

The 1st column of this file contains all the stimuli from img/pics.

Each row represents a trial with the item in the first column being the query and all that follow being the references.

Fill in the references for each trial to set up fixed trials. See the example below for a 3 choose 1 experiment.

Query	1st Ref	2nd Ref	3rd Ref	4th Ref	5th Ref	6th Ref	7th Ref	8th Ref
A1.png	A3.png	B3.png	B1.png					
A2.png	B2.png	A1.png	B3.png					
A3.png	B2.png	B1.png	A2.png					
B1.png	A2.png	A3.png	B2.png					
B2.png	A2.png	A1.png	B3.png					
B3.png	B1.png	A3.png	A1.png					

** Note that you only fill in as many references as specified by your embedding choice, so in this example the 5 leftmost columns are left blank as a 3 choose 1 experiment only uses 3 reference images.**

With fixed trial experiments in the GUI when you select to use fixed trials it disables several parameters, that's because you are manually setting those parameters when you populate fixed_trials.csv.

For Repetitions in fixed trial experiments simply copy the first column from the first stimuli and paste below. Here's an example:

Query	1st Ref	2nd Ref	3rd Ref	4th Ref	5th Ref	6th Ref	7th Ref	8th Ref
A1.png	A3.png	B3.png	B1.png					
A2.png	B2.png	A1.png	B3.png					
A3.png	B2.png	B1.png	A2.png					

B1.png	A2.png	A3.png	B2.png					
B2.png	A2.png	A1.png	B3.png					
B3.png	B1.png	A3.png	A1.png					
A1.png	A3.png	B3.png	B1.png					
A2.png	B2.png	A1.png	B3.png					
A3.png	B2.png	B1.png	A2.png					
B1.png	A2.png	A3.png	B2.png					
B2.png	A2.png	A1.png	B3.png					
B3.png	B1.png	A3.png	A1.png					

5: FAQ