Stroop Task experiment & analysis documentation

Contents

Summary

In the Stroop task, the participant needs to report the ink colour of the word on the screen, while ignoring the word itself. The ink colour and word are congruent (red Respond red) or incongruent (red Respond green). Participants reports the ink colour by pressing the corresponding key as fast and accurate as they can. Reaction times are normally higher with incongruent stimuli than with congruent stimuli.

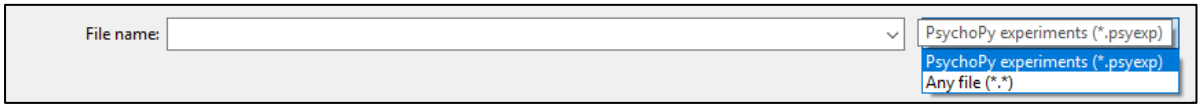
Running the experiment

Before you start running the experiment on a new computer setup, check the following:

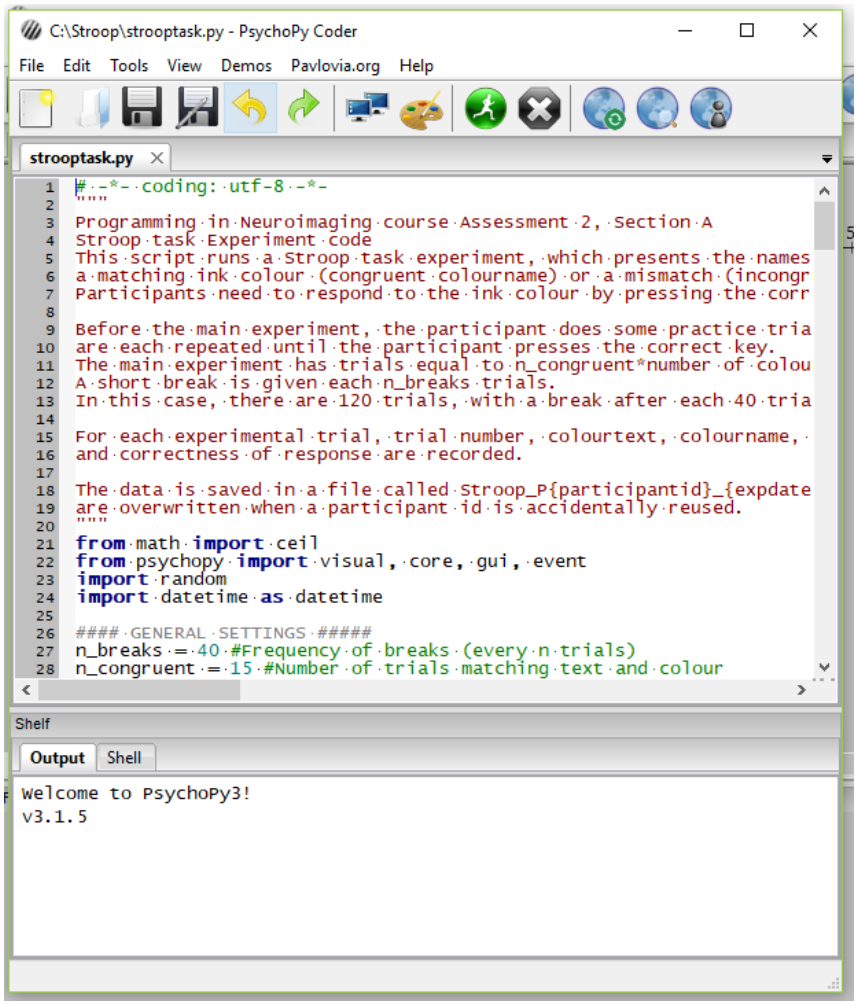
1. Automatic sleep mode is turned off:
    a. Open Settings → System → Power and Sleep. Set **Screen** and **Sleep** to Never.
2. Keyboard has the colour markers on the correct keys, if not, get stickers and mark the keys:
    a. f: red; g: blue; h: green; j: yellow – which forms a left to right line on the centre row of the keyboard in between the d and k keys.

Opening the Experiment file

To prepare for the first experiment of the day, turn on the computer and open PsychoPy3. Click **File** in the top bar, then click **Open**. Change the file type next to filename to **any file (*.*)** as shown below.

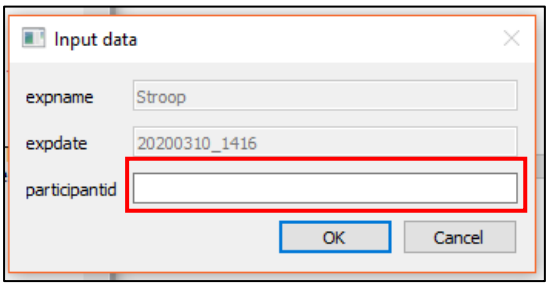


Now, navigate to **C:\Stroop**, select **'strooptask.py'** and click **open**. This should open a new window, which looks like this:

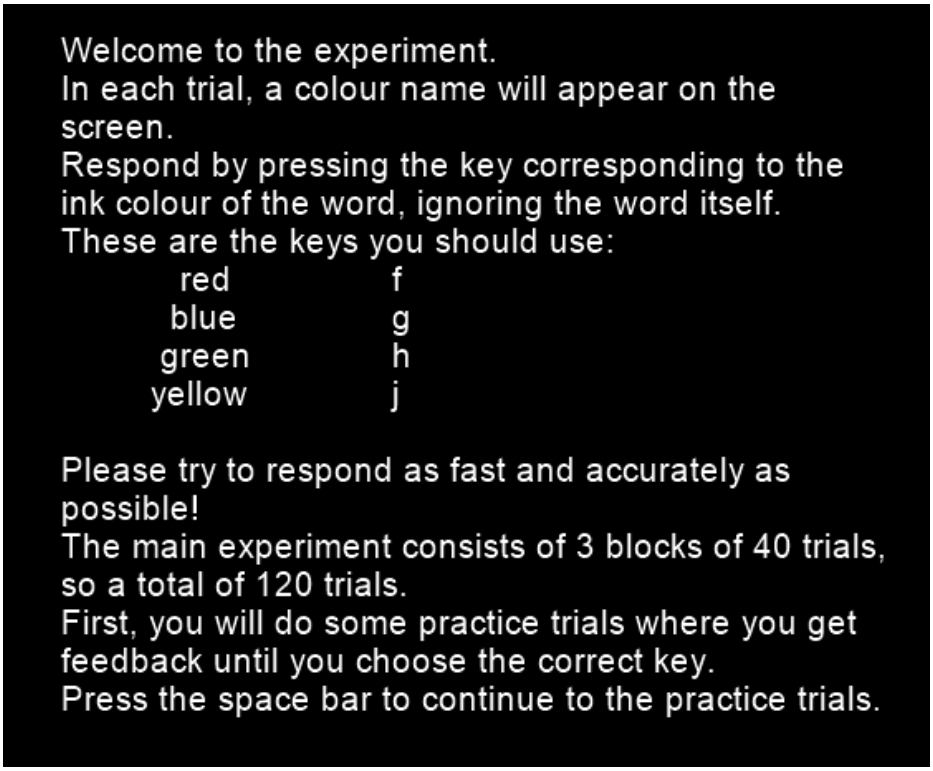


Running a participant

1. Give the participant these basic instructions:
    - In this experiment, you need to press the key corresponding to the <u>ink colour of the word</u> you see on the screen. For example, if the word 'yellow' is printed in green, respond green.
    - The keys are marked with coloured stickers, so you can easily recognise them *[show them the keyboard]*
    - The experiment will start with instructions and practice trials. If there are any problems, please let me know before starting the main experiment.
2. Make sure they understand the task and have them sign the consent form.
3. Press the run button  → This will bring up a small window, where you need to enter their participant ID. Enter their number and click OK to start the experiment.



4. A full screen window with the following text in the centre of the screen will open:



5. Let the participant sit down and read these instructions. Keep an eye out in case they have any problems or questions, but the experiment should run automatically.

Aborting the experiment

If the experiment needs to be exited partway through, you can press the escape key when on a trial. If the experiment is on a different screen (instructions, ready screen, break screen), press the space bar to continue to a trial, then press escape. This will save data measured until that trial into the data file before exiting the program.

Data file

Once the experiment is completed/aborted, a datafile will be available in the **C:\Stroop** folder. This file is named *'Stroop_P{participantid}_{expdate}.csv'*. The participantid will be what you entered when running this participant, the expdate is a string of the date and time that you pressed the run button to start the experiment, formatted as HourMinute_DayMonthYear, so you can identify when someone was measured.

Analysing the experiment

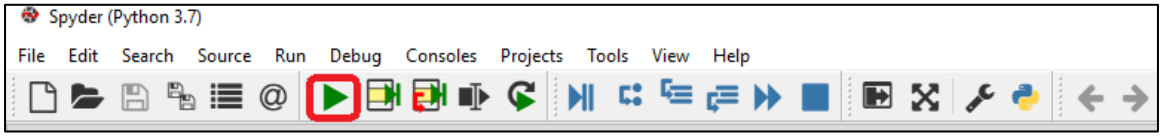
Preparing data

Put all the participant files that you want to analyse in the **C:\Stroop\data** folder. **Do NOT put any other .csv files in this folder!!!**

Analysing data

Open Spyder or Spyder3. Click **File** in the top bar → **Open**. Navigate to **C:\Stroop**, select **'analysis.py'** and click **open**.

Press the green triangle icon to run the analysis.



Analysis produces two outputs: a table and a figure.

Reaction times table

The table is printed into the IPython console (the bottom right part of the screen). An example output is shown below. The table shows the Mean reaction time ± STD in seconds, and the percentage correct for the congruent and incongruent trials per subject.

IPython console

Console 1/A

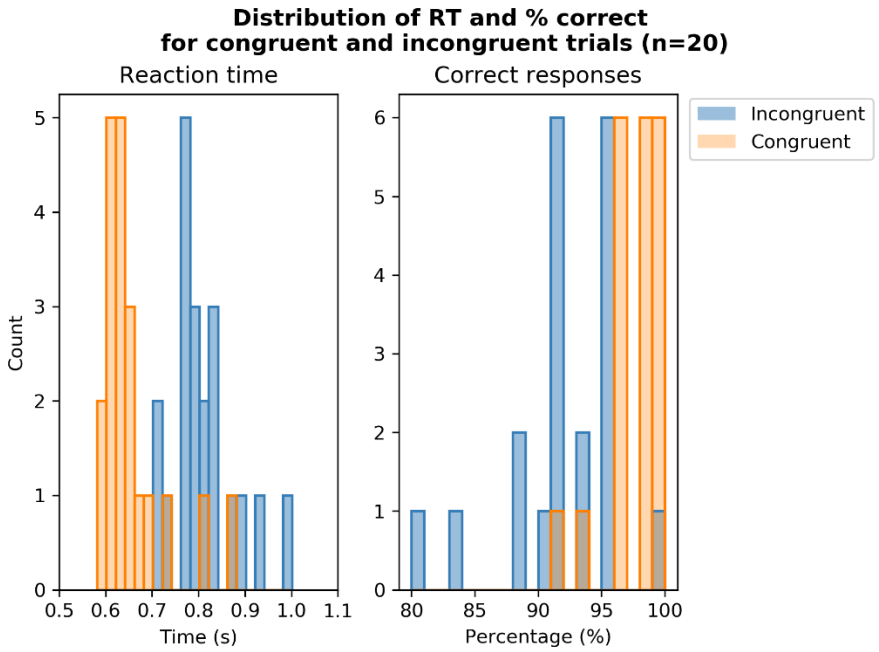
```
                ### REACTION TIMES TABLE ###
Participant        Congruent                    Incongruent
             Mean RT ± STD   %correct     Mean RT ± STD   %correct
1          0.879  ±  0.518 , 91.67 %    0.996  ±  0.362 , 91.67 %
2          0.585  ±  0.092 , 96.67 %    0.727  ±  0.187 , 83.33 %
3          0.809  ±  0.473 , 100.00%    0.934  ±  0.401 , 91.67 %
4          0.687  ±  0.563 , 98.33 %    0.901  ±  0.447 , 95.00 %
5          0.722  ±  0.184 , 96.67 %    0.786  ±  0.180 , 95.00 %
6          0.655  ±  0.150 , 96.67 %    0.822  ±  0.250 , 80.00 %
7          0.655  ±  0.178 , 100.00%    0.867  ±  0.217 , 91.67 %
8          0.656  ±  0.128 , 98.33 %    0.780  ±  0.181 , 90.00 %
9          0.602  ±  0.133 , 93.33 %    0.824  ±  0.272 , 88.33 %
10         0.611  ±  0.085 , 98.33 %    0.832  ±  0.239 , 91.67 %
11         0.637  ±  0.123 , 96.67 %    0.775  ±  0.214 , 93.33 %
12         0.630  ±  0.100 , 100.00%    0.802  ±  0.182 , 88.33 %
13         0.614  ±  0.116 , 98.33 %    0.762  ±  0.182 , 91.67 %
14         0.678  ±  0.127 , 100.00%    0.809  ±  0.164 , 100.00%
15         0.617  ±  0.180 , 98.33 %    0.798  ±  0.206 , 93.33 %
16         0.606  ±  0.107 , 98.33 %    0.765  ±  0.205 , 95.00 %
17         0.632  ±  0.095 , 100.00%    0.765  ±  0.184 , 91.67 %
18         0.632  ±  0.134 , 100.00%    0.706  ±  0.152 , 95.00 %
19         0.633  ±  0.128 , 96.67 %    0.712  ±  0.142 , 95.00 %
20         0.582  ±  0.082 , 96.67 %    0.786  ±  0.214 , 95.00 %
```

The table data is also automatically saved in the **C:\Stroop** folder as *'strooptask_summary_{analysisdate}.csv'* with analysisdate formatted as HourMinute_DayMonthYear. This allows you to view the data at a later time using Excel.

Distribution figure

The figure will contain the distribution of reaction times and percentages correct for congruent and incongruent trials of all analysed participants.

This figure will look something like this:



The figure is automatically saved in the **C:\Stroop** folder as *'group.png'*. **Watch out, running the analysis code again with new data will overwrite this figure, so be sure to rename the previous image or move it to a different folder if you want to save it.**

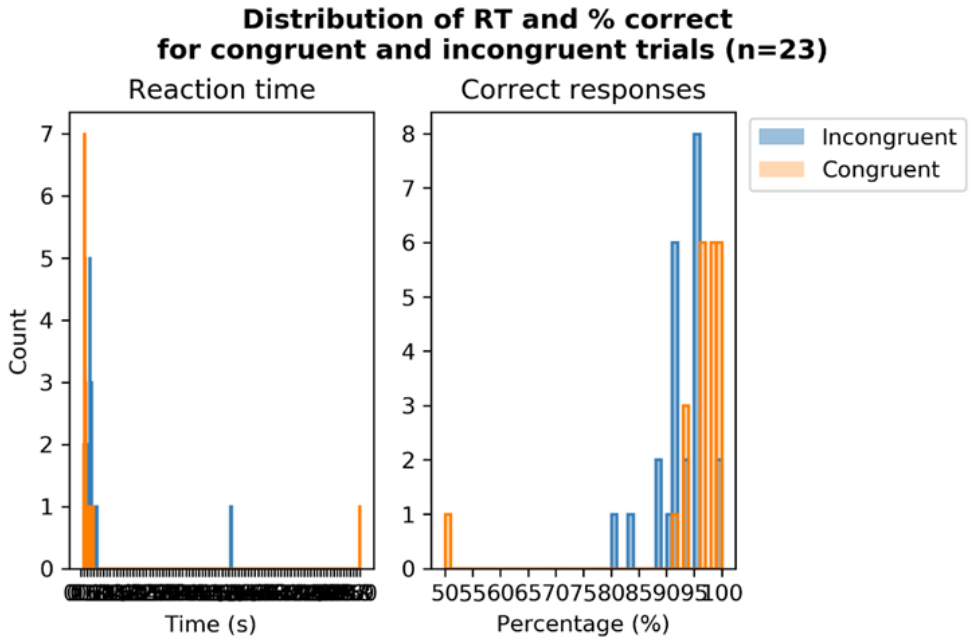
X-axis configuration

If the axes of the figure are too crowded, you will need to change the x-tick step size. In the analysis.py file, you need to change the Plot settings.

These are the default settings:

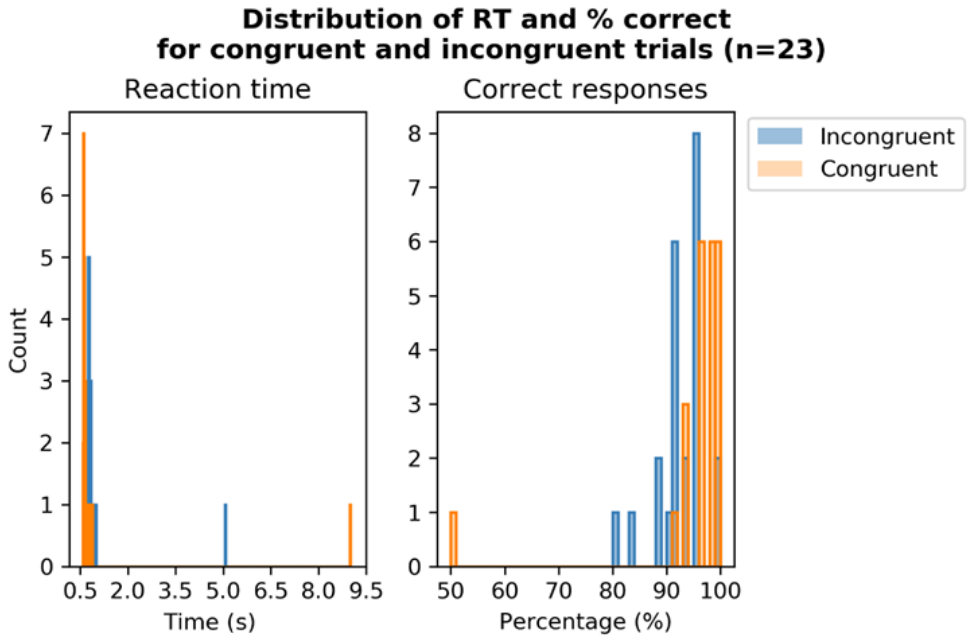
```
19 #### Plot Settings ####
20 xtickstep_rt = 0.1 #x ticks every xtickstep_rt seconds for the reaction time plot, change this value for bigger/smaller steps
21 xtickstep_percent = 5 #x ticks every xtickstep_percent % for the correct responses plot, change this value for bigger/smaller steps
22
```

Here is an example of a problematic plot with crowded x-axes for both plots.



Changing the xtickstep_rt to 1.5 seconds and xtickstep_percent to 10% gives a figure with usable x axes:

```
19 #### Plot Settings ####
20 xtickstep_rt = 1.5 #x ticks every xtickstep_rt seconds for the reaction time plot, change this value for bigger/smaller steps
21 xtickstep_percent = 10 #x ticks every xtickstep_percent % for the correct responses plot, change this value for bigger/smaller steps
22
```



Play around with the values until you get a nice plot. **Change these settings back to the defaults when you are done!**