

Stroop Task experiment & analysis documentation

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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:

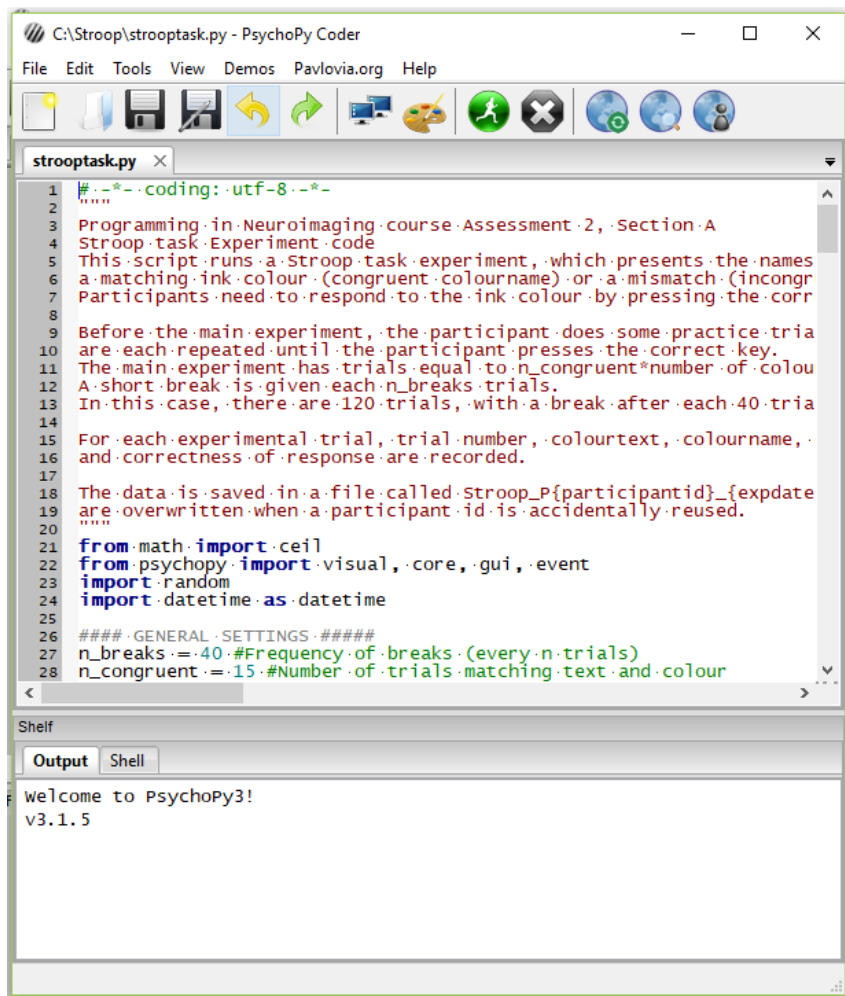
1. Automatic sleep mode is turned off:
 - a. Open Settings → System → Power and Sleep. Set **Screen** and **Sleep** to Never.
2. Keyboard has the colour markers on the correct keys, if not, get stickers and mark the keys:
 - a. f: red; g: blue; h: green; j: yellow – which forms a left to right line on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

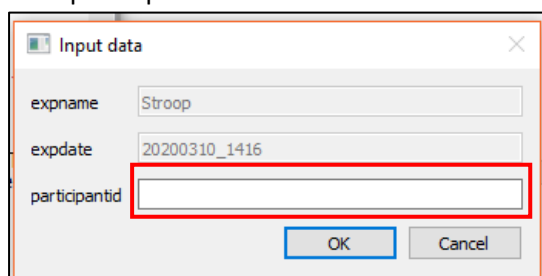


The screenshot shows the PsychoPy3 code editor with the file 'strooptask.py' open. The code is written in Python and includes comments explaining the experiment. The code defines variables for the number of breaks and congruent trials, imports necessary modules, and sets up the experiment structure. The 'Output' window at the bottom shows the message 'Welcome to PsychoPy3! v3.1.5'.

```
1  #-*-coding: utf-8 -*-
2  """
3  Programming in Neuroimaging course Assessment 2, Section A
4  Stroop task Experiment code
5  This script runs a Stroop task experiment, which presents the names
6  a matching ink colour (congruent colourname) or a mismatch (incongr
7  Participants need to respond to the ink colour by pressing the corr
8
9  Before the main experiment, the participant does some practice tria
10 are each repeated until the participant presses the correct key.
11 The main experiment has trials equal to n_congruent*number of colou
12 A short break is given each n_breaks trials.
13 In this case, there are 120 trials, with a break after each 40 tria
14
15 For each experimental trial, trial number, colourtext, colourname,
16 and correctness of response are recorded.
17
18 The data is saved in a file called Stroop_P{participantid}_{expdate
19 are overwritten when a participant id is accidentally reused.
20 """
21 from math import ceil
22 from psychopy import visual, core, gui, event
23 import random
24 import datetime as datetime
25
26 ##### GENERAL SETTINGS #####
27 n_breaks = 40 #Frequency of breaks (every n trials)
28 n_congruent = 15 #Number of trials matching text and colour
```

Running a participant

1. Give the participant these basic instructions:
 - In this experiment, you need to press the key corresponding to the ink colour of the word 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.



The screenshot shows the 'Input data' dialog box. It has three input fields: 'expname' with the value 'Stroop', 'expdate' with the value '20200310_1416', and 'participantid' which is empty. The 'participantid' field is highlighted with a red rectangle. There are 'OK' and 'Cancel' buttons at the bottom.

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

Welcome to the experiment.
In each trial, a colour name will appear on the screen.
Respond by pressing the key corresponding to the ink colour of the word, ignoring the word itself.
These are the keys you should use:

red	f
blue	g
green	h
yellow	j

Please try to respond as fast and accurately as possible!
The main experiment consists of 3 blocks of 40 trials, so a total of 120 trials.
First, you will do some practice trials where you get feedback until you choose the correct key.
Press the space bar to continue to the practice trials.

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

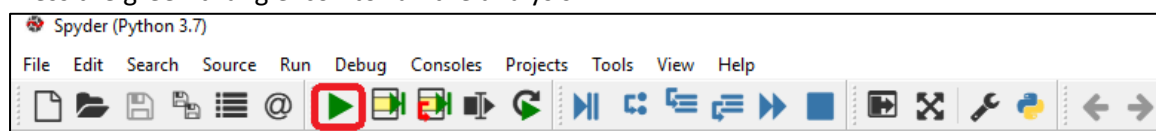
Preparing data

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**.

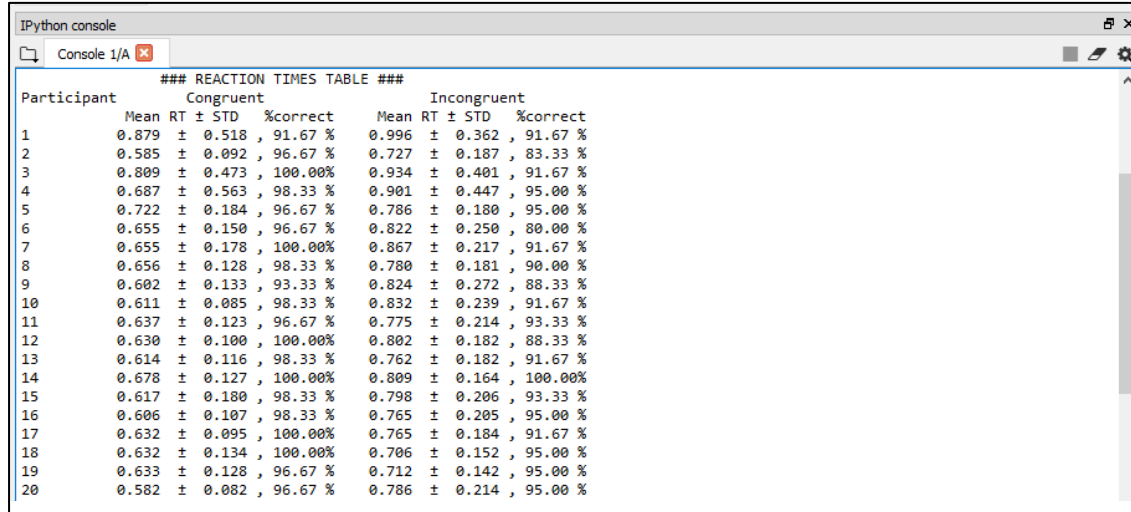
Press the green triangle icon to run the analysis.



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 \pm STD in seconds, and the percentage correct for the congruent and incongruent trials per subject.



IPython console

Console 1/A

REACTION TIMES TABLE

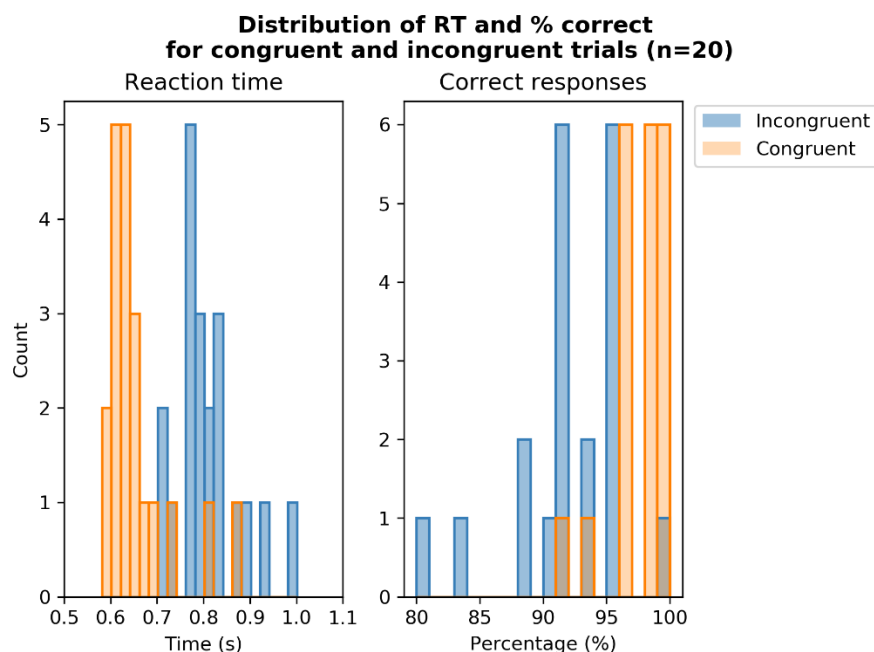
Participant	Congruent			Incongruent		
	Mean RT	\pm STD	%correct	Mean RT	\pm STD	%correct
1	0.879	\pm 0.518	91.67 %	0.996	\pm 0.362	91.67 %
2	0.585	\pm 0.092	96.67 %	0.727	\pm 0.187	83.33 %
3	0.809	\pm 0.473	100.00 %	0.934	\pm 0.401	91.67 %
4	0.687	\pm 0.563	98.33 %	0.901	\pm 0.447	95.00 %
5	0.722	\pm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

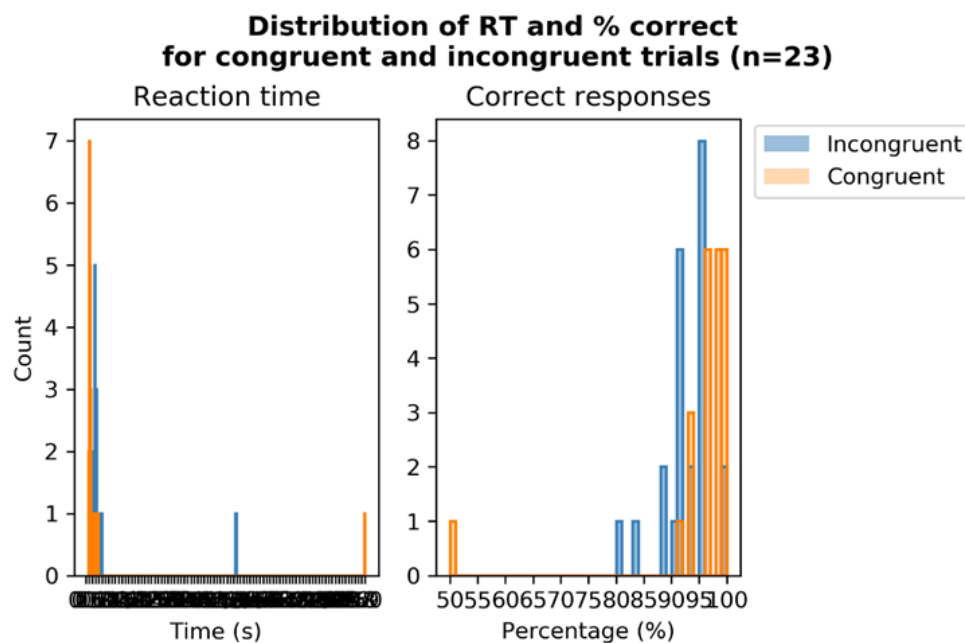
X-axis configuration

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
```

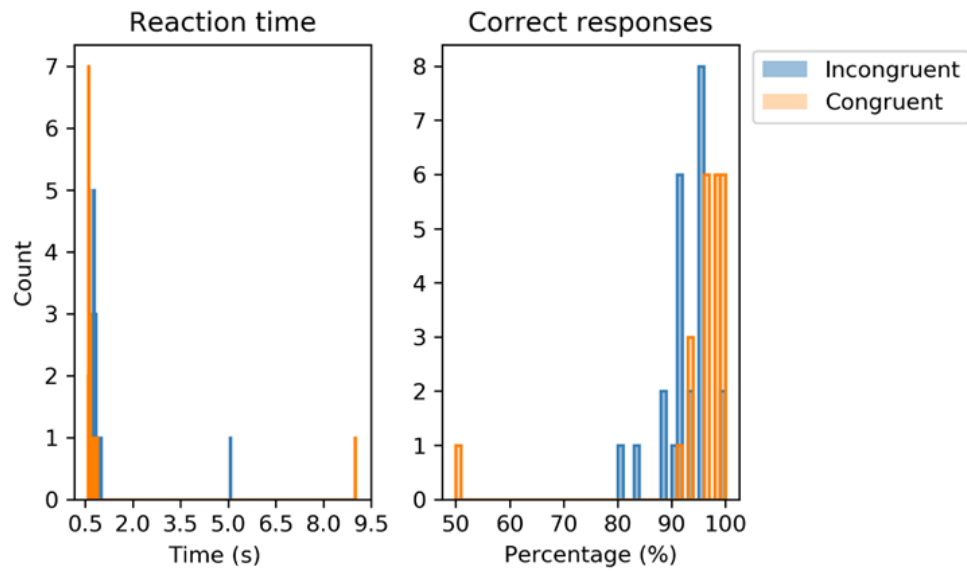
Here is an example of a problematic plot with crowded x-axes for both plots.



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
```

**Distribution of RT and % correct
for congruent and incongruent trials (n=23)**



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