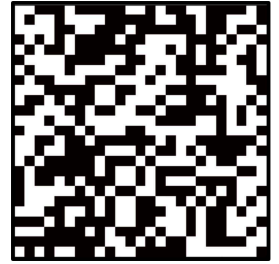


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A Simple Exploration of Simulated Annealing: Protocol

DOI

<https://dx.doi.org/10.17504/protocols.io.eq2lyj77plx9/v1>



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Protocol status: Working

We use this protocol and it's working

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Abstract

This protocol describes technical steps to understand the computational environment for A Simple Exploration of Simulated Annealing hosted on **Code Ocean**.

Safety warnings

❗ Code can take a considerable amount of time. Be cautious when modifying.

Reproducing the Data Analysis

- 1 Access the capsule for this project at [Code Ocean](#). Select "**Edit Capsule**" to work with your own copy.
- 2 The analysis was completed with Python in a Jupyter Notebook. The following notebook is found in the **code** folder in the file manager:

```
analysis.ipynb
```

- 2.1 Details about the computational environment, including the versions of Python, Jupyter, and other libraries are found in the **environment** section of the file manager, which contains a Dockerfile.
- 2.2 Data for the analysis is found in separate folders in the **data** folder in the file manager:
 - **grid_sample**: A .npy file of the sample grid used in simulated annealing
 - **separated_grids**: Multiple .npy files for every grid resulting from a simulation
 - **simulation_data**: Multiple .csv files with run details at every iteration of a simulation

- 3 To execute **analysis.ipynb**, select "**Reproducible Run**"



- 4 Once the reproducible run is complete, the resulting figures, an HTML copy of the executed **analysis.ipynb**, and a run output log are stored in the **results** section found in the file manager.

Running Additional Simulations and Producing New Data

- 5 Each simulation can be run again, with the same sample grid, by executing the following Jupyter Notebook found in the **code** folder:



```
production.ipynb
```

6 **WARNING:** Running **production.ipynb** will overwrite all of the data in each subdirectory of **data**. 

6.1 Copy each subdirectory in a new folder with a title such as "**original**" or something that is more descriptive. Do this before each subsequent run of **production.ipynb**. Update file paths in **analysis.ipynb** if you wish to analyze data that was moved.

7 Modify line 10 of the **run** file inside the **code** section to select **production.ipynb** to run in a reproducible run:

```
--execute production.ipynb \
```

8 Select "**Reproducible Run**" to run additional simulations and produce new data. 

9 To reanalyze the new data, modify line 10 of the **run** file to select **analysis.ipynb**. 

Note

WARNING: Any files that are in **results** may be overwritten. Move these files into a new folder before proceeding.

10 Select "**Reproducible Run**" to execute a new analysis.

11 There are various ways to alter parameters to run additional simulations:

STEP CASE

Changing parameters to create a new sample grid

3 steps

12 There are several parameters that can be changed in **production.ipynb** to produce a new sample grid:

- **rows:** number of rows in the grid
- **cols:** number of columns in the grid



- **percentage:** composition of 1's in the randomly generated grid of mixed 1's and 0's
- **seed:** defines the random number seed used to generate the random mixture of 1's and 0's

- 13 Change any of these parameters (individually or in combination), and after running **production.ipynb**, a new .npz file will be generated in **data/grid_sample**.



Note

WARNING: If the seed is not changed, the .npz file for the previous sample will likely be overwritten. Make sure to relocate or rename these files before running.

- 14 Repeat all steps in "**Running Additional Simulations and Producing New Data**" to produce new data from the new sample.

Protocol references

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