Instructions on how to run and compare the results of optimization vs forward integration

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1 Instructions on how to submit the minAone annealing procedure as a batch job after running forward integration

1.1 Required files and packages

This is an instruction sheet on how to submit annealing procedures generated by the minAone packages, as computational jobs on SLURM-HPC. The following are the system requirements for this procedure to run:

- Python version 3.0 or higher
- Latest version of IPOPT

The required files to run the annealing procedure:

- minAone.py
- discAone.py
- malecppAone.py
- makehppAone.py
- makemakeAone.py
- makeoptAone.py

- equations.txt
- specs.txt
- submit.sbatch
- Any other file defined in specs(e.g injection current, timestep size, boundary condition files etc)

1.2 Forward integration instructions

To run the forward integration procedure, which should be run before the annealing procedure starts, the following files are required:

- forward_integration.ipynb
- Experiment-sepcific files e.g output_solarModel_Bahcall.txt etc

These coding files can be run only on Jupyter Notebook, which can be accessed by following the instructions on "HPC_SLURM_Guideline". The code found on "forward_integration.ipynb" calculates the Jacobian and Hessian matrices of the model (more information on this topic can be found at journals.aps.org/prd/abstract/10.1103/PhysRevD.105.103003), and copies the solution of those matrices to the same directory as the solution files of the annealing procedure.

1.3 Submitting the optimization job/task

List of commands to run an annealing procedure generated by minAone as a batch job on SLURM-HPC:

```
$ python minAone.py
$ make
$ ./neutrinos.cpp
$ Ctrl + Z
$ sbatch submit.sbatch
```

. There a possibility of running into errors at each step of this process. If there is an error after running "python minAone.py", the most likely source of error would be in "equations.txt". To identify the specific error it is recommended to check if the "equations.txt" follows the syntax rules described at the Userguide. If there is an error after running "./neutrinos.cpp", the cause of this error is most likely found in "specs.txt". It might be that a file was not addressed properly or an indentation error. For better assistance in finding the error, it is

recommended to go over the Userguide. Lastly, if an error message is shown while submitting the job with "sbatch submit.sbatch", the user is recommended to look at all the parameters assigned on the batch file for any inconsistencies.

The output that is generated should show the job id , which can be used to cancel the job or change the priority of it (if the user has such privilges). The command to cancel a job on SLURM is scancel and is used as follows:

```
$ scancel job-id ## the latter being usually a 5-6 digit number
```

1.4 Plotting the results

In order to plot the results, the following file is required:

- plotting_code.ipynb

The plotting code plots the forward integration solutions against the optimization solutions as a way of measuring the accuracy of the optimization job.