MANUAL

This manual shall provide a detailed insight into TREMOL_Singlets from a user's and developer's perspective.

Table of Contents

Coding style

- 4 spaces per indentation level.
- Float and Integers are written lower case, while vectors and arrays start with a capital letter.
- Comment convention for functions is as follows:

```
output1 = function(Arg1, arg2):
    """
     This is a function.
      Parameters
      - `Arg1:: Int`: array of dimensions ...
      - `arg2:: String`: string that ...
      return
      - `output1::Float`: float that ...
    """
```

- Inline comments are rare and indicated by a "#"-symbol (e.g. # This is a comment).

Requirements

- TREMOL_Singlets has been tested and runs smoothly on **Linux** operating system, whereas errors may occur on Windows operating systems frequently
- **Julia** (version 0.6.4 has been tested): https://julialang.org/downloads/oldreleases.html
- **PyPlot** package to generate the plots: https://github.com/JuliaPy/PyPlot.jl

TREMOL_Singlets directory structure

After the download of TREMOL_Singlets on https://github.com/monterrubio-velasco/TREMOL_singlets, a user should see the following folders and files:

Name	**Description**
doc/	Source files for TREMOL_Singlets documentation
examples/	Templates of basic scripts for TREMOL_Singlets modeling
TREMOL_singlets/	Source code
Description.pdf	Summary of TREMOL_Singlets features and requirements
License.pdf	License file
README.pdf	Readme file

The source code is located in the `TREMOL_Singlets/` folder, which is divided into three subfolders.

Name	Description
main/	Main scripts to execute the simulation
preprocessing/	Definition of the input parameters by the user
postprocessing/	Analysis of the raw data coming from main/

TREMOL_Singlets workflow

Figure 1 shows the workflow of the code of TREMOL_Singlets. Pre-processing processing and post-processing phases are included.

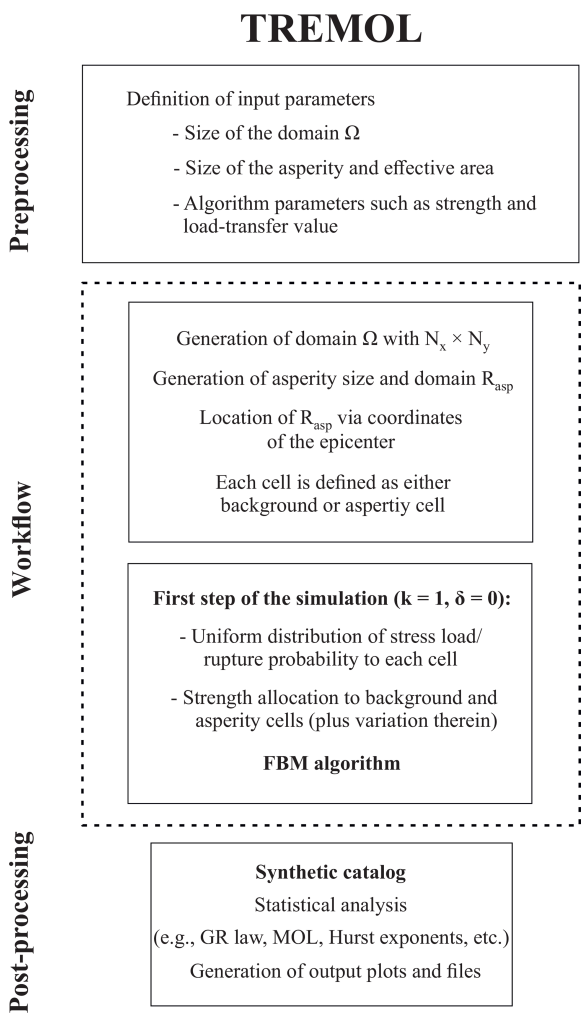

Figure 1. The workflow of the TREMOL_Singlets code.

TREMOL_Singlets preprocessing: Parameter definition

The first step in order to use TREMOL_Singlets code is to define the initial parameters within the ***preprocessing.jl*** file. Those input parameters will be used by the main algorithm to model the asperity rupture.

This file is structured as follows:

```
"""
Define you path
        YOURPATH = “path user”
Include an external function
        include("TREMOL_Singlets.jl")
Arguments
Parameters to assigned the initial conditions to the simulated domain
- `VecID ::String: Name to identify the simulated event.
- `fhi_asp::Float`: percentage of load to be transferred for any ruptured cell in the asperity domain
- `fhi_bkg::Float or Vector`: percentage of load to be transferred for any ruptured cell in the
  background
- `strength_asp::Integer`: strength value to define the asperity cells.
- `nbox::Integer`: Number of cells assigned to each Seismic Source.
- `nk::Integer`: Number of times that will execute a same experiment to obtain statistics

Parameters coming from the finite fault source method
- `DurTeo::Float Vector`: rupture duration given by finite fault computation [seconds]
- `VelAsp :: Float Vector`: rupture velocity given by finite fault computation [km/s]
- `Leff::Float Vector`: Effective length size of the effective rupture area [km]
- `Weff::Float Vector`: Effective wide size of the effective rupture area [km]
- `VectorSeff::Float Vector`: Effective area [km²]
- `SaOri::Float Vector`: Ratio of the asperity size
- `YsizeOri::Float Vector`: Asperity area [km²]

"""
YOURPATH = “path user”
include("TREMOL_Singlets.jl")

TREMOL_Singlets(VecID,fhi_asp,fhi_bkg,strength_asp,DurTeo,VelAsp,Leff,Weff,VectorSeff,SaOri,YsizeOri,nbox,nk)
```

Running a simulation

1. Install **Julia v0.6**. Note that newer versions may not be compatible with TREMOL_Singlets.
2. Add **PyPlot package** following the instructions defined on https://github.com/JuliaPy/PyPlot.jl.
3. Locate the downloaded TREMOL_Singlets-master folder in a path of your choice (e.g. desktop, documents).

4. Define **YOURPATH** (the path where you just placed the TREMOL_Singlets-master folder) in the **preprocessing.jl** and **TREMOL_Singlets.jl** files. Those files can be found at:

`~YOURPATH/TREMOL_singlets-master/TREMOL_singlets/preprocessing/preprocessing.jl

`~YOURPATH/TREMOL_singlets-master/TREMOL_singlets/main/TREMOL_Singlets.jl

5. Afterwards, the input parameters can be defined in the ***preprocessing.jl*** script. We suggest the default values in order to reproduce our results (see Monterrubio-Velasco et al., 2019).
6. To execute TREMOL_Singlets there are two options:

a) from a Linux bash run

```
$ julia YOURPATH/TREMOL_singlets/TREMOL_singlets/preprocessing.jl
```

This option does not show the plots right after their production – excepting TkInter has been installed on Linux beforehand. Nevertheless, the generated figures will be saved in an output folder which is located at /YOURPATH/TREMOL_singlets-master/Results_PlotFiles.

b) from a julia prompt

```
include(joinpath("/YOURPATH/TREMOL_singlets-master/TREMOL_singlets/preprocessing/", "preprocessing.jl"))
```

Alternatively, one can run the code manually by entering the processing subfolder via cd("YOURPATH/TREMOL_singlets-master/TREMOL_singlets/preprocessing/") and run through include("preprocessing.jl"). The simulation ends as soon as the final value of time-steps as well as the absolute number of loops (nk) has been reached.

Visualization of results

TREMOL_Singlets outputs eight different plots in ".pdf"-format as well as one ASCII file as ".dat". Those plots are generated by four different functions in TREMOL_singlets.jl, calcuMagniSpaceTimeSinglets.jl, plotcoordenadasSingletes.jl and gutenberRichAspDef.jl.

- TREMOL_singlets.jl generates a plot of the initial strength configuration: **"EventID*AsperezaSpatial.pdf"**

- calcuMagniSpaceTimeSinglets.jl creates three plots:
  1. **"EventID-MagnitudeTime.pdf":** the magnitude of the events as function of the computed time
  2. **"EventID-FrequencyMagnitude.pdf":** a histogram of the frequency of the magnitudes of the simulated earthquakes
  3. **"EventID-DurationFrequency.pdf:** the rupture duration of each simulated earthquake

- gutenberRichAspDef.jl produces the cumulative number of earthquakes vs magnitude for four different scale relations: **"EventID-Grfit.pdf"**

- plotcoordenadasSingletes.jl: this function generates three plots

1. **"EventID-Mean_Load.pdf":** mean load of the system with time
2. **"EventID-IntereventRate.pdf":** the inter-event rate of the synthetic earthquakes
3. **"EventID-SpatialDistribution.pdf":** Final spatial distribution of differing rupture-groups indicated by different colors

These plots are saved in the directory /YOURPATH/TREMOL_singlets-master/Results_PlotFiles. Plot generation may be deactivated by putting a "#"-symbol at the beginning of every **PyPlot** line for any figure. Furthermore, users may modify or add plots.
If the number of realizations of each experiment is larger than one (nk >1) then the plots **"EventoID*AsperezaSpatial.pdf"** and **"EventID-SpatialDistribution.pdf"** is configured to be saved only for the first realization (i.e. nk=1).

The file **"EventID-MagnitudeStatisticalResults.dat"** contains 18 columns with following information:

1. b-value computed through the function bmemag.jl using Somerville relation (Somerville et al., 1999)
2. maximum magnitude using Somerville relation
3. b-value computed trough the function bmemag.jl using Mai relation (Mai et al., 2000)
4. maximum magnitude using Mai relation
5. b-value computed trough the function bmemag.jl using Mai-VL relation (Mai et al., 2000)
6. maximum magnitude using Mai-VL relation
7. b-value computed trough the function bmemag.jl using Ramirez relation (Rodríguez and Otemöller, 2013)
8. maximum magnitude using Ramirez relation
9. ratio of the largest simulated earthquake [cells] and the total number of cells
10. largest simulated earthquake in [cells]
11. the size of the asperity defined in the random range
12. the random number to define the size of the asperity size
13. original asperity size coming from preprocessing input data
14. number of steps realized in the algorithm
15. maximum magnitude using Somerville relation
16. duration of the computed rupture area (in km^2) divided by the rupture velocity (km/s).
17. equivalent rupture time in seconds, considering the longest rupture duration divided by the rupture velocity
18. equivalent rupture time in seconds considering the root square of the area divided by the rupture velocity
19. rupture velocity, velAsp
20. area of the largest simulated earthquake
21. sqrt(area of the largest simulated earthquake)/velAsp
22. sqrt(area of the largest simulated earthquake)/DurTeo
23. velAsp*DurTeo
24. sqrt(area of the largest simulated earthquake)/velAsp

Each row corresponds to one execution controlled by the number **"nk"** defined in preprocessing.jl script.
The user may perform the corresponding statistics by analyzing the ruptured area or the equivalent magnitude with four different scale-relations (see calcuMagniSpaceTimeSinglets.jl script) by using the file **"EventID-MagnitudeStatisticalResults.dat"**

Example

Modelling the magnitude and ruptured area of the earthquake Mw=7.0, 07/06/1982

The initial values within the **preprocessing.jl** file are:

```
VecID =  ["Mw7-1982"]
fhi_bkg =  0.67
fhi_asp =  0.90
strength_asp = 4
nbox = 100
nk = 10
DurTeo = [40]
VelAsp = [3.2]
Leff = [34.47]
Weff = [17.81]
VectorSeff = [Leff[1].*Weff[1]]
SaOri = [0.23]
YsizeOri = [Leff[1].*Weff[1].*SaOri[1]]
```

The values of *DurTeo*, *VelAsp*, *SaOri*, *Leff* and *Weff* were computed by Rodríguez-Pérez & Ottemöller, (2013), whereas *fhi_bkg*, *fhi_asp*, *strength_asp*, *nbox*, were defined by Monterrubio-Velasco et al. (2019) in order to explore the behavior of the algorithm TREMOL_Singlets.

The output plots and file are saved in the folder
"/YOURPATH/TREMOL_singlets/examples/ExampleMw7_0-1982/Results_PlotsFilesMw7_1982/"

To compare the user results with the expected you can use the files saved in the folder
"~/YOURPATH/TREMOL_singlets/examples/ ExampleMw7_0-1982
/Results_PlotsFilesMw7_1982/Expected_Output_Mw7_0_1982"

Code documentation

Following sub-sections are dedicated to described the **parameters** and **return** parameters of scripts of the code documentation TREMOL_Singlets.

preprocessing/

preprocessing.jl : Define the input by the user and call the function TREMOL_Singlets to pass the input values as arguments

```
Import modules
  using PyPlot
  using PyCall
  @pyimport matplotlib.colors as matcolors
  @pyimport matplotlib as mpl
```

@pyimport matplotlib.patches as patches

Import functions
- include(joinpath("/YOURPATH/TREMOL_singlets/main/","TREMOL_Singlets.jl"))

Parameters that assigned the initial conditions to the simulated domain
- `VecID ::String: Name to identify the simulated event.
- `fhi_asp::Float`: percentage of load to be transferred for any ruptured cell in the asperity domain
- `fhi_bkg::Float or Vector`: percentage of load to be transferred for any ruptured cell in the background
- `strength_asp::Integer`: strength value to define the asperity cells.
- `nbox::Integer`: Number of cells assigned to each Seismic Source.
- `nk::Integer`: Number of times that will execute a same experiment to obtain statistics

Parameters coming from the finite fault source method
- `DurTeo::Float Vector`: rupture duration given by finite fault computation [seconds]
- `VelAsp :: Float Vector`: rupture velocity given by finite fault computation [km/s]
- `Leff::Float Vector`: Effective length size of the effective rupture area [km]
- `Weff::Float Vector`: Effective wide size of the effective rupture area [km]
- `VectorSeff::Float Vector`: Effective area [km²]
- `SaOri::Float Vector`: Ratio of the asperity size
- `YsizeOri::Float Vector`: Asperity area [km²]

main/

TREMOL_Singlets.jl

Main program that define the size and shape to the effective domain and asperity domain. Also this script gives the input values as arguments to the FBM algorithm. Lastly, the output values goes to the postprocessing function.

Import functions
- include(joinpath("/YOURPATH/TREMOL_singlets/main/","FBM_Singlets.jl"))
- include(joinpath("/YOURPATH/TREMOL_singlets/postprocessing/","postprocessing.jl"))

Parameters
- `VecID::String`: Name to identify the simulated event.
- `fhi_asp::Float`: percentage of load to be transferred for any ruptured cell in the asperity domain
- `fhi_bkg::Float or Vector`: percentage of load to be transferred for any ruptured cell in the background
- `strength_asp::Integer`: strength value to define the asperity cells.
- `DurTeo::Float Vector`: rupture duration given by finite fault computation [seconds]
- `VelAsp :: Float Vector`: rupture velocity given by finite fault computation [km/s]
- `Leff::Float Vector`: Effective length size of the effective rupture area [km]
- `Weff::Float Vector`: Effective wide size of the effective rupture area [km]
- `VectorSeff::Float Vector`: Effective area [km²]
- `SaOri::Float Vector`: Ratio of the asperity size
- `YsizeOri::Float Vector`: Asperity area [km²]
- `nbox::Integer`: Number of cells assigned to each Seismic Source.
- `nk::Integer`: Number of times that will execute a same experiment to obtain statistics

return
- `VecMagni::Vector`: Array that contains the results of the magnitude analysis coming from the function postprocessing.jl

FBM_Singlets.jl

This function carry out the FBM asperity algorithm

Import function
- include(joinpath("/YOURPATH/TREMOL_singlets/main/","contaravalan_Asp.jl"))
- include(joinpath("/YOURPATH/TREMOL_singlets/main/","distmayorLLS_Asp.jl"))
- include(joinpath("/YOURPATH/TREMOL_singlets/main/","distmenorLLS_Asp.jl"))

Parameters
- `nbox_x::Integer`: number of cells in X-axis of the domain \Omega
- `nbox_y::Integer`: number of cells in Y-axis of the domain \Omega
- `smin::Integer`: number of steps that realize the algorithm
- `VecPosi::Array`: size(nbox_x,nbox_y), Matrix of the load values. Dynamical matrix because changes the value of some cells at each step.
- `MatrizStrengtInitial::Array`: size(nbox_x,nbox_y), Initial Matrix of the strength value.
- `VecAsperi::Array`: size(nbox_x,nbox_y), Matrix of the strength value. This matrix evolves at each step
- `fhiFuera::Float`: load-transfer value assigned to the cells located in the domain
- `fhiDentro::Float`: load-transfer value assigned to the cells located in the asperity domain
- `VecPhi::Array`: size(nbox_x,nbox_y), Matrix of the load-transfer values.

return
- `vectk1::Array`: size(smin+10,12). Raw data that contains the results of the transfer, accumulation and rupture process following the FBM rules. At each step each row contains:
    1. k:number of step
    2. acumt: cumulative time (T_k = sum(time[1:k]))
    3. tiempo[k]: inter-event time [dimensionless]
    4. (0 or 1): counter that indicates if is normal or avalanche event
    5. suma: sum of the load in all the cells
    6. sumarho= 1/tiempo[k] (rupture rate)
    7. parametrosigma: load value of the cell chosen to fail
    8. a: coordinate in the X-axis, of the cell chosen to fail
    9. b: coordinate in the Y-axis, of the cell chosen to fail
    10. fhi: load-transfer value
    11-12. (iorigi,jorigi): coordinates of the cell chosen to fail at the first stage of the searching algorithm defined in the function contaravalan_Asp.
- `vectparamestad::Array`: size(smin+10,2). Mean and Standard deviation of the load in the system, computed at each time step considering only the cells active
- `VecPosiFinal::Array`: size(nbox_x,nbox_y). Final configuration of VecPosi.

contaravalan_Asp.jl

Compute the number of cells that overpass the threshold load value (STAGE 1). But also in this version the cells that fails is chosen considering not only its load but also the strength criterion defined in TREMOL algorithm (STAGE 2)

Parameters

- `nx::Integer`: number of cells in X-axis of the domain \Omega
- `ny::Integer`: number of cells in Y-axis of the domain \Omega

- `VectorP::Array`: size(nbox_x,nbox_y), Matrix of the load values. Dynamical matrix because changes the value of some cells at each step.
- `VecAsperi::Array`: size(nbox_x,nbox_y), Matrix of the strength value. This matrix evolves at each step
- `VecPhi:Array`: size(nbox_x,nbox_y), Matrix of the load-transfer values.
- `rho::Integer`: Weibull exponent, we take it as a constant 30
- `k::Integer`: step of number

return

- `contador::Integer`: number of cells that overpass the threshold load value
- `Nflag1::Integer` : code that indicates if the rupture is normal or avalanche
- `maxtempo1::Float` : maximum load value
- `iout1::Integer`: x coordinate in the array of the chosen cell to fail
- `jout1::Integer`: y coordinate in the array of the chosen cell to fail
- `VecAsperi::Array`: updated matrix of the strength
- `iout::Integer`: x coordinate in the array of the chosen cell to fail at STAGE 1
- `jout::Integer`: Y coordinate in the array of the chosen cell to fail at STAGE 1

distmayorLLS_Asp.jl

Function that distribute the load following the avalanche events algorithm (avalanche event is the cell that overpass their threshold values)

Import function
 - include(joinpath("/YOURPATH/TREMOL_singlets/main/","vecinosLLS.jl"))

Parameters

- `vector::Array`:vector of nine positions that contains the neighbors and failed cell, being: vector[9], vector[3], vector[7] and vector[1] diagonal neighbors; vector[8], vector[2], vector[4] and vector[6] perpendicular neighbors. Finally vector[5] is the failed cell.
- `fhi::Float`: load-transfer value assigned to the failed cell.

return

- `vector::Array`: updated vector of nine positions after the load transfer of the failed cell.

distmenorLLS_Asp.jl

Function that distributes the load following the normal-events algorithm (when any cell overpasses its threshold values)

Import function
 - include(joinpath("/YOURPATH/TREMOL_singlets/main/","vecinosLLS.jl"))

Parameters
- `vector1::Array`:vector of nine positions that contains the neighbors and failed cell, being: vector1[9], vector1[3], vector1[7] and vector1[1] diagonal neighbors; vector1[8], vector1[2], vector1[4] and vector1[6] perpendicular neighbors. Finally vector1[5] is the failed cell.
- `fhi::Float`: load-transfer value assigned to the failed cell

return

- `vecreload::Array`: updated vector of nine positions after the load transfer of the failed cell.

vecinosLLS.jl

This function distributed the load for the orthogonal neighbors (N,S,E,W) that are allowed to received load.

Import function
- include(joinpath("/YOURPATH/TREMOL_singlets/main/","veciProhiDiag.jl"))

Parameters
- `vector::Array`:vector of nine positions that contains the neighbors and failed cell, being: vector[9], vector[3], vector[7] and vector[1] diagonal neighbors; vector[8], vector[2], vector[4] and vector[6] perpendicular neighbors.
- `vecEsfTot::Float`: Load value of the failed cell.

return
- `vectclon::Array`: Updated vector of nine positions after the load transfer of the failed cell.

veciProhiDiag.jl

Compute the number of cells that overpass the threshold load value. But also in this version it choose the cells that is ruptured because the strength criterion defined in TREMOL algorithm

Parameters

- `vector::Array`:vector of nine positions that contains the neighbors and failed cell, being: vector[9], vector[3], vector[7] and vector[1] diagonal neighbors; vector[8], vector[2], vector[4] and vector[6] perpendicular neighbors.`
- `vecEsfDiag::Float`: Load value will be transfer to the Diagonal neighbors. `
- `A::Array`:vector of four positions that contains the diagonal neighbors

return
- `B::Array`: updated vector of four positions that contains the new amount of load given to the diagonal neighbors

postprocessing/

postprocessing.jl

Main program that assigns the size and shape to the effective domain and asperity domain. Also this script gives the input values to the FBM algorithm. Lastly the output values goes to the postprocess function.

Import function
- include(joinpath("/YOURPATH/TREMOL_singlets/main/","calcuMagniSpaceTimeMultiSinglets.jl"))
- include(joinpath("/YOURPATH/TREMOL_singlets/postprocessing/","plotcoordenadasSingletesbis.jl"))

Parameters

- `datos::Array`: size(smin,12) raw data coming from the FBM algorithm. This data base contains the rupture information of model
Each row contains:

1. k: number of steps
2. acumt: cummulative time (T_k = sum(time[1:k]))
3. tiempo[k]: inter-event time [dimensionless]
4. (0 or 1): identifier to normal or avalanche event
5. suma: sum of the load in all the cells
6. sumarho= 1/time[k] (rupture rate)
7. parametrosigma: load value of the cell chosen to fail
8. a: coordinate in the X-axis, of the cell chosen to fail
9. b: coordinate in the Y-axis, of the cell chosen to fail
10. fhi: load-transfer value
11-12. (iorigi,jorigi): coordinates of the cell chosen to fail at the first stage of the searching algorithm defined in the function contaravalan_Asp.

- `VectorCenterAperities::Vector Integer`: size(1), Central coordinates of the asperity (x,y)
- `VectorSaOriLateralSize_y::Vector`: Asperity lateral size in the Y-axis
- `VectorSaOriLateralSize_x::Vector`: Asperity lateral size in the X-axis
- `VectorCoordsAperities_x::Vector Integer`: coordinates of the asperity vertex in the X-axis
- `VectorCoordsAperities_y::Vector Integer`: coordinates of the asperity vertex in the Y-axis
- `nbox_x::Integer`: number of cells in X-axis of the domain \Omega
- `nbox_y::Integer`: number of cells in Y-axis of the domain \Omega
- `smin::Integer`: number of steps that realize the algorithm
- `vecEstadistico::Array`: size(smin+10,2). Mean and Standard deviation of the load in the system, computed at each time step considering only the cells active
- `VectorSaOri::Float Vector`: Random size of the asperity
- `SaOri::Float Vector`: Original Ratio of the asperity size
- `TotalNumberCells::Integer`: number of cells in the domain \Omega (nbox_x * nbox_y)
- `a::Float`: random number
- `CellSize::Float`: Size of a cell in km²
- `velAsp::Float`: rupture velocity
- `Weff::Float`: width of the effective area in km
- `Leff::Float`: length of the effective area in km
- `DurTeo::Float`: rupture duration

return

- `vecMagniLoop::Array`: results of the magnitude analysis
Each row contains:
1. vecMagniLoop[1,1]: b-value computed trough the function bmemag.jl using Somerville relation
2. vecMagniLoop[1,2]: maximum magnitude using Somerville relation
3. vecMagniLoop[1,3]: b-value computed trough the function bmemag.jl using Mai relation
4. vecMagniLoop[1,4]: maximum magnitude using Mai relation
5. vecMagniLoop[1,5]: b-value computed trough the function bmemag.jl using Mai-VL relation
6. vecMagniLoop[1,6]: maximum magnitude using Mai-VL relation
7. vecMagniLoop[1,7]: b-value computed trough the function bmemag.jl using Ramirez relation
8. vecMagniLoop[1,8]: maximum magnitude using Ramirez relation
9. vecMagniLoop[1,9]: ratio of the largest simulated earthquake [cells] and the total number of cells
10. vecMagniLoop[1,10]: largest simulated earthquake in [cells]
11. vecMagniLoop[1,11]: VectorSaOri
12. vecMagniLoop[1,12]: a
13. vecMagniLoop[1,13]: SaOri
14. vecMagniLoop[1,14]: smin
15. vecMagniLoop[1,15]: maximum magnitude using Somerville relation
16. vecMagniLoop[1,16]: length of the area earthquake (in km^2) divided by the rupture velocity (km/s)

17. vecMagniLoop[1,17]: equivalent rupture time in seconds, considering the longest length divided by the rupture velocity
18. vecMagniLoop[1,18]: equivalent rupture time in seconds considering the root square of the area divided by the rupture velocity
19. vecMagniLoop[1,19]: rupture velocity, velAsp
20. vecMagniLoop[1,20]: area of the largest simulated earthquake
21. vecMagniLoop[1,21]: sqrt(area of the largest simulated earthquake)/velAsp
22. vecMagniLoop[1,22]: sqrt(area of the largest simulated earthquake)/DurTeo
23. vecMagniLoop[1,23]: velAsp*DurTeo
24. vecMagniLoop[1,24]: sqrt(area of the largest simulated earthquake)/velAsp

calcuMagniSpaceTimeSinglets.jl

Cluster the avalanches considering the time and space criterion. Also is computed the equivalent magnitude at each new group.

Import function
- include(joinpath("/YOURPATH/TREMOL_singlets/postprocessing/","gutenberRichAspDef.jl"))
- include(joinpath("/YOURPATH/TREMOL_singlets/postprocessing/","bmemag.jl"))

Parameters
- `Y::Array`:raw data coming from the FBM algorithm. This data base contains the rupture information of model
  Each row contains:
  1. k:number of step
  2. acumt: accumulated time (T_k = sum(time[1:k]))
  3. tiempo[k]: inter-event time [dimensionless]
  4. (0 or 1): identifier to normal or avalanche event
  5. suma: sum of the load in all the cells
  6. sumarho= 1/time [k] (rupture rate)
  7. parametrosigma: load value of the cell chosen to fail
  8. a: coordinate in the X-axis, of the cell chosen to fail
  9. b: coordinate in the Y-axis, of the cell chosen to fail
  10. fhi: load-transfer value
  11-12. (iorigi,jorigi): coordinates of the cell chosen to fail at the first stage of the searching algorithm defined in the function contaravalan_Asp.

- `Nbox_x::Integer`: number of cells in X-axis of the domain \Omega
- `Nbox_y::Integer`: number of cells in Y-axis of the domain \Omega`
- `smin::Integer`: number of steps that realize the algorithm
- `VectorCenterAperities::Vector Integer`: size(1), Central coordinates of the asperity (x,y)
- `VectorSaOriLateralSize_y::Vector`: Asperity lateral size in the Y-axis
- `VectorSaOriLateralSize_x::Vector`: Asperity lateral size in the X-axis
- `VectorCoordsAperities_x::Vector Integer`: coordinates of the asperity vertex in the X-axis
- `VectorCoordsAperities_y::Vector Integer`: coordinates of the asperity vertex in the Y-axis
- `CellSize::Float`: Size of a cell in km²`
- `velAsp::Float`: rupture velocity
- `Weff::Float`: width of the effective area in km
- `Leff::Float`: length of the effective area in km

return
- `vecMagni::Array`: matrix that contains the results of the magnitude analysis

- VecNewAvalSpaceTime::Array`: matrix that contains the data of the regrouping algorithm coming from the Y matrix
Each row contains:
1. VecNewAvalSpaceTime[contNumAvalSpaceTime,1] = contadorAval: number of elements considering in the regrouping algorithm
2. VecNewAvalSpaceTime[contNumAvalSpaceTime,2] = original number in the raw catalog Y
3. VecNewAvalSpaceTime[contNumAvalSpaceTime,3] = cumulative time (T_k = sum(tiempo[1:k])) computed in the raw catalog Y
4. VecNewAvalSpaceTime[contNumAvalSpaceTime,4] = inter-event time [dimensionless] computed in the raw catalog Y
5. VecNewAvalSpaceTime[contNumAvalSpaceTime,5] = normal-avalanche code considered in the new regrouping
6. VecNewAvalSpaceTime[contNumAvalSpaceTime,6] = x coordinate
7. VecNewAvalSpaceTime[contNumAvalSpaceTime,7] = y coordinate
8. VecNewAvalSpaceTime[contNumAvalSpaceTime,8] = rupture rate

bmemag.jl

Function calculates the mean magnitude, the b-value based on the mean and the standard deviation

Parameters
- `VecMag ::Array`: Vector that contains the equivalent magnitudes

return
- `meanm1::Float`: mean value of VecMag vector
- `b1::Float`: b-value
- `sig1::Float`: standard deviation
- `av2::Float`: a-value

gutenberRichAspDef.jl

Function that computes the Gutenberg-Richter fit relation using the method of least squares

Parameters
- `VecMagHB1::Array`: Vector that contains the equivalent magnitudes
- `nflag::Integer`: Identifier
- `AreaSUB::Float`: Cell area ion km²

return
- `paramGRAreaWY::Array`: results of the Gutenberg-Richter fitting using the least square method
  1. paramGRAreaWY[1]=magMax
  2. paramGRAreaWY[2]=magMin
  3. paramGRAreaWY[3]=p1 (a-value)
  4. paramGRAreaWY[4]=p2 (b-value)
  5. paramGRAreaWY[5]=rho (correlation coefficient)
- `cuenrep::Integer`: number of times that a same frequency of magnitudes is repeated for different magnitudes
- `vecWrite::Array`: vector that contains the frequency-magnitude data.

References

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