

Instruction Guide¹

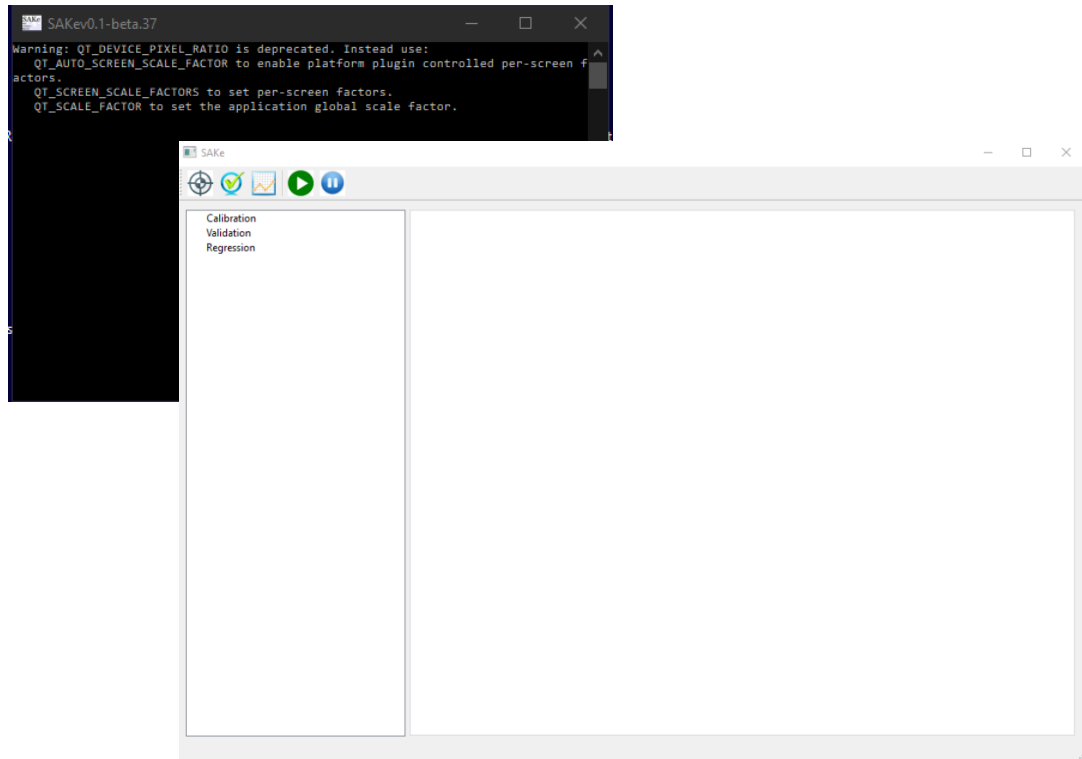
Examples and details on model application²

Start

To start the model, double click the executable file **SAKev0.1-beta.39.exe**

The following two windows will open:

- the first (in black) is the “terminal window”, that may be useful for checking program messages during execution (note: do not close it, otherwise the application ends);
- the second (in white/grey) is the main application window.




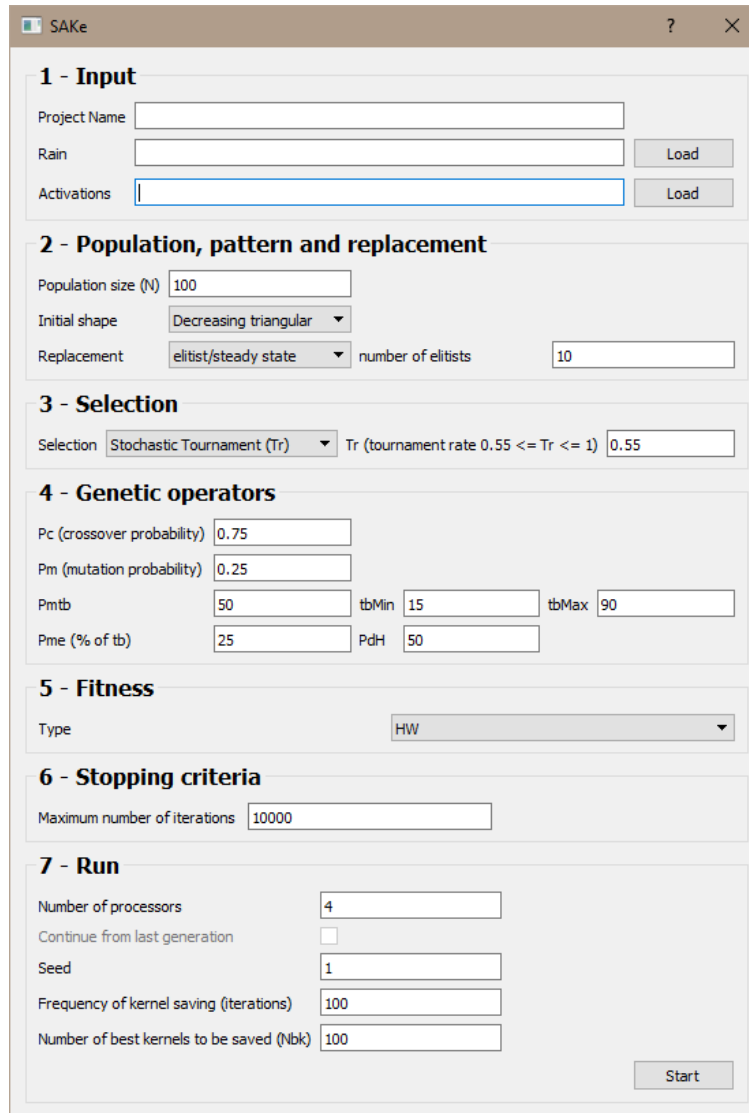
¹ The present Instruction Guide refers to the Microsoft Windows operating system.

² For more details, please refer to: De Rango A, Terranova A, D'Ambrosio D, Lupiano V, Mendicino G, Terranova OG, Iovine G (*submitted*). GA SAKe-2.0 – An advanced hydrological model to predict the activation of landslides.

Calibration

For calibrating the model, the following steps are required (for more details, cf. §3 - Model calibration³):

- select the button  on the tool bar (top left). The following input mask will open:



The screenshot shows the SAKe calibration input mask, which is a window titled "SAKe" with a question mark icon and a close button. The mask is divided into seven sections:

- 1 - Input**: Contains three text input fields: "Project Name", "Rain", and "Activations". Each field has a "Load" button to its right.
- 2 - Population, pattern and replacement**: Contains a "Population size (N)" input field (value: 100), an "Initial shape" dropdown menu (value: Decreasing triangular), a "Replacement" dropdown menu (value: elitist/steady state), and a "number of elitists" input field (value: 10).
- 3 - Selection**: Contains a "Selection" dropdown menu (value: Stochastic Tournament (Tr)) and a "Tr (tournament rate 0.55 <= Tr <= 1)" input field (value: 0.55).
- 4 - Genetic operators**: Contains several input fields: "Pc (crossover probability)" (value: 0.75), "Pm (mutation probability)" (value: 0.25), "Pmtb" (value: 50), "tbMin" (value: 15), "tbMax" (value: 90), "Pme (% of tb)" (value: 25), and "PdH" (value: 50).
- 5 - Fitness**: Contains a "Type" dropdown menu (value: HW).
- 6 - Stopping criteria**: Contains a "Maximum number of iterations" input field (value: 10000).
- 7 - Run**: Contains several input fields: "Number of processors" (value: 4), "Continue from last generation" (checkbox), "Seed" (value: 1), "Frequency of kernel saving (iterations)" (value: 100), and "Number of best kernels to be saved (Nbk)" (value: 100). A "Start" button is located at the bottom right of this section.

- The three fields of section **1 - Input** must be initialized, by specifying a unique *Project Name*, and the complete paths (file names included, in csv format) for *Rain* and *Activations*. The remaining field of sections **2-7** are pre-compiled. In Figure A-1, an example of initialization of the mask for the “benchmark

³ For details on mentioned sections, please refer to: De Rango A, Terranova A, D'Ambrosio D, Lupiano V, Mendicino G, Terranova OG, Iovine G (*submitted*). GA SAKe-2.0 – An advanced hydrological model to predict the activation of landslides.

experiment” (cf. [Appendix B.1](#)) is provided. Note that pre-compiled fields can be changed to allow for exploring different experimental setups (for details on fields and values, cf. [Figure A-2](#), §3 and [Appendix B.1](#)).

- To start the calibration experiment, press the *Start* button on the bottom-right corner.

Note that, both calibration and regression experiments (see below) can be paused and re-started, by pressing the

following buttons  on the tool bar.

Multiple experiments can be executed simultaneously. Per each experiment, the results are shown on a specific window (cf. [Appendix B.1](#)).

By default, the output files are stored in the following path:

C:\Users\name\Documents\workspace\calibration\Project Name.

SAKe

1 - Input

Project Name: C&G_b0

Rain: F:/SAKe/case studies/S.FILI/Frega17/SFILI_rain_C.csv

Activations: F:/SAKe/case studies/S.FILI/Frega17/SFILI_activation_C_(Frega17).csv

2 - Population, pattern and replacement

Population size (N): 100

Initial shape: Decreasing triangular

Replacement: elitist/steady state number of elitists: 10

3 - Selection

Selection: Stochastic Tournament (Tr) Tr (tournament rate $0.55 \leq Tr \leq 1$): 0.55

4 - Genetic operators

Pc (crossover probability): 0.75

Pm (mutation probability): 0.25

Pmtb: 5 tbMin: 15 tbMax: 180

Pme (% of tb): 25 PdH: 50

5 - Fitness

Type: HW

6 - Stopping criteria

Maximum number of iterations: 10000

7 - Run

Number of processors: 4

Continue from last generation: ☐

Seed: 1

Frequency of kernel saving (iterations): 100

Number of best kernels to be saved (Nbk): 100

Figure A-1 – SAKe 2.0 – Example of calibration mask (“benchmark experiment” – cf. Appendix B.1).

SAKe

1 - Input

Project Name: C&G_b0

Rain: F:/SAKe/case studies/S.FILI/Frega17/SFILI_rain_C.csv

Activations: F:/SAKe/case studies/S.FILI/Frega17/SFILI_activation_C_(Frega17).csv

2 - Population, pattern and replacement

Population size (N): 100

Initial shape: Decreasing triangular

Replacement: elitist/steady state number of elitists: 10

3 - Selection

Selection: Stochastic Tournament (Tr) Tr (tournament rate $0.55 \leq Tr \leq 1$): 0.55

4 - Genetic operators

Pc (crossover probability): 0.75

Pm (mutation probability): 0.25

Pmtb: 5 tbMin: 15 tbMax: 180

Pme (% of tb): 25 PdH: 50

5 - Fitness

Type: HW

6 - Stopping criteria

Maximum number of iterations: 10000

7 - Run

Number of processors: 4

Continue from last generation: ☐

Seed: 1

Frequency of kernel saving (iterations): 100

Number of best kernels to be saved (Nbk): 100

<h3>2 - Population, pattern and replacement</h3> <p>Population size (N) <input type="text" value="100"/></p> <p>Initial shape <input type="text" value="Decreasing triangular"/></p> <p>Replacement <input type="text" value="generational"/></p>
<h3>2 - Population, pattern and replacement</h3> <p>Population size (N) <input type="text" value="100"/></p> <p>Initial shape <input type="text" value="Decreasing triangular"/></p> <p>Replacement <input type="text" value="elitist/steady state"/> number of elitists <input type="text" value="10"/></p>
<h3>3 - Selection</h3> <p>Selection <input type="text" value="Stochastic Tournament (Tr)"/> Tr (tournament rate $0.55 \leq Tr \leq 1$) <input type="text" value="0.55"/></p>
<h3>3 - Selection</h3> <p>Selection <input type="text" value="Deterministic Tournament (Ts)"/> Ts (tournament size $2 \leq Ts \leq N$) <input type="text" value="2"/></p>
<h3>3 - Selection</h3> <p>Selection <input type="text" value="Ranking (s)"/> selective pressure $0 < s < 1$ (exponential) $1 \leq s \leq 2$ (linear) <input type="text" value="2"/></p>
<h3>3 - Selection</h3> <p>Selection <input type="text" value="Roulette"/></p>

Figure A-2a – SAKe 2.0 – Details on sections of the calibration mask.

4 - Genetic operators Pc (crossover probability) <input type="text" value="0.75"/> Pm (mutation probability) <input type="text" value="0.25"/> Pmtb <input type="text" value="5"/> tbMin <input type="text" value="15"/> tbMax <input type="text" value="180"/> Pme (% of tb) <input type="text" value="25"/> PdH <input type="text" value="50"/>					
5 - Fitness Type <input type="text" value="HW"/>					
5 - Fitness Type <input type="text" value="EW"/>					
5 - Fitness Type <input type="text" value="AUC ROC"/> ROC AUC Number of Thresholds (ntr) <input type="text" value="10"/>					
6 - Stopping criteria Maximum number of iterations <input type="text" value="10000"/>					
7 - Run Number of processors <input type="text" value="4"/> Continue from last generation <input type="checkbox"/> Seed <input type="text" value="1"/> Frequency of kernel saving (iterations) <input type="text" value="100"/> Number of best kernels to be saved (Nbk) <input type="text" value="100"/>					

Figure A-2b – SAKe 2.0 – Details on sections of the calibration mask.


In **Figure A-3**, an example of output for the “benchmark experiment” (cf. **Appendix B.1**) is provided.



Figure A-3 – SAKe 2.0 – Example of output of calibration (“benchmark experiment” – cf. **Appendix B.1**).

Validation

For validating the model, the following steps are required (for more details, cf. **§4 - Model validation**):

- select the button , on the tool bar. The following input mask will open:

Validation

Project name

Rain

Load

Activation

Load

Kernel

Load

ROC AUC Number of Thresholds (ntr)

10

OK

- The fields must be initialized, by specifying a unique *Project Name*, the complete paths (file names included, in csv format) for *Rain*, *Activations*, and *Kernel*, and the number of thresholds to be employed for ROC evaluation. Note that this latter is pre-compiled, and can be changed to allow for exploring different

experimental setups (for details on fields and values, cf. §4 and Appendix B.2). In Figure A-4, an example of initialization of the mask for the “benchmark experiment” (cf. Appendix B.1) is provided.

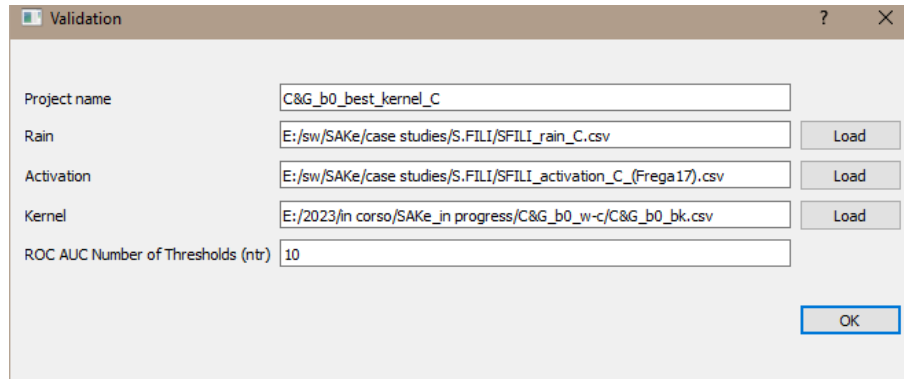


Figure A-4 – SAKe 2.0 – Example of validation mask (best kernel, “benchmark experiment” – cf. Appendix B.1).

- To start the validation experiment, press the *OK* button on the bottom-right corner.

The model will perform one single iteration, by applying the three fitness functions (HW, EW, ROC). The results are shown on a specific window (cf. Appendix B.2). By default, the output files are stored in the following path:

C:\Users\name\Documents\workspace\validation\Project Name.


In Figure A-5, an example of output for the “benchmark experiment” (cf. Appendix B.1) is provided.



Figure A-5 – SAKe 2.0 – Example of output of validation (best kernel, “benchmark experiment” - cf. Appendix B.1).

Regression

For a regression experiment, the following steps are required (for more details, cf. §5 - Regression (reduction of kernel variability for physical interpretation):

- select the button , on the tool bar. The following input mask will open:

1 - Input

Project name

Starting Kernel

2 - Population, Replacement

Population size (N)

Replacement number of elitists

3 - Selection

Selection

Tr (tournament rate $0.55 \leq Tr \leq 1$)

4 - Genetic Operators

Pc (crossover probability)

Pm (mutation probability)

5 - Stopping criteria

Maximum number of iterations

6 - Run

Number of processors

Continue from last generation ☐

Seed

Frequency of population saving (iterations)

Number of functions with alpha ≥ 1

N.	pha m	pha m	eta m	eta m	ight n	ight n	lpha %	beta %	eight	ift m	ift m	ift %
1	8	1	100	20	2	0.02	0.03	0.03	0.03	10	1	1.5

Number of linear functions

N.	n max	n min	q max	q min	ight n	ight n	m %	q %	eight	ift m	ift m	ift %
1	0.0005	0.0005	0.003	0.1	0.2	2	0.03	0.03	0.03	0.03	0.03	0.03

- The two fields of section **1 - Input** must be initialized, by specifying a unique *Project Name*, and the complete path (file name included, in csv format) of the *Starting Kernel*. The remaining field of sections **2-6** are pre-compiled. They can be changed to allow for exploring different experimental setups (for details on fields and values, cf. §4 and Appendix B.3). In Figure A-6a, an example of initialization of the mask is provided.
- To start the validation experiment, press the *Start* button on the bottom.

The model will perform the pre-fixed number of iterations. The results are shown on a specific window (cf. Appendix B.3). By default, the output files are stored in the following path:

C:\Users\name\Documents\workspace\regression\Project Name.

In **Figure A-6b**, an example of output is provided.

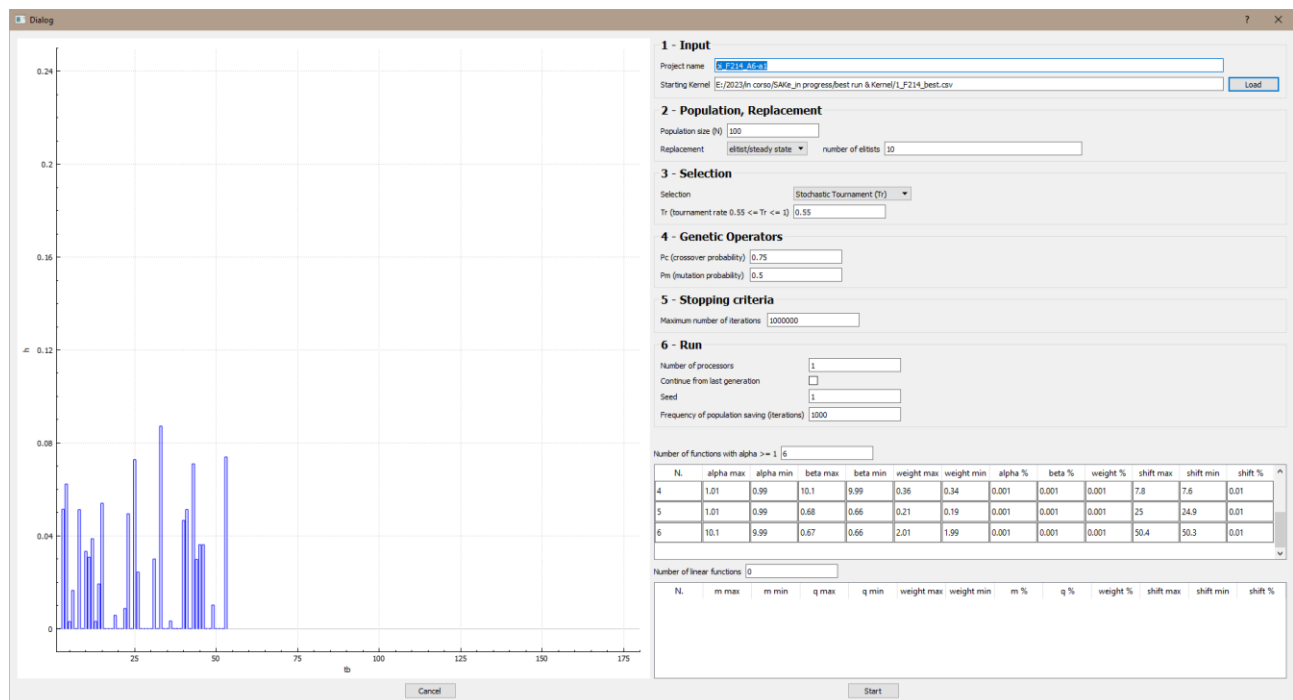


Figure A-6a – SAKe 2.0 Post-processing panel. Initialization of the regression.



Figure A-6b – SAKe 2.0 Post-processing panel. Output of regression.

Please note: the model is in beta version, as checks are in progress to resolve an error that occurs in the Regression after several hundred thousand iterations. In any case, the tool already provides useful results for understanding the dynamics of the landslide phenomenon and the underground water circulation responsible for its activation.