

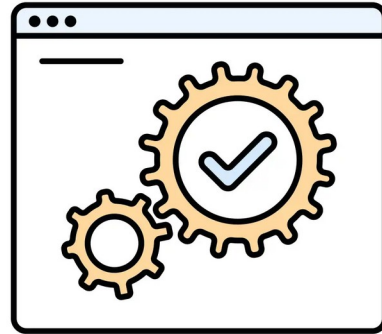
MODELOS EVOLUTIVOS EN CÁNCER: MEJORAS Y EXTENSIONES A WEB APPS INTERACTIVAS

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Tutor: Ramón Díaz Uriarte

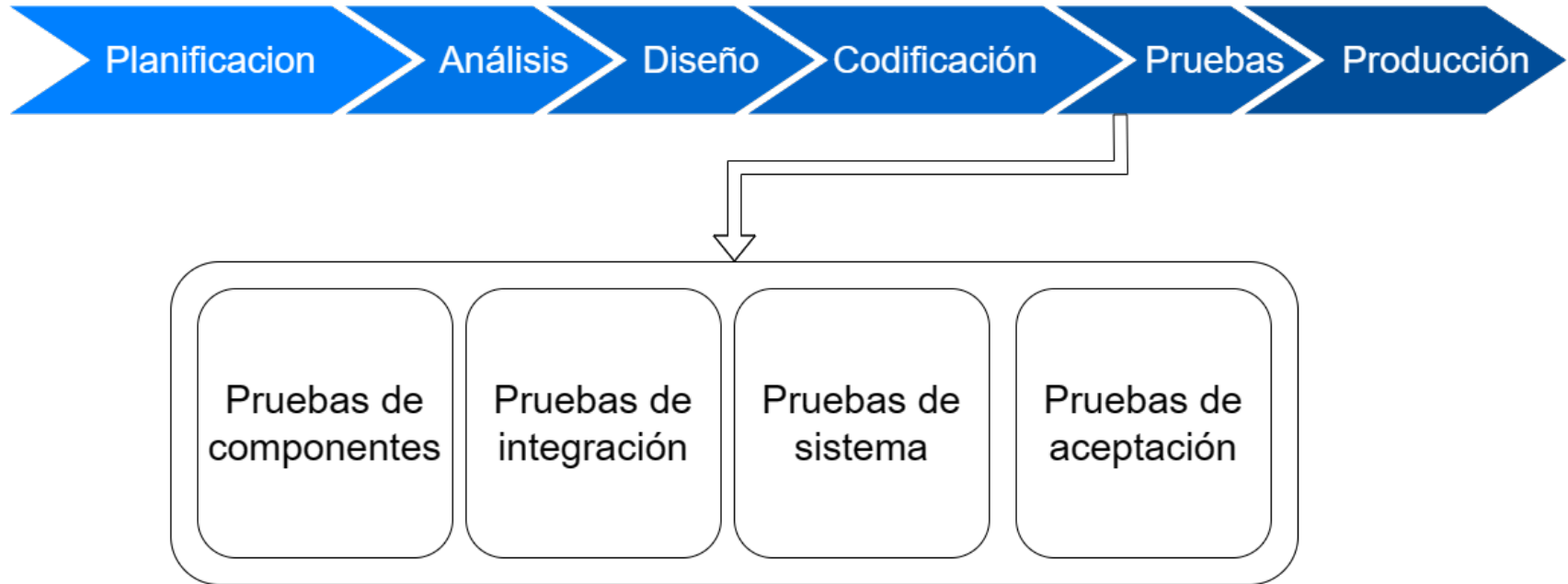
INTRODUCCIÓN Y MOTIVACIÓN

Software de calidad

- ▷ Utiliza los recursos de forma eficiente.
- ▷ Es confiable; los resultados no varían al procesar los mismos datos.
- ▷ Es facil de utilizar.
- ▷ Es seguro.
- ▷ Es facil de mantener.



Fase de pruebas



EvAM-Tools



About EvAM-Tools

User input

Results

Cross-sectional data. Upload, create, generate, modify.

Enter cross-sectional data:

☐ Upload file
☐ Enter genotype frequencies manually

Generate cross-sectional data from CPM models:

☐ DAG and reference proba.
☐ Matrix log-CP matrix

Examples and user's data:

☐ DAG_Fish_3
☒ DAG_Fish_4
☐ DAG_Limma
☐ DAG_AND
☐ DAG_OR
☐ DAG_XOR
☐ DAG_A_O_X

evamtools R package version 2.1.15

Set the number of genes (using 7 or more genes can lead to very long execution times for some methods and crowded figures)

Number of genes

Use different gene names

Define a Directed Acyclic Graph (DAG) and generate data from it. [Help](#)

1. Define DAG

Type of model
Model: ☐ OT ☐ OncBN ☒ CBNH-ESBCH

New edge

From (parent node) ☒ Root ☐ A ☐ B ☐ C ☐ D

To (child node) ☒ A ☐ B ☐ C ☐ D

If you want to decrease the number of genes first remove edges and nodes from the DAG and only then modify 'Set the number of genes'. (We cannot know which edges/nodes you want to remove).
If you want to increase the number of genes use 'Set the number of genes' to increase the available gene labels, and then increase the number of nodes in the DAG.

DAG table

Remember to hit Ctrl-Enter when you are done editing the DAG table for changes to take effect.

From	To	Relation	Lambdas
Root	A	Single	0.6
Root	B	Single	0.7
A	C	Single	0.9
B	D	Single	0.3

2. Generate data from the DAG model

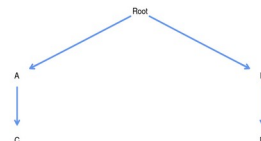
spikeL

For OT (types) and OncBN (s) only: probability that children nodes not allowed by the model (the DAG) occur. Accepted values: [0, 1]. This setting affects predicted probabilities.

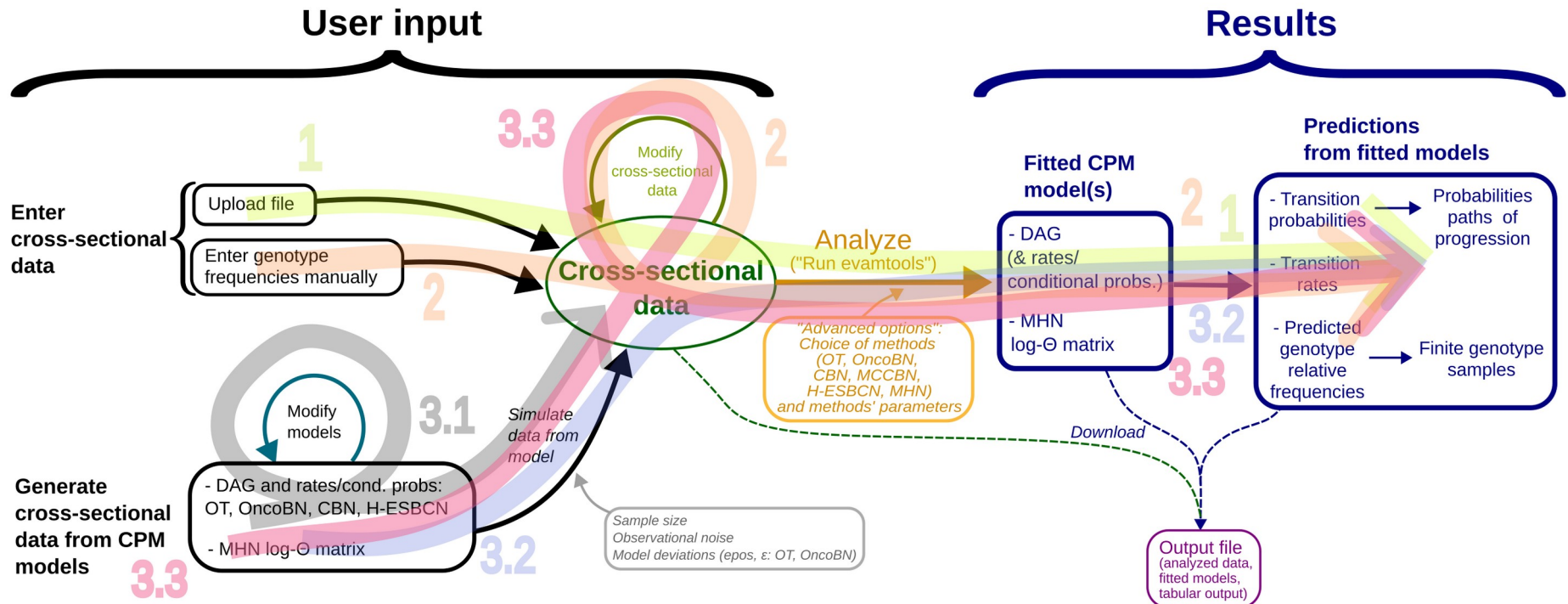
Run evamtools

Advanced options and CPMs to use

Legend:
- Single
- AND
- OR
- XOR

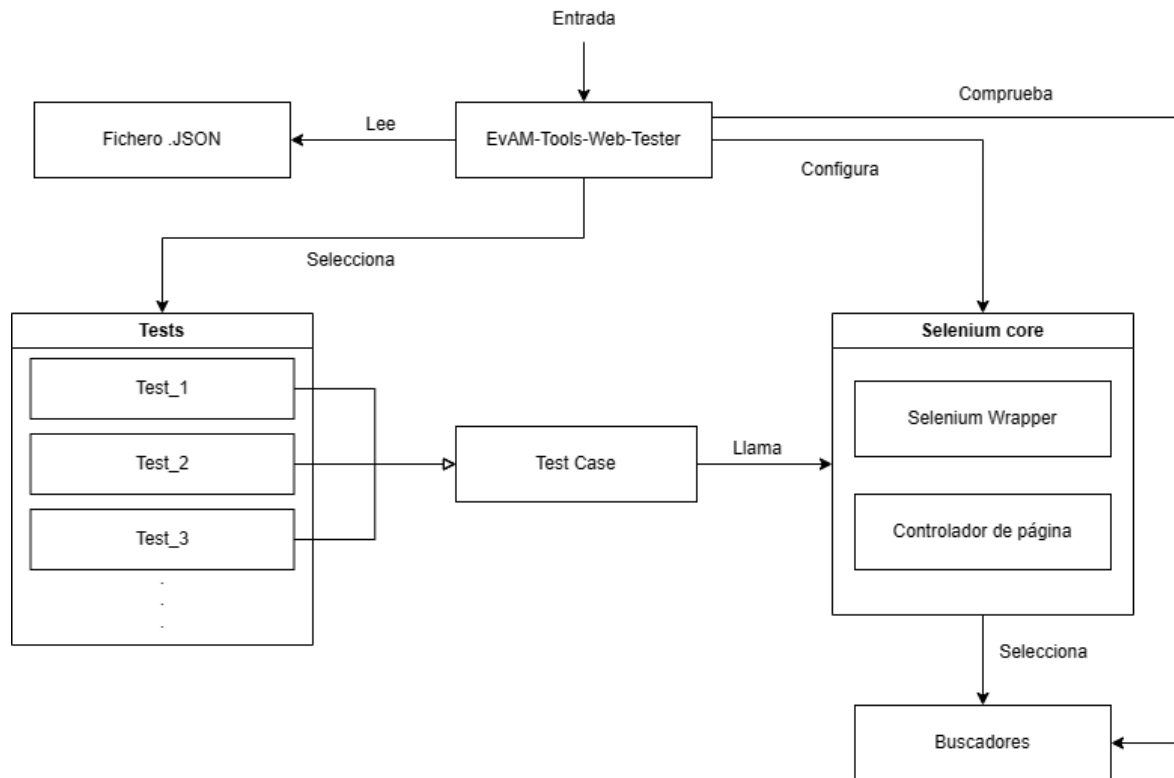


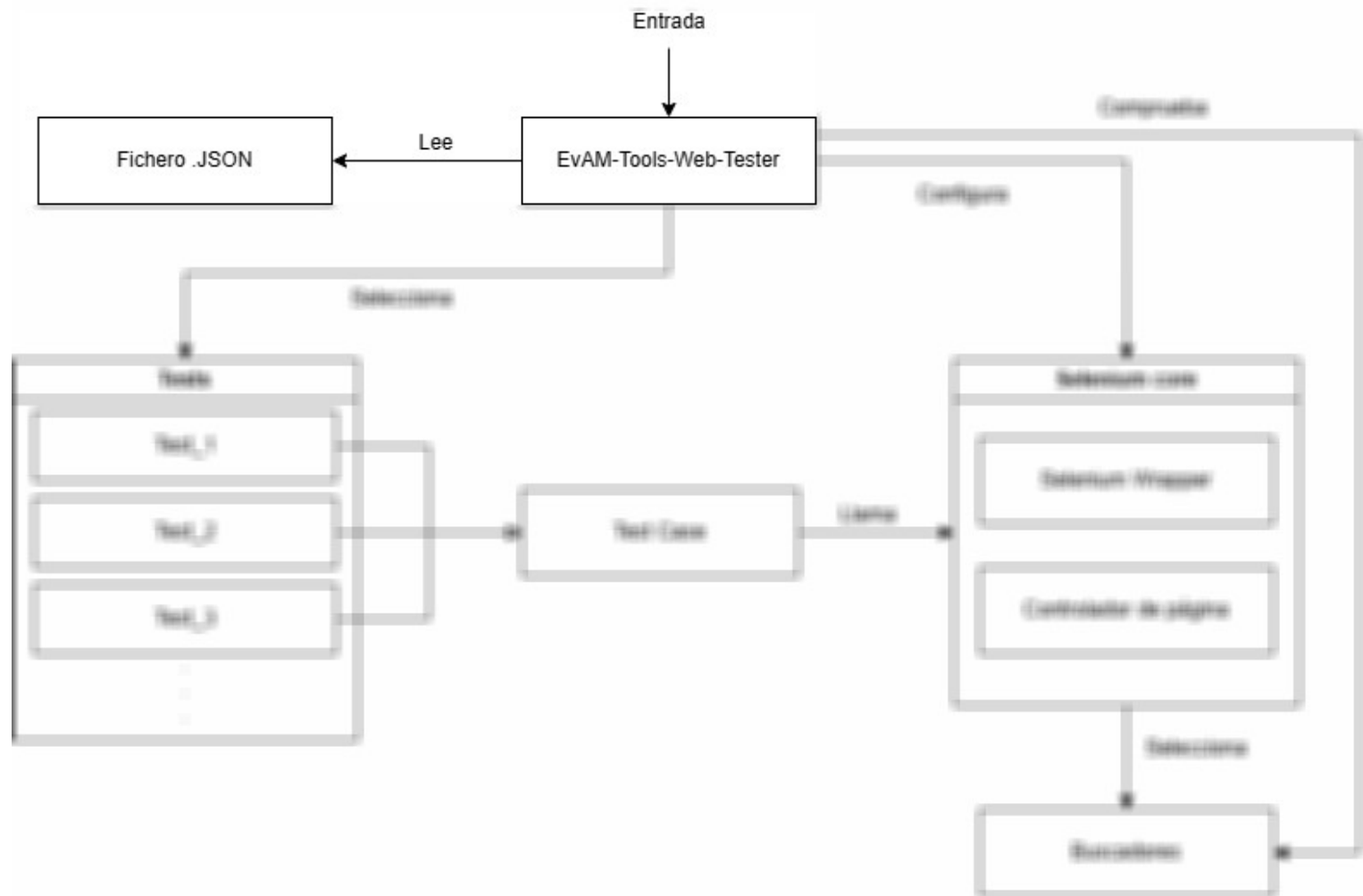
EvAM-Tools



DISEÑO DE LA HERRAMIENTA

Estructura general





Configuración de la herramienta

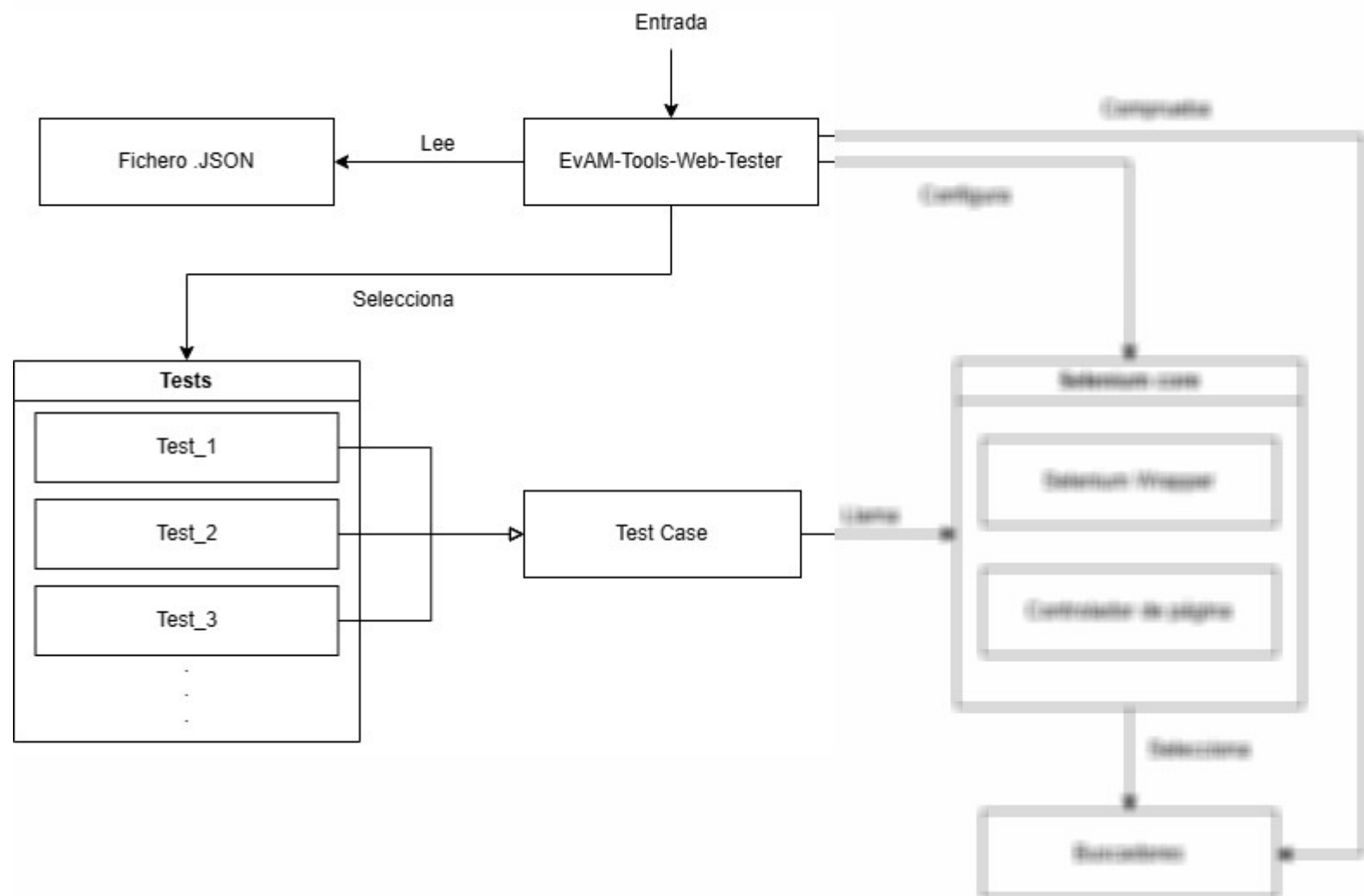
	Prueba 1	Prueba 2	Prueba 3
Grupo 1	✗	✓	✓
Grupo 2	✓	✗	✗
Grupo 3	✗	✓	✗
Grupo 4	✗	✗	✓
Grupo 5	✓	✓	✓

Configuración de la herramienta

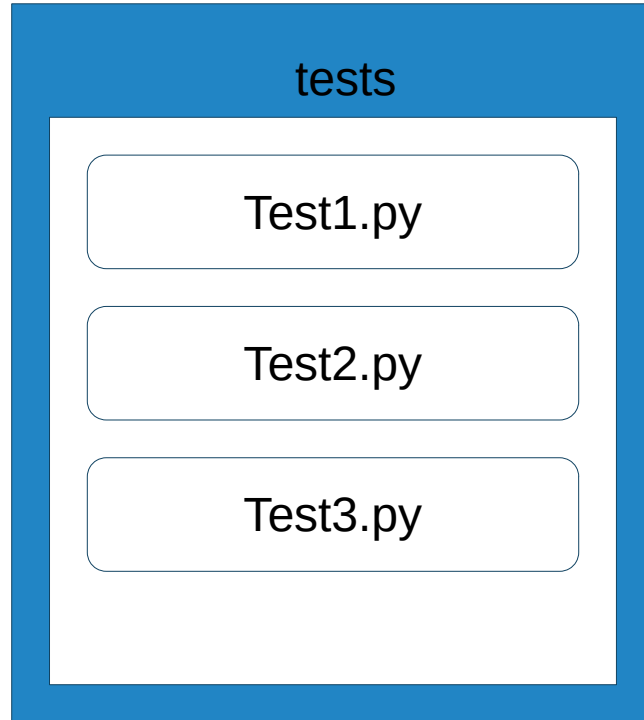
	Prueba 1	Prueba 2	Prueba 3
Grupo 1	✗	✓	✓
Grupo 2	✓	✗	✗
Grupo 3	✗	✓	✗
Grupo 4	✗	✗	✓
Grupo 5	✓	✓	✓



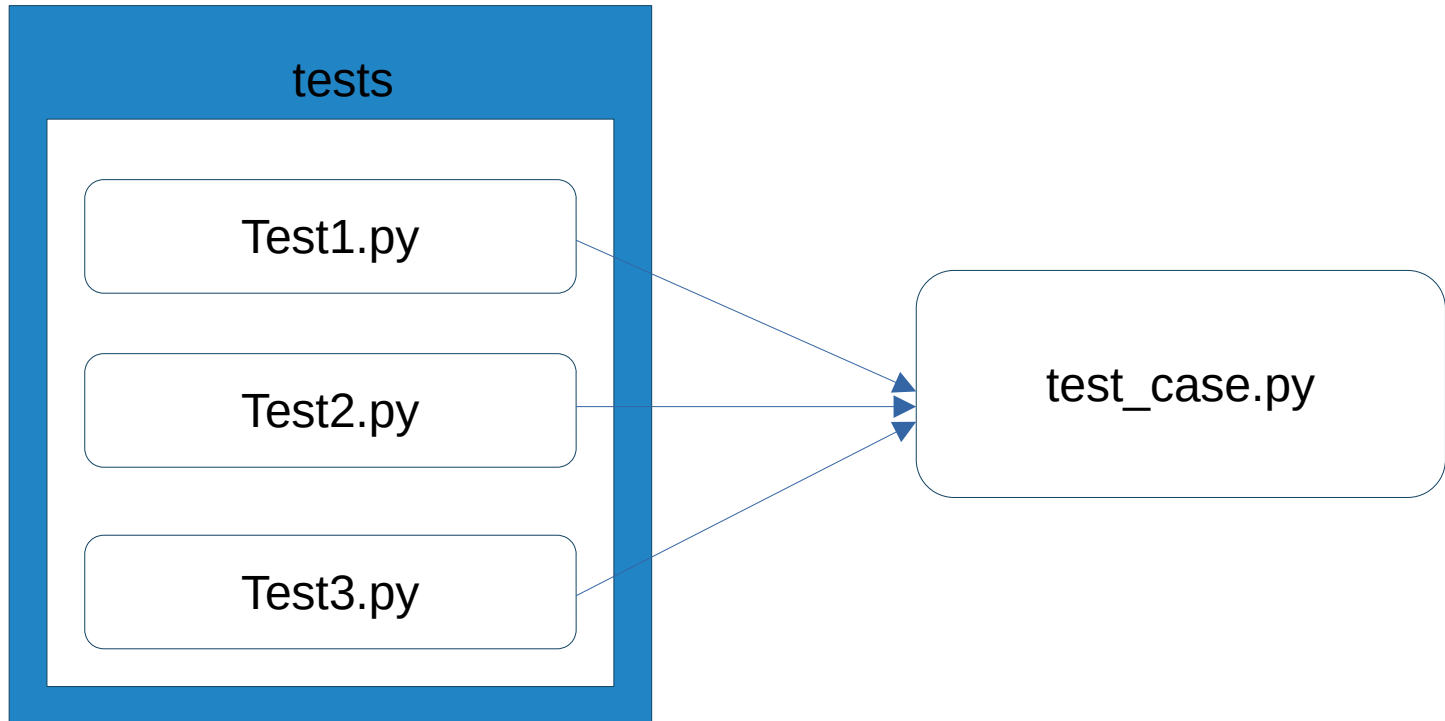
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  ]  
}
```

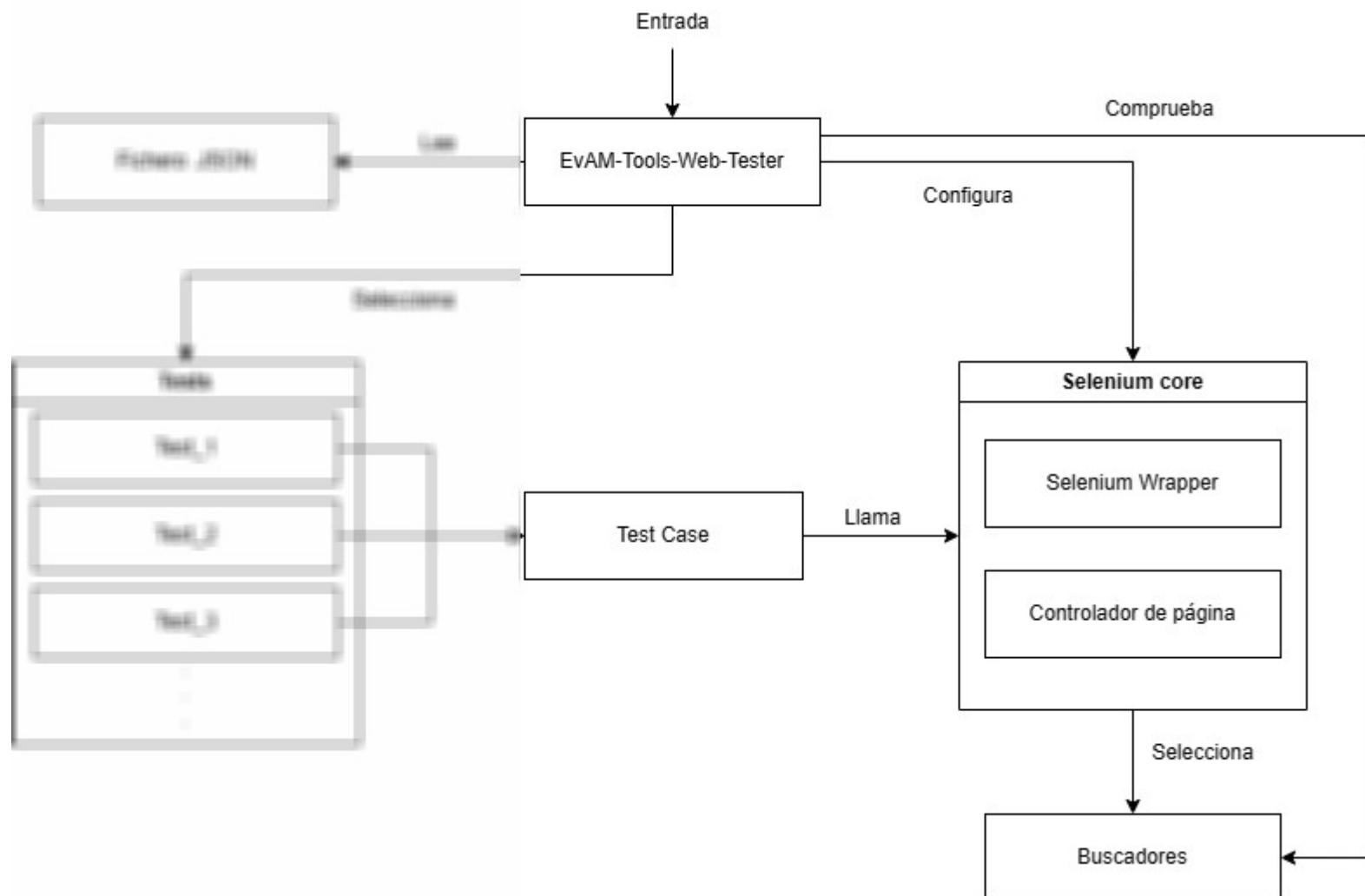


Módulo 'tests'

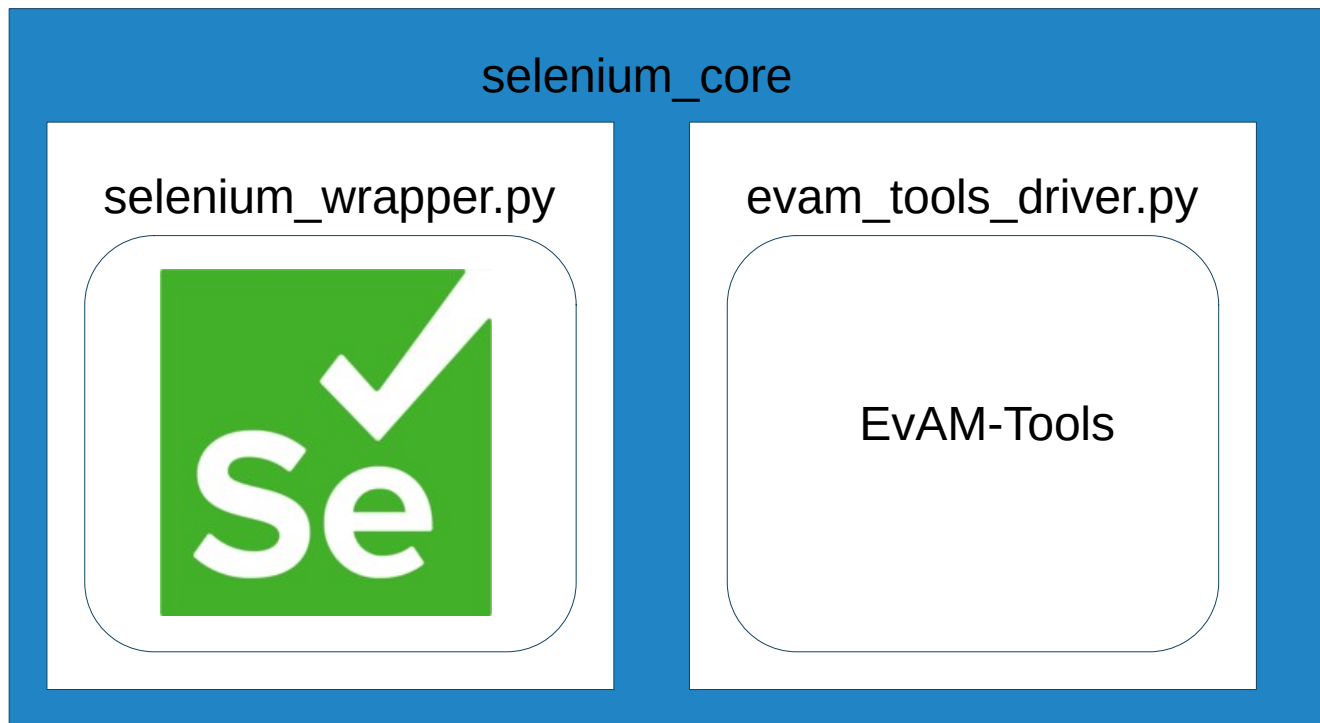


Módulo 'tests'





Módulo 'Selenium core'



1

al
data.
Upload,
create,
generate,
modify:

Enter
cross-sectional
data:

☐ Upload file

☐ Enter
genotype
frequencies
manually

Generate
cross-sectional
data from CPM
models:

☒ DAG and
rates/cond.
probs.

☐ MHN
log- Θ
matrix

Examples and
user's data:

☐ DAG_Fork_3

☒ DAG_Fork_4

☐ DAG_Linear

☐ DAG_AND

2

number of genes (Using 7 or more genes can lead to very long execution times for
s and crowded figures.)

Number of
genes



Define a Directed Acyclic Graph (DAG) and generate data from it.

1. Define DAG

Type of model

Model: ☐ OT ☐ OncoBN ☒ CBN/H-ESBCN

New edge

From (parent node) ☒ Root ☐ A ☐ B ☐ C ☐ D

To (child node) ☒ A ☐ B ☐ C ☐ D

If you want to decrease the number of genes first remove edges and nodes from the DAG and only then modify 'Set the number of genes'. (We cannot know which edges/nodes you want to remove).

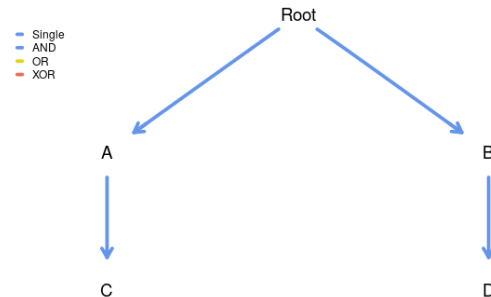
If you want to increase the number of genes use 'Set the number of genes' to increase the available gene labels, and then increase the number of nodes in the DAG.

DAG table

Remember to hit Ctrl-Enter when you are done editing the DAG table for changes to take effect.

From	To	Relation	Lambdas
Root	A	Single	0.5
Root	B	Single	0.7
A	C	Single	0.9

3



1

Upload, create, generate, modify:

Enter cross-sectional data:

☐ Upload file

☐ Enter genotype frequencies manually

Generate cross-sectional data from CPM models:

☒ DAG and rates/cond. probs.

☐ MHN log- Θ matrix

Examples and user's data:

☐ DAG_Fork_3

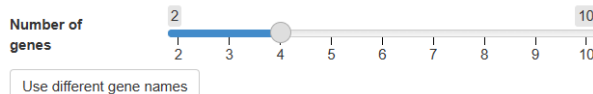
☒ DAG_Fork_4

☐ DAG_Linear

☐ DAG_AND

2

number of genes (Using 7 or more genes can lead to very long execution times for some methods and crowded figures.)



Define a Directed Acyclic Graph (DAG) and generate data from it.

Help

1. Define DAG

Type of model

Model: ☐ OT ☐ OncoBN ☒ CBN/H-ESBCN

New edge

From (parent node) ☒ Root ☐ A ☐ B ☐ C ☐ D

To (child node) ☒ A ☐ B ☐ C ☐ D

Add edge Remove edge

If you want to decrease the number of genes first remove edges and nodes from the DAG and only then modify 'Set the number of genes'. (We cannot know which edges/nodes you want to remove).

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DAG table

Remember to hit Ctrl-Enter when you are done editing the DAG table for changes to take effect.

From	To	Relation	Lambdas
Root	A	Single	0.5
Root	B	Single	0.7
A	C	Single	0.9

3

Run evamtools

Advanced options and CPMs to use

(See additional details for all options in the help of the `evam` and `sample_evam` functions available from the 'Package evamtools' help files in the [Additional documentation](#)).

- ☒ CBN
- ☒ OT
- ☒ OncoBN
- CPMs to use ☒ MHN
- ☐ MCCBN
- ☐ H-ESBCN

Beware: MCCBN may take hours to run. H-ESBCN often takes longer than the remaining methods (except MCCBN) for small numbers of genes (5 or less). For 7 or more genes, CBN can be much slower than OT, OncoBN, or MHN (e.g., data analyzed in < 1 second by those three methods can take 45 with CBN), and also often slower than H-ESBCN.

Return paths to maximum(a) FALSE

(Paths to the maximum/maxima and their probabilities. These are not part of the tabular or graphical output (because of their possibly huge number) but if requested are included in the result object you can download)

Sample genotypes: FALSE

Generate a finite sample of genotypes according to the predicted frequencies of the model.

Number of samples 10000

Number of genotypes to generate when generating a finite sample of genotypes according to the predicted frequencies of from model.

Observation noise 0

If > 0, the proportion of observations in the sampled matrix with error (for instance, genotyping error). This proportion of observations will have 0s flipped to 1s, and 1s flipped to 0s.

Generate
cross-sectional data from
CPM models:

☒ DAG and
rates/cond.
probs.

☐ MHN
log- Θ
matrix

Examples and user's
data:

☐ DAG Fork 3

```
<div class="radio">
  <label>
    <input type="radio" name="input2build" checked="checked">
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      "DAG and"
      <br>
      "rates/cond."
      <br>
      " probs."
    </span>
  </label>
</div>
```

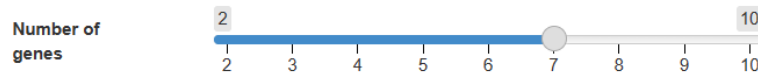
```
<div class="radio">
  <label>
    <input type="radio" name="input2build">
    <span>
      "MHN "
      <br>
      "log- $\Theta$ "
      <br>
      " matrix"
    </span>
  </label>
</div>
```

Set the number of genes (Using 7 or more genes can lead to very long execution times for some methods and crowded figures.)



Use different gene names

Set the number of genes (Using 7 or more genes can lead to very long execution times for some methods and crowded figures.)



Use different gene names

Define MHN's log-Theta matrix ($\log-\Theta$) and generate data from it.

Help

1. Define MHN's θ s

Entries are lower case thetas, θ s, range $\pm \infty$

Remember to hit Ctrl-Enter when you are done editing the matrix for changes to take effect.

	A	B	C	D
A	0	0	0	0
B	0	0	0	0
C	0	0	0	0
D	0	0	0	0

Define MHN's log-Theta matrix ($\log-\Theta$) and generate data from it.

Help

1. Define MHN's θ s

Entries are lower case thetas, θ s, range $\pm \infty$

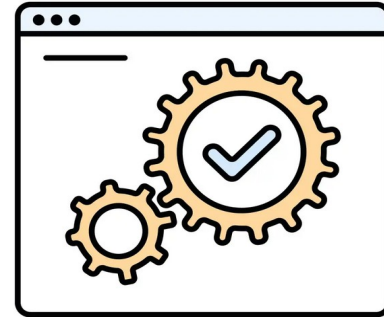
Remember to hit Ctrl-Enter when you are done editing the matrix for changes to take effect.

	A	B	C	D	E	F	G
A	0	0	0	0	0	0	0
B	0	0	0	0	0	0	0
C	0	0	0	0	0	0	0
D	0	0	0	0	0	0	0
E	0	0	0	0	0	0	0
F	0	0	0	0	0	0	0
G	0	0	0	0	0	0	0

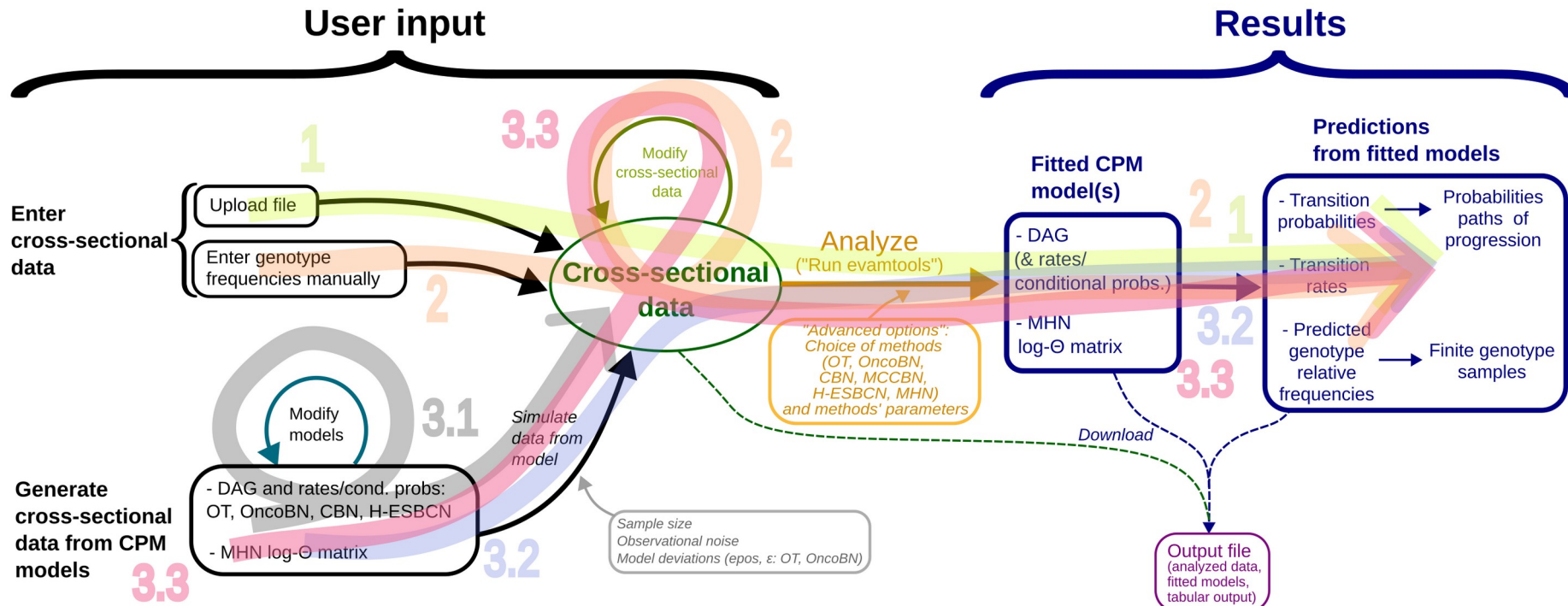
PRUEBAS

Pruebas realizadas sobre la herramienta

- ▷ Pruebas de rendimiento.
- ▷ Pruebas de sus componentes.
- ▷ Pruebas de integración.
- ▷ Pruebas de sistema.
- ▷ Pruebas de validación.



EvAM-Tools



CONCLUSIONES

Conclusiones

- ▷ Casos de prueba completados.
- ▷ Ejecuciones automaticas.
- ▷ Ejecuciones desatendidas.
- ▷ Fácil expansión y mantenimiento.

TRABAJO FUTURO



Propuestas

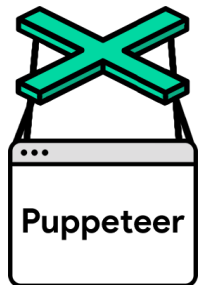
- ▷ Expansión a nuevos buscadores.
- ▷ Expansión de los informes de ejecución.
- ▷ Dockerización.
- ▷ Soporte para diferentes OS.

Muchas gracias

Turno de preguntas

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Escuela Politécnica Superior

Tecnologías actuales



- ▷ Desarrollados por Google y Microsoft.
- ▷ Simples y orientados a pruebas de rendimiento



- ▷ Pruebas en JavaScript



- ▷ Para AngularJS y Angular



- ▷ Orientado a móviles

Lenguajes disponibles con selenium

- ▷ C#
- ▷ Java
- ▷ JavaScript
- ▷ Ruby
- ▷ Python
- ▷ PHP