

Meeting 2

Vendredi 24 Octobre 2025

Model 0D (C++) used for Sobol analysis

The (20) parameters that can be sampled are:

```
params = ["Cm", "gNa", "gNaCa", "gS", "eNa", "S", "gi", "ge", "cEts", "cTs", "rPulse", "rGnd", "rWTip", "rWRing", "rBlock", "rCharge", "rTip", "rRing", "cTip", "cRing"]
```

To note:

ionic components for Beeler-Reuter (BR77) model are fixed in literature: $gNa = 0.04$ and $gNaCa = 3e-5$

Stimulation controlled parameters:

```
# 0D model controlled parameters.
start_time: 0.0 # in ms
end_time: 2500 # in ms
stimulation:
  start: 100 # in ms
  duration: 1 # in ms
  amplitude: 2500 # in mV
  period: 600 # in ms

# Numerical parameters
time_steps: # in ms
  wait: 0.01
  pulse: 0.001
  switch: 0.001
  ocd: 0.01
```

Model 0D (C++) results (n_samples=1024)

Configuration

n_samples : 1024
num_vars: 3

names: ["S", "gi", "ge"]

bounds:

- [0.5, 500.0]
- [0.00015, 2500.0]
- [0.00015, 2500.0]

log_sampling: [True, True, True]

0D model controlled parameters.

start_time: 0.0 # in ms

end_time: 2500 # in ms

stimulation:

start: 100 # in ms

duration: 1 # in ms

amplitude: 2500 # in mV

period: 600 # in ms

Numerical parameters

time_steps: # in ms

wait: 0.01

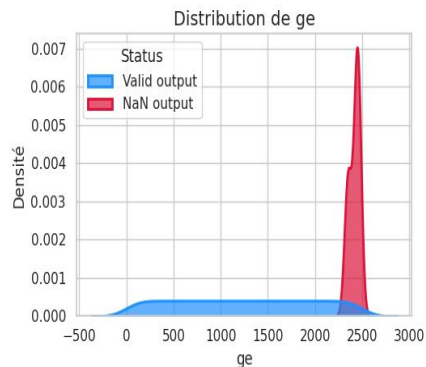
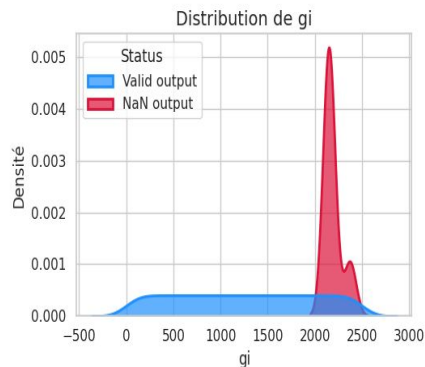
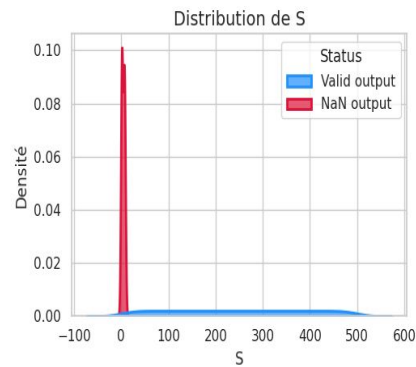
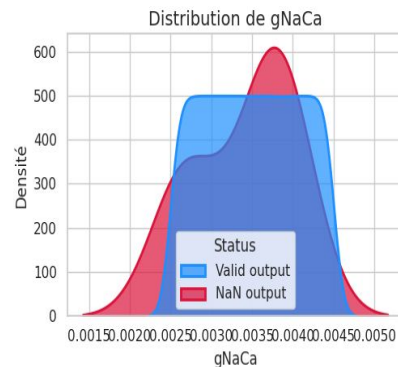
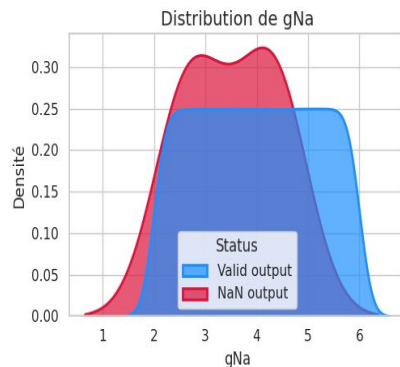
pulse: 0.001

switch: 0.001

ocd: 0.01



Comparaison des distributions — Valeurs valides vs NaN

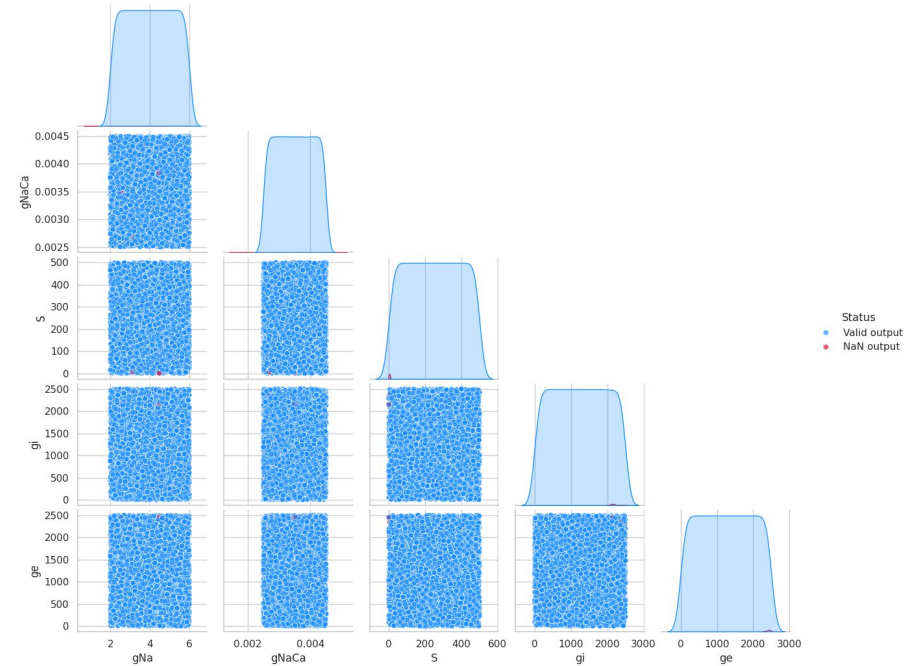
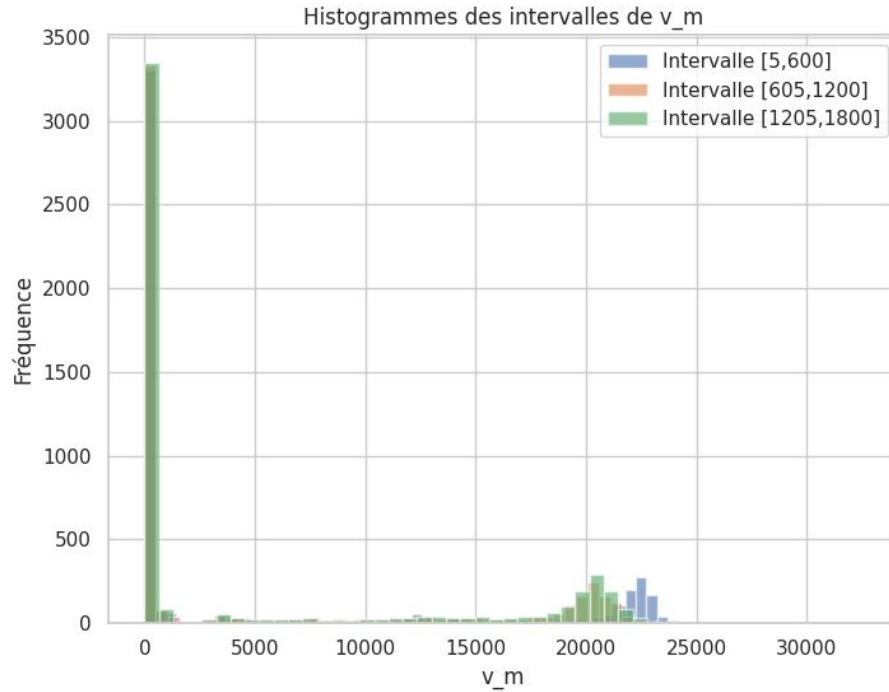


On a des **NaNs** dans 2 cas (pour 5120 au total) :

S, gi, ge = 5.247665, 2479.783211, 2361.869812

S, gi, ge = 2.154008, 2213.327136, 2286.392474

Histos des trois outputs v_m



Reduction of maximal value for gi and ge to 2000

Configuration

n_samples : 1024
num_vars: 3

names: ["S", "gi", "ge"]

bounds:

- [0.5, 500.0]

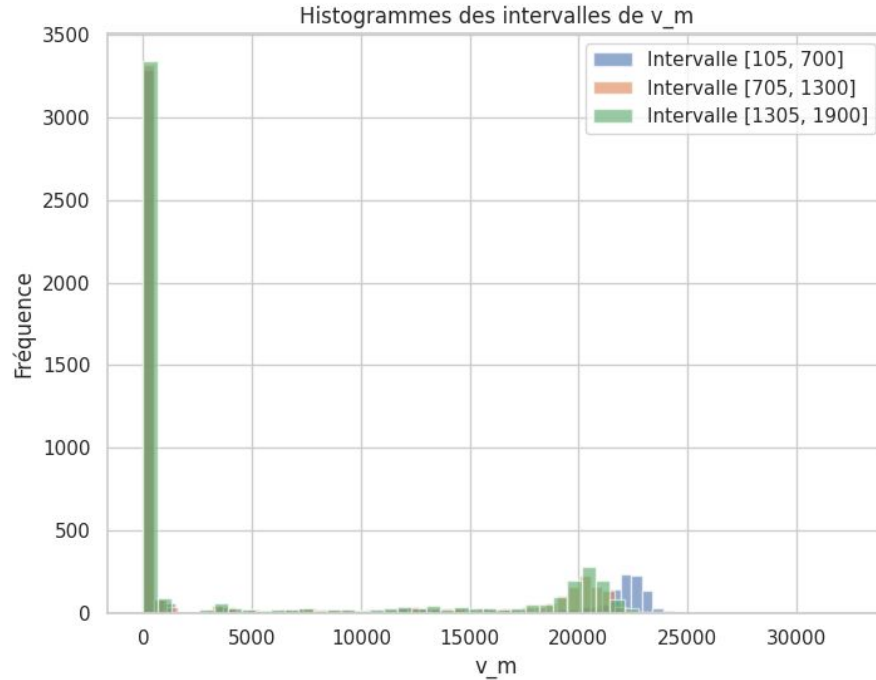
- [0.00015, 2000.0]

- [0.00015, 2000.0]



On n'a pas des **Nans**

log_sampling: [True, True, True]



Test 0D (random values for 7 variables in FIMH 2025)

```
names: [ "S", "gi", "ge", "rRing", "cRing", "rTip", "cTip"]
```

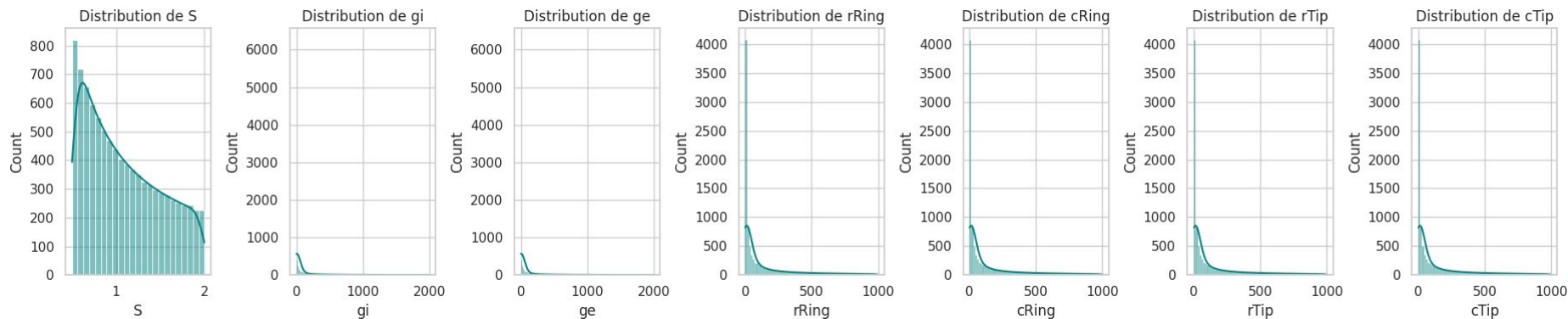
```
bounds:
```

- [0.5, 2.0]
- [0.00015, 2000.0]
- [0.00015, 2000.0]
- [0.5, 1000.0]
- [0.5, 1000.0]
- [0.5, 1000.0]
- [0.5, 1000.0]

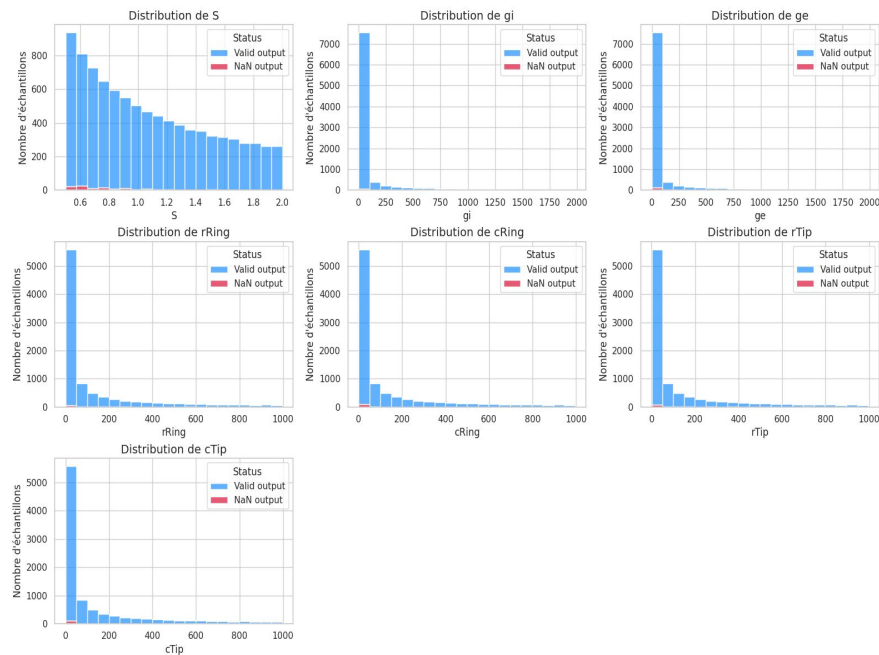
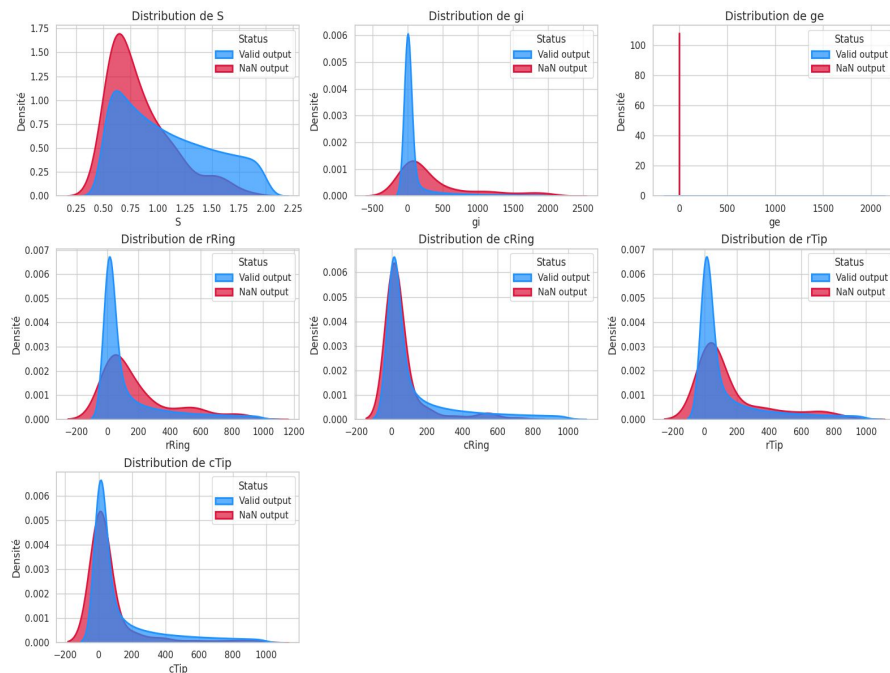


On a des **Nans** dans 141 cas (pour 9216 au total) :

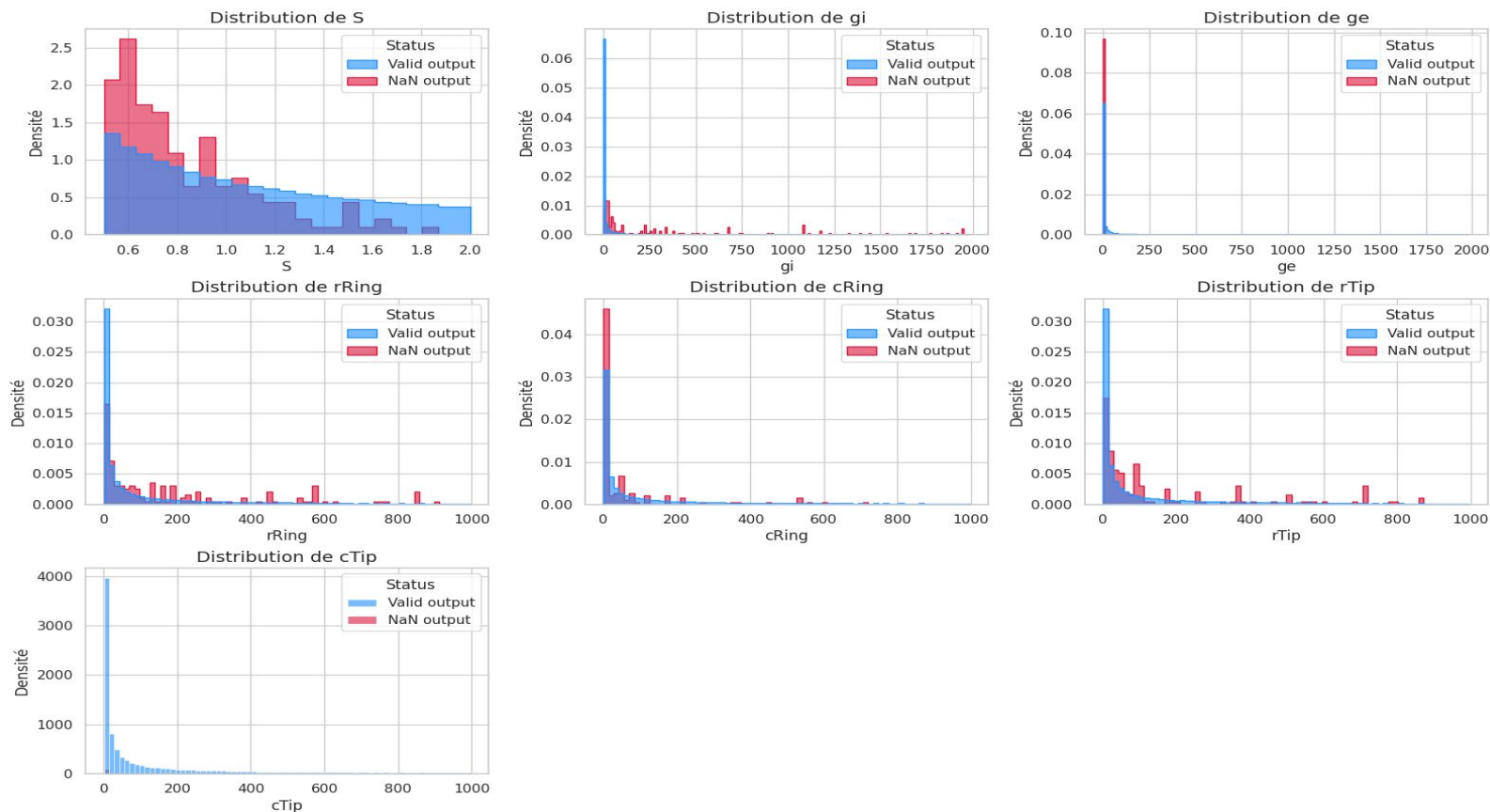
```
log_sampling: [ True,True,True, True,True,True, True ]
```



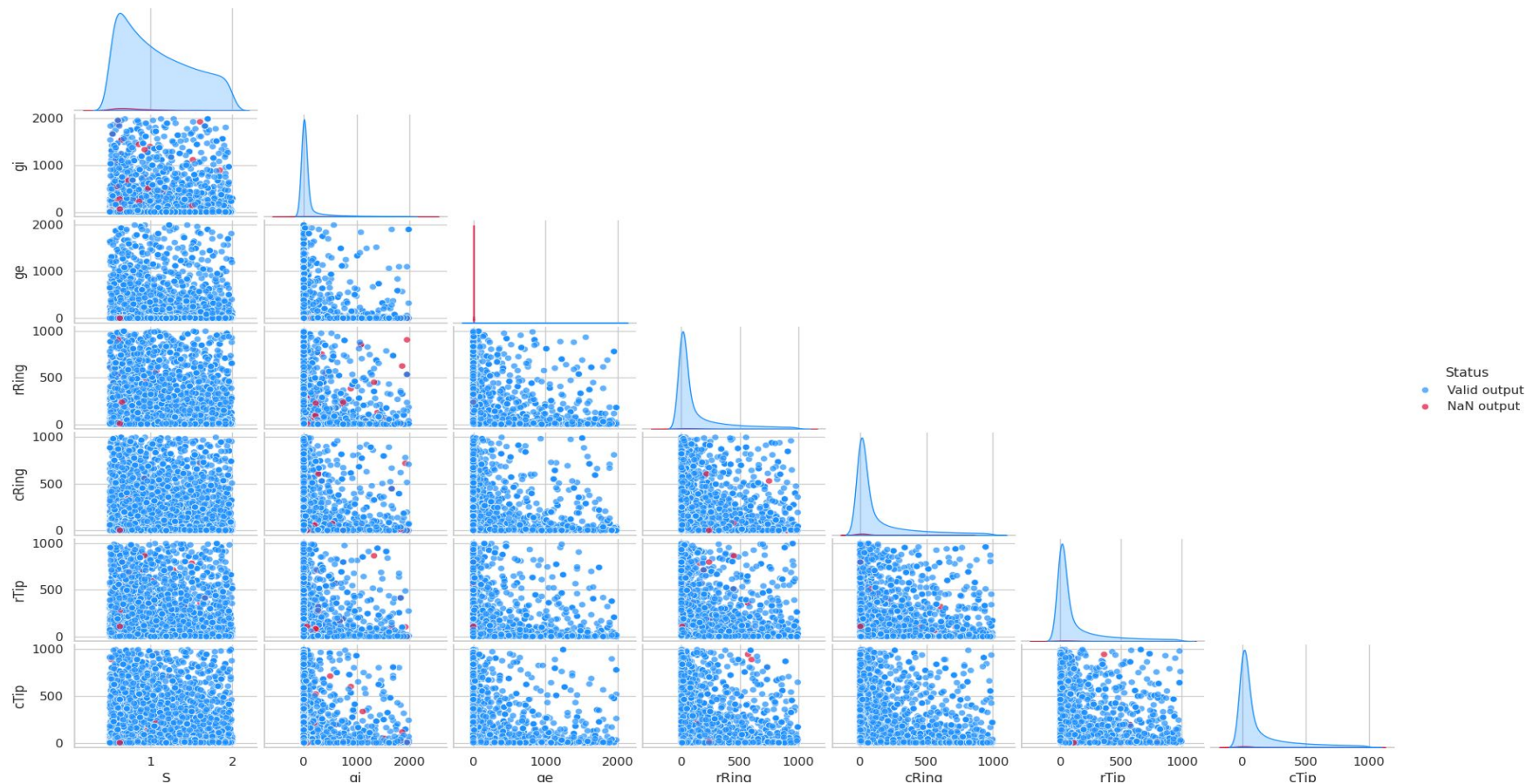
Test 0D (random values for 7 variables in FIMH 2025)



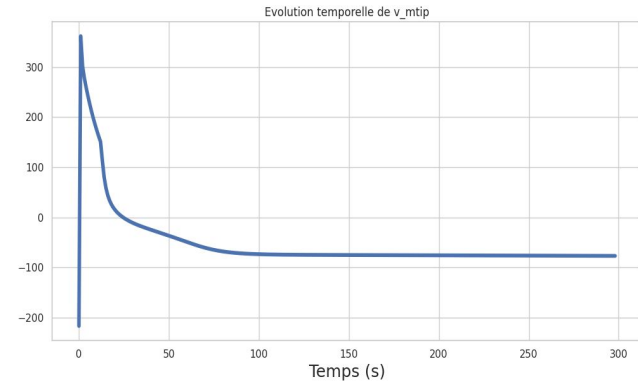
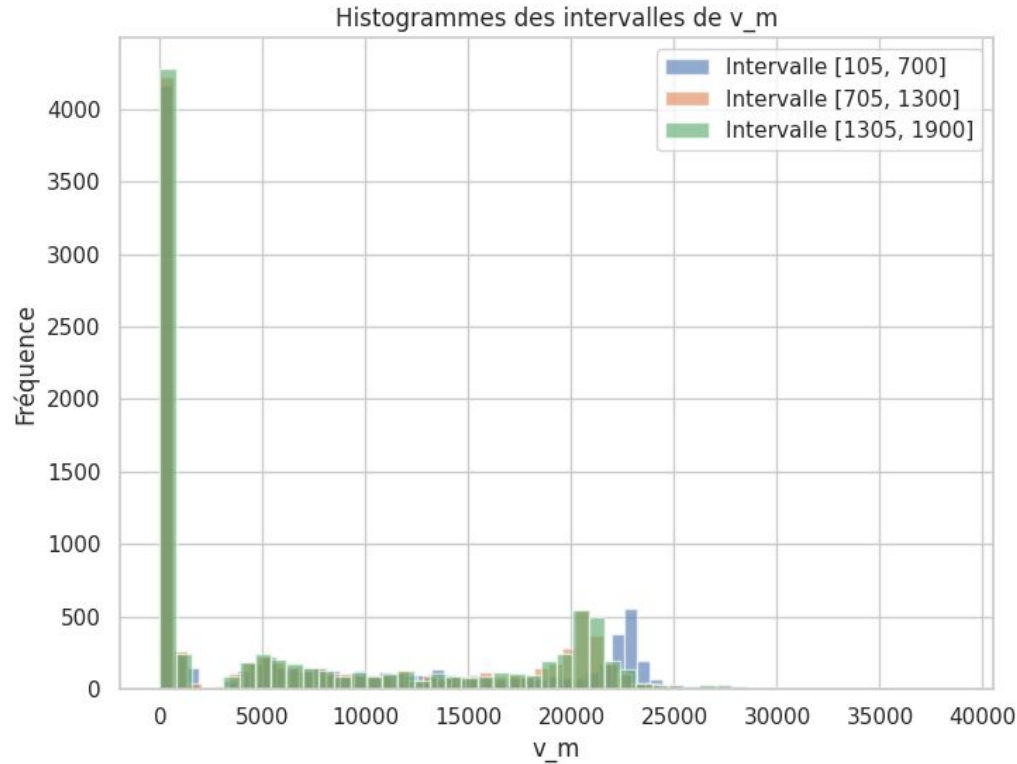
Test 0D (random values for 7 variables in FIMH 2025)



Test 0D (random values for 7 variables in FIMH 2025)

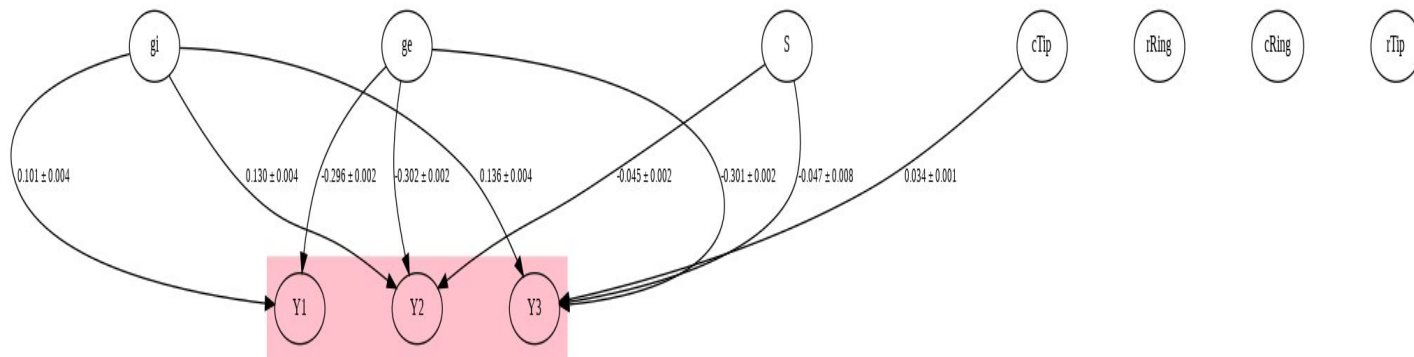


Test 0D (random values for 7 variables in FIMH 2025)

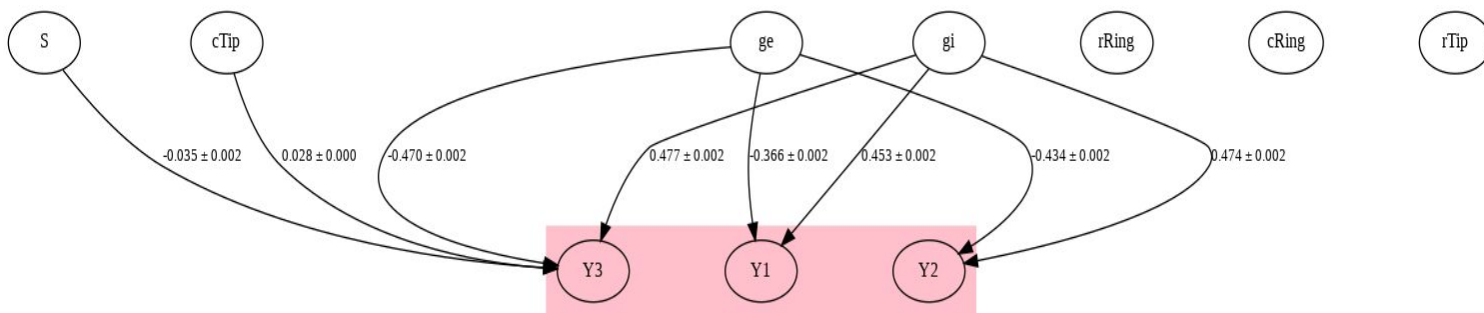


Test 0D (random values for 7 variables in FIMH 2025)

Standard
scaling



Log
scaling



Data modèle

ceps_data is extracted from `sim_data["ceps_results"]`

```
{'durations': [0.25, 0.5, 0.75, 1.0, 1.25, 1.5, 2.0], 'thresholds': [1.8, 1.2, 0.8, 0.7, 0.7, 0.6, 0.3],  
'frequency': 90, 'out': 0.5, 'Am': 2500, 'linear_solver_absolute_tolerance': 1e-12,  
'linear_solver_relative_tolerance': 1e-12, 'pde_time_step': 0.01, 'mesh_refine': 1.0, 'device':  
'PSA'}
```

circe_data is extracted from `sim_data["circe_results"]`

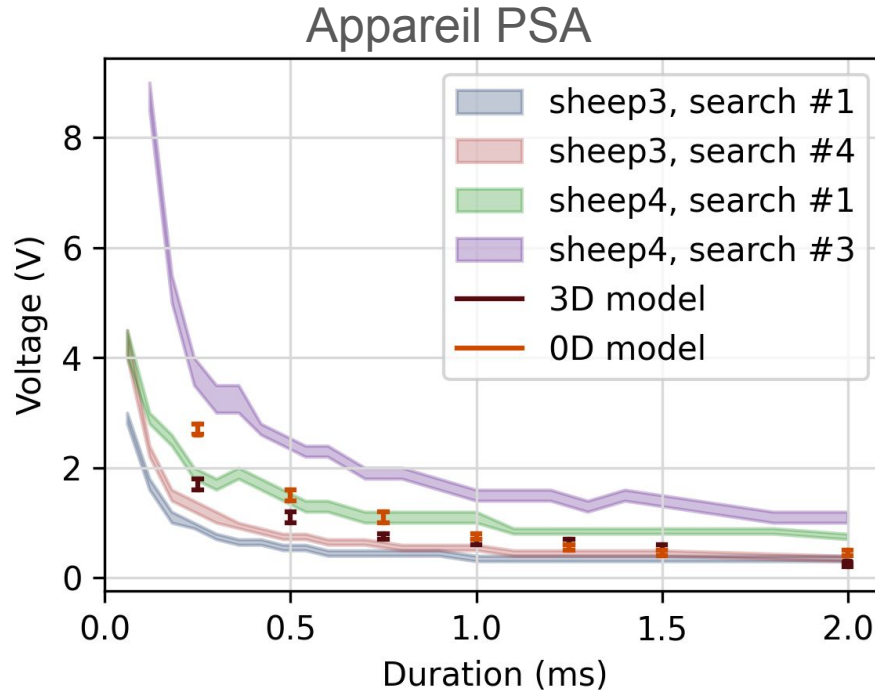
```
{'durations': [0.25, 0.5, 0.75, 1.0, 1.25, 1.5, 2.0, 5.0, 6.0, 7.0, 8.0, 10.0], 'thresholds': [2.8, 1.6,  
1.2, 0.8, 0.6, 0.5, 0.5, 0.3, 0.3, 0.3, 0.3, 0.3], 'frequency': 90, 'se': 15.0, 'device': 'PSA'}
```

Data expérimentale

exp_data is extracted from `exp_data = json.load(open("./data_experiments.json", 'r'))`

```
{'sheep1': {'date': '7 june 2022', 'comments': 'pilote', 'searches': [{'comments': 'Borea', 'order': 'D', 'n spikes': 5, 'bpm': 90, 'site': 'RV ENDO APEX', 'tissue': 'healthy', 'bath': 14.3, 'impedance': 361, 'durations': [0.12, 0.25, 0.35, 1.0], 'thresholds': [0.75, 0.5, 0.5, 0.0]}]}, 'sheep2': {'date': '8 november 2022', 'comments': '', 'searches': [{'comments': 'Borea', 'order': 'D', 'n spikes': 3, 'bpm': 90, 'site': 'RV ENDO APEX', 'tissue': 'healthy', 'bath': 14.3, 'impedance': 338, 'durations': [0.12, 0.25, 0.35, 0.5, 0.6, 0.75, 0.85, 1.0, 1.5, 2.0], 'thresholds': [1, 0.75, 0.75, 0.5, 0.5, 0.5, 0.5, 0.25, 0.25, 0.25]}, {'comments': 'Borea', 'order': 'D', 'n spikes': 5, 'bpm': 90, 'site': 'RV ENDO SEPTUM', 'tissue': 'healthy', 'bath': 14.3, 'impedance': 546, 'durations': [0.12, 0.25, 0.35, 0.5, 0.6, 0.75, 0.85, 1.0, 1.5, 2.0], 'thresholds': [0.75, 0.5, 0.5, 0.25, 0.25, 0.25, 0.25, 0.25, 0.25, 0.25]}, {'comments': 'Borea', 'order': 'D', 'n spikes': 5, 'bpm': 90, 'site': 'RV ENDO BASE (RVOT)', 'tissue': 'healthy', 'bath': 14.3, 'impedance': 342, 'durations': [0.12, 0.25, 0.35, 0.5, 0.75, 0.85, 1.0], 'thresholds': [1.5, 1.0, 0.75, 0.75, 0.75, 0.5, 0.5]}]}, 'sheep3': {'date': '18 october 2023', 'comments': '', 'searches': [{'comments': 'PSA', 'order': 'A', 'n spikes': 8, 'bpm': 90, 'site': 'RV ENDO APEX', 'tissue': 'healthy', 'bath': 16.9, 'impedance': 259, 'durations': [0.06, 0.12, 0.18, 0.24, 0.3, 0.36, 0.42, 0.48, 0.54, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.5, 2.0], 'thresholds': [3.0, 1.8, 1.2, 1.0, 0.8, 0.7, 0.7, 0.6, 0.6, 0.5, 0.5, 0.5, 0.5, 0.4, 0.4, 0.4, 0.4]}, {'comments': 'PSA', 'order': 'D', 'n spikes': 8, 'bpm': 90, 'site': 'RV ENDO APEX', 'tissue': 'healthy', 'bath': 16.9, 'impedance': 259, 'durations': [0.06, 0.12, 0.18, 0.24, 0.3, 0.36, 0.42, 0.48, 0.54, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.5, 2.0], 'thresholds': [3.0, 1.8, 1.2, 1.0, 0.8, 0.7, 0.7, 0.6, 0.6, 0.6, 0.5, 0.5, 0.5, 0.5, 0.5, 0.4]}, {'comments': 'Borea', 'order': 'D', 'n spikes': 5, 'bpm': 90, 'site': 'RV ENDO SEPTUM', 'tissue': 'healthy', 'bath': 16.9, 'impedance': 473, 'durations': [0.12, 0.25, 0.35, 0.5, 0.6, 0.75, 0.85, 1.0], 'thresholds': [1.5, 1.0, 0.75, 0.5, 0.5, 0.5, 0.5, 0.5]}, {'comments': 'PSA', 'order': 'D', 'n spikes': 8, 'bpm': 120, 'site': 'RV ENDO SEPTUM', 'tissue': 'healthy', 'bath': 16.9, 'impedance': 497, 'durations': [0.06, 0.12, 0.18, 0.24, 0.3, 0.36, 0.42, 0.48, 0.54, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.5, 2.0], 'thresholds': [4.5, 2.4, 1.6, 1.4, 1.2, 1.0, 0.9, 0.8, 0.8, 0.7, 0.7, 0.6, 0.6, 0.6, 0.5, 0.5, 0.4]}]}, ...}
```

Exemple courbe Lapicque (expériences vs modèles)



Code `plotSimVsExpLapicque.py`