

# A Graph-Based, In-Memory Workflow Library for Brain/MINDS 2.0

NEST Conference 2025

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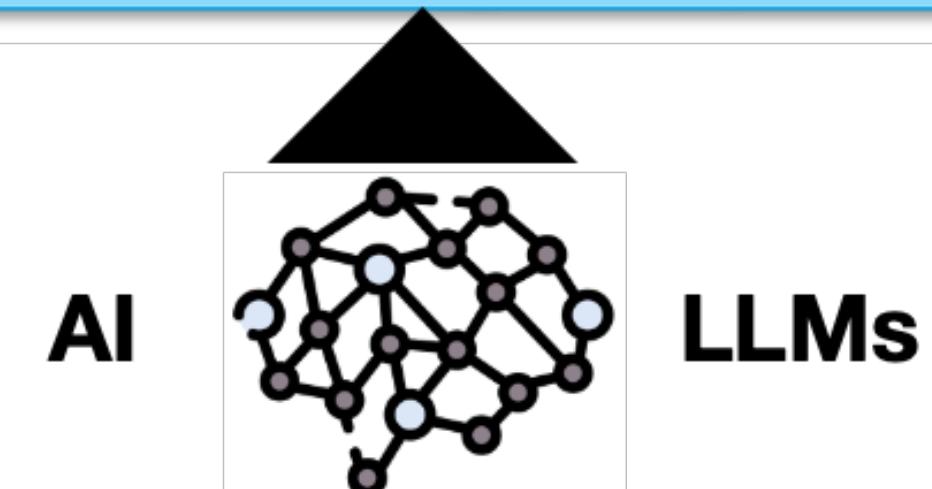
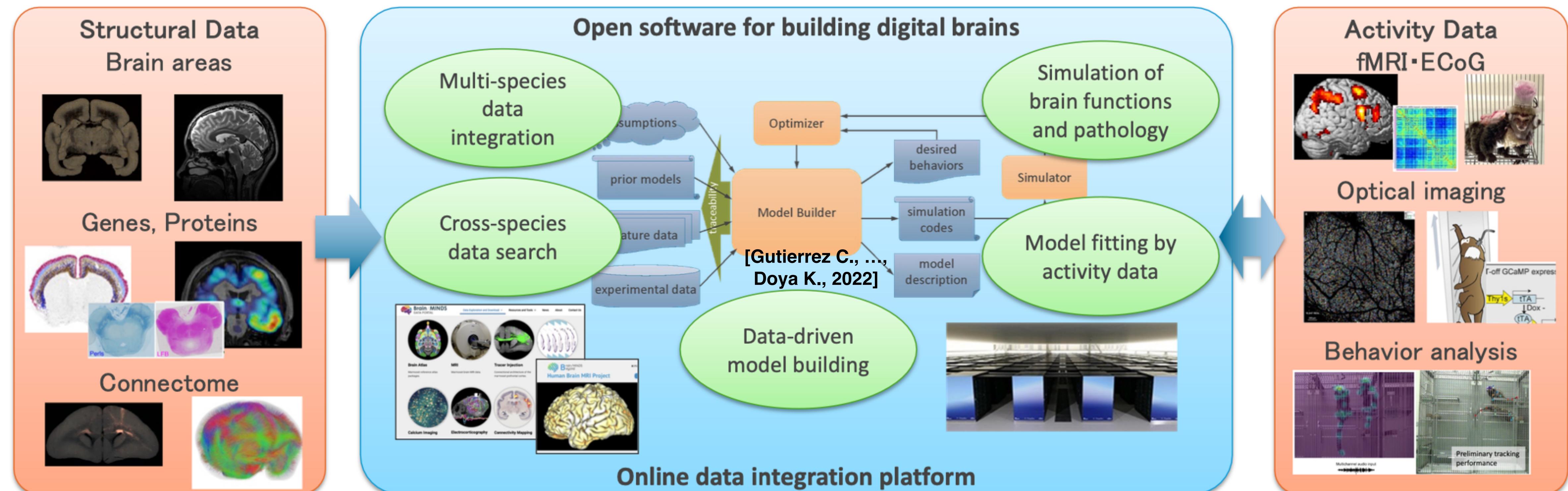
(1) Okinawa Institute of Science and Technology Graduate University

(2) RIKEN CBS



# Brain/MINDS 2.0 - The Digital Brain Project

**Goal:** open software for building digital brains  
-online platform for data integration, model building and simulations-

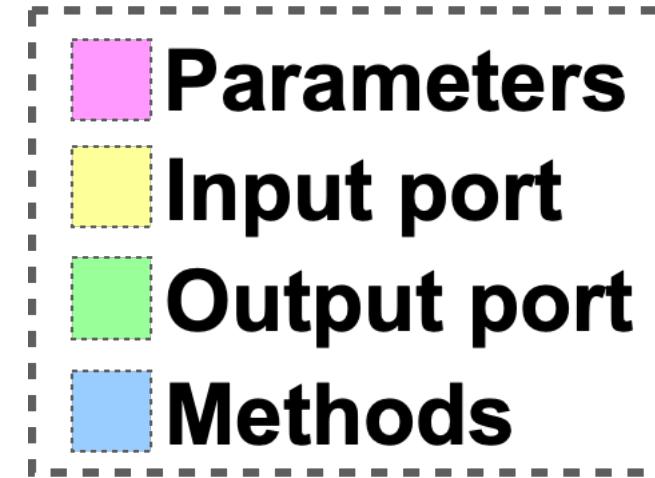


# The Digital Brain as a graph-based framework

- The BM2 aims to create a framework that supports **interoperability with open data and popular neuroscience tools** by leveraging their Python interfaces.
- Modern brain modeling and simulation require complex sequences of data processing, model configuration, and analysis steps. While **powerful tools** exist, they frequently **demand advanced programming knowledge, limiting accessibility and collaboration potential**. **Shared models are frequently difficult to understand, execute and expand.**
- We present a python-based graph framework that **transforms brain modeling steps into modular, interpretable, reusable components through a node-edge architecture**.

# Neuro-WorkFlow

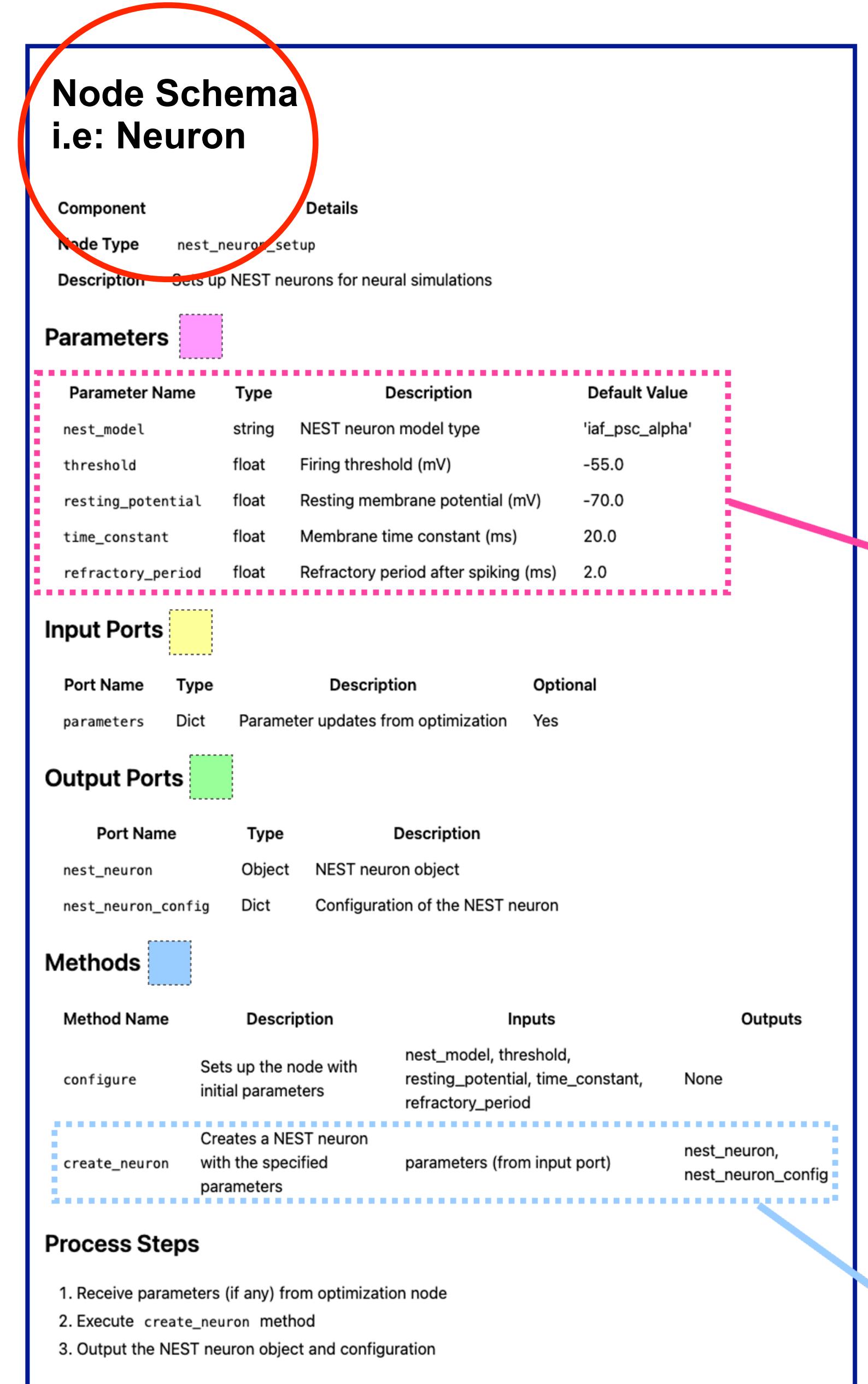
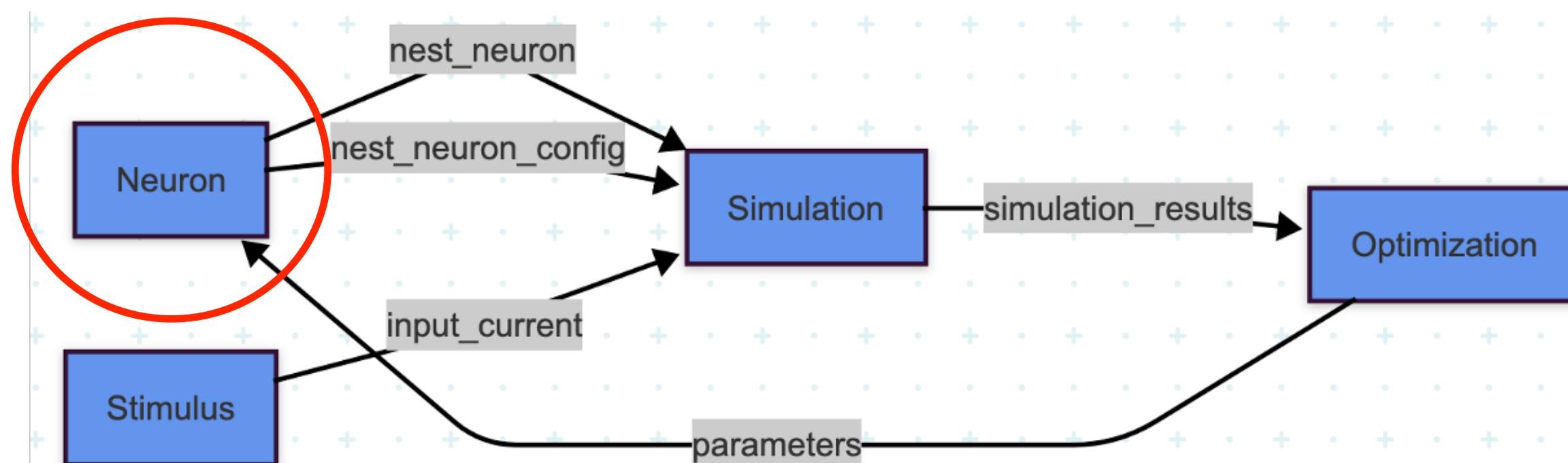
## ► A NODE defines



## ► NODES are connected by PORTS

## ► A NODE is a python class with a defined schema (structure)

## ► Example of a neuro-workflow with 4 NODES



## In Python a Node is defined as a Class:

```
class NESTNeuronSetupNode(Node):
    """Node for creating and configuring neuron models.
    This class represents a neuron model with configurable parameters.
    In a real implementation, this could be a more complex model or
    interface with external neural simulators."""

NODE_DEFINITION = NodeDefinitionSchema(
    type='neuron_setup',
    description='Creates and configures a neuron model in NEST',
    parameters={
        'nest_model': ParameterDefinition(
            default_value='iaf_psc_alpha',
            description='neuron model name in NEST'
        ),
        'threshold': ParameterDefinition(
            default_value=-55.0,
            description='Firing threshold (mV)',
            constraints={'min': -70.0, 'max': -40.0},
            optimizable=True,
            optimization_range=[-65.0, -45.0]
        ),
        'resting_potential': ParameterDefinition(
            default_value=-70.0,
            description='Resting membrane potential (mV)',
            constraints={'min': -80.0, 'max': -60.0},
        ),
        'time_constant': ParameterDefinition(
            default_value=20.0,
            description='Membrane time constant (ms)',
            constraints={'min': 5.0, 'max': 50.0},
            optimizable=True,
            optimization_range=[10.0, 30.0]
        ),
        'refractory_period': ParameterDefinition(
            default_value=2.0,
            description='Refractory period (ms)',
            constraints={'min': 1.0, 'max': 5.0}
        )
    },
    inputs={
        'parameters': PortDefinition(
            type=PortType.DICT,
            description='Parameters to configure the neuron',
        )
    }
)

def create_neuron(self, parameters: Optional[Dict[str, Any]] = None) ->
    """Create and configure a neuron model.

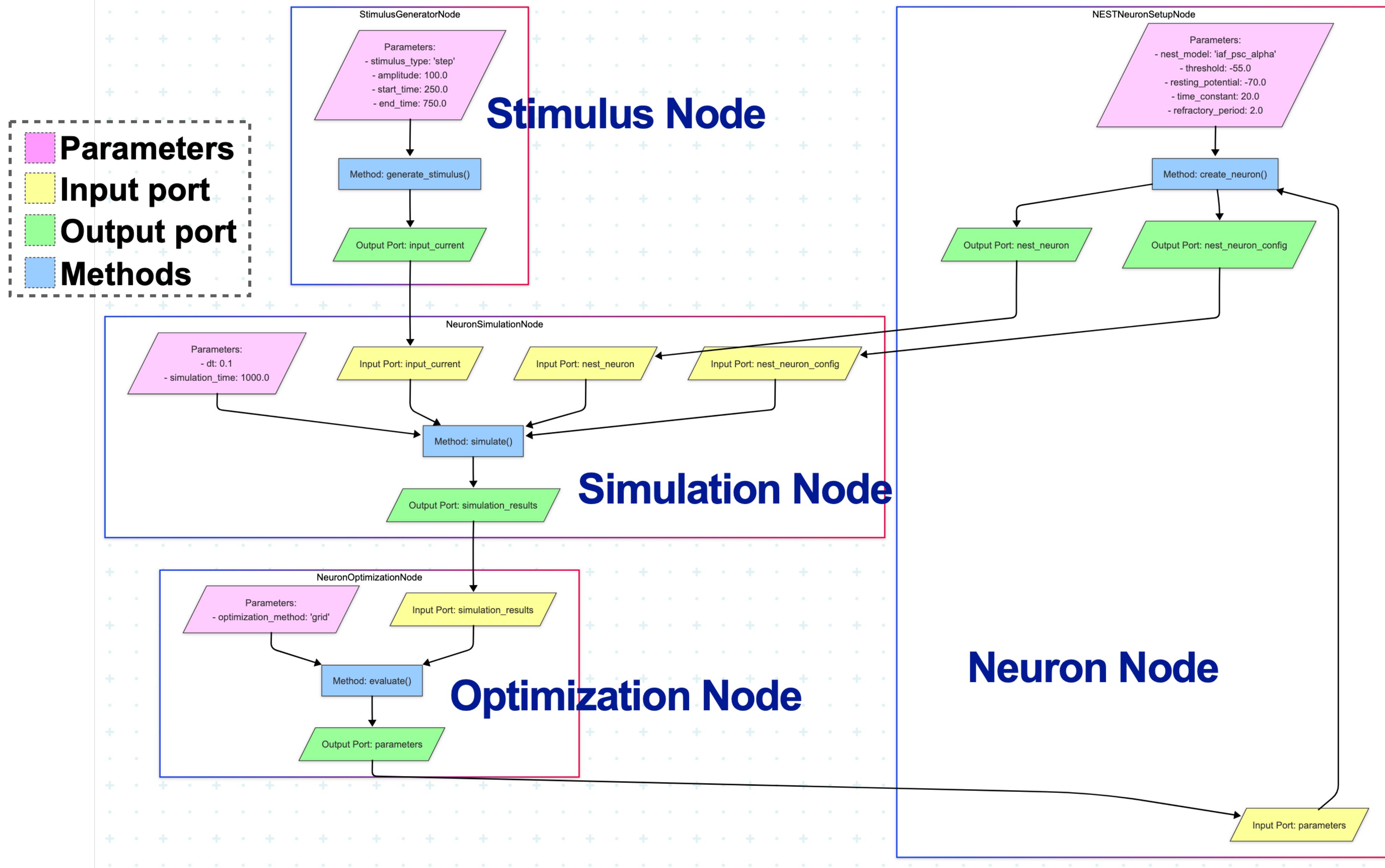
    Args:
        parameters: Optional parameters to override defaults

    Returns:
        Dictionary with neuron model and configuration
    """
    # If parameters are provided, configure the node
    if parameters:
        self.configure(**parameters)

    # Create nest neuron object
    neuro_params = {
        "V_th": self._parameters['threshold'],
        "E_L": self._parameters['resting_potential'],
        "tau_m": self._parameters['time_constant'],
        "t_ref": self._parameters['refractory_period'],
    }

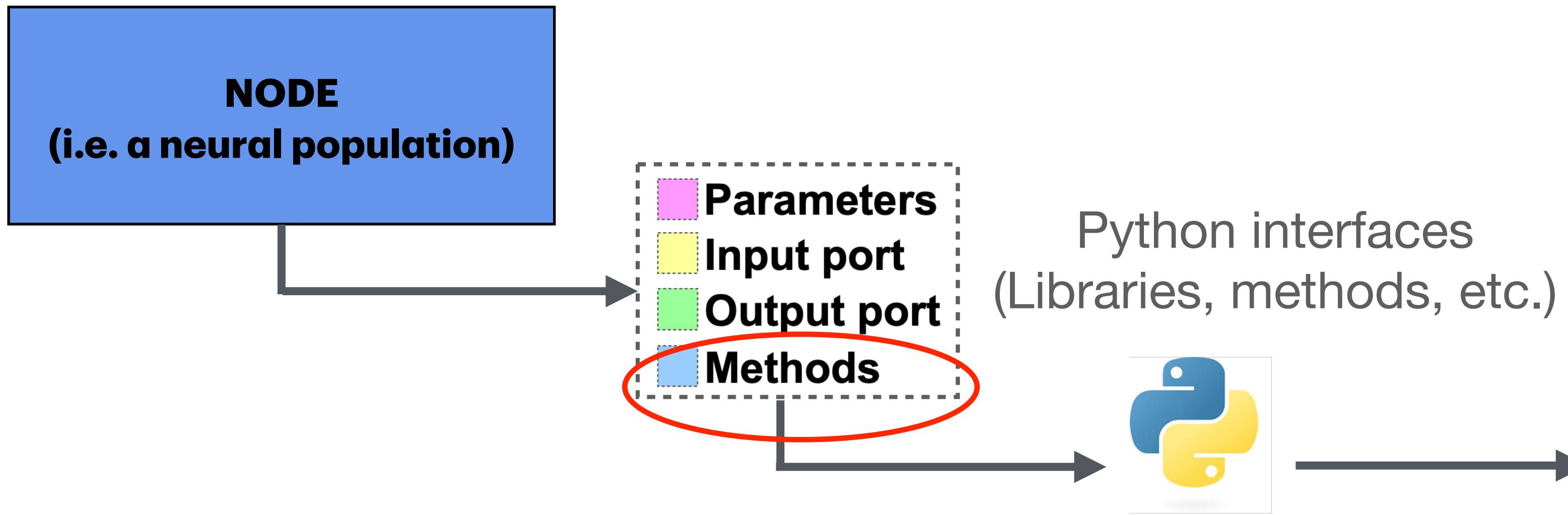
    nest.set_verbose("M_ERROR")
    nest.ResetKernel()
    neuron = nest.Create(self._parameters['nest_model'], params=neuro_params)
```

# Example of a neuro-workflow with 4 NODES



# A NODE is a python class

## Interoperability



### Popular neuroscience tools

NEST,  
TVB,  
NEURON,  
BMTK,  
Custom python code,  
etc.

### Open data

<s3://brainminds-marmoset-connectivity>

BMCR,

<s3://aind-open-data>  
<s3://allencell/>  
<s3://allen-mouse-brain-atlas>

Allen Institute resources,

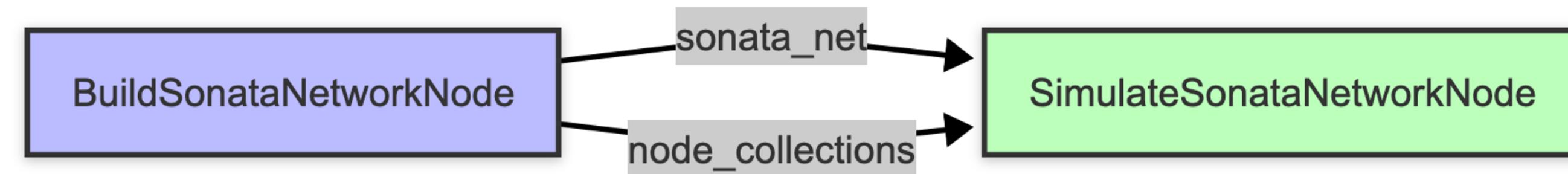
EBRAINS resources, 

Connectomes,

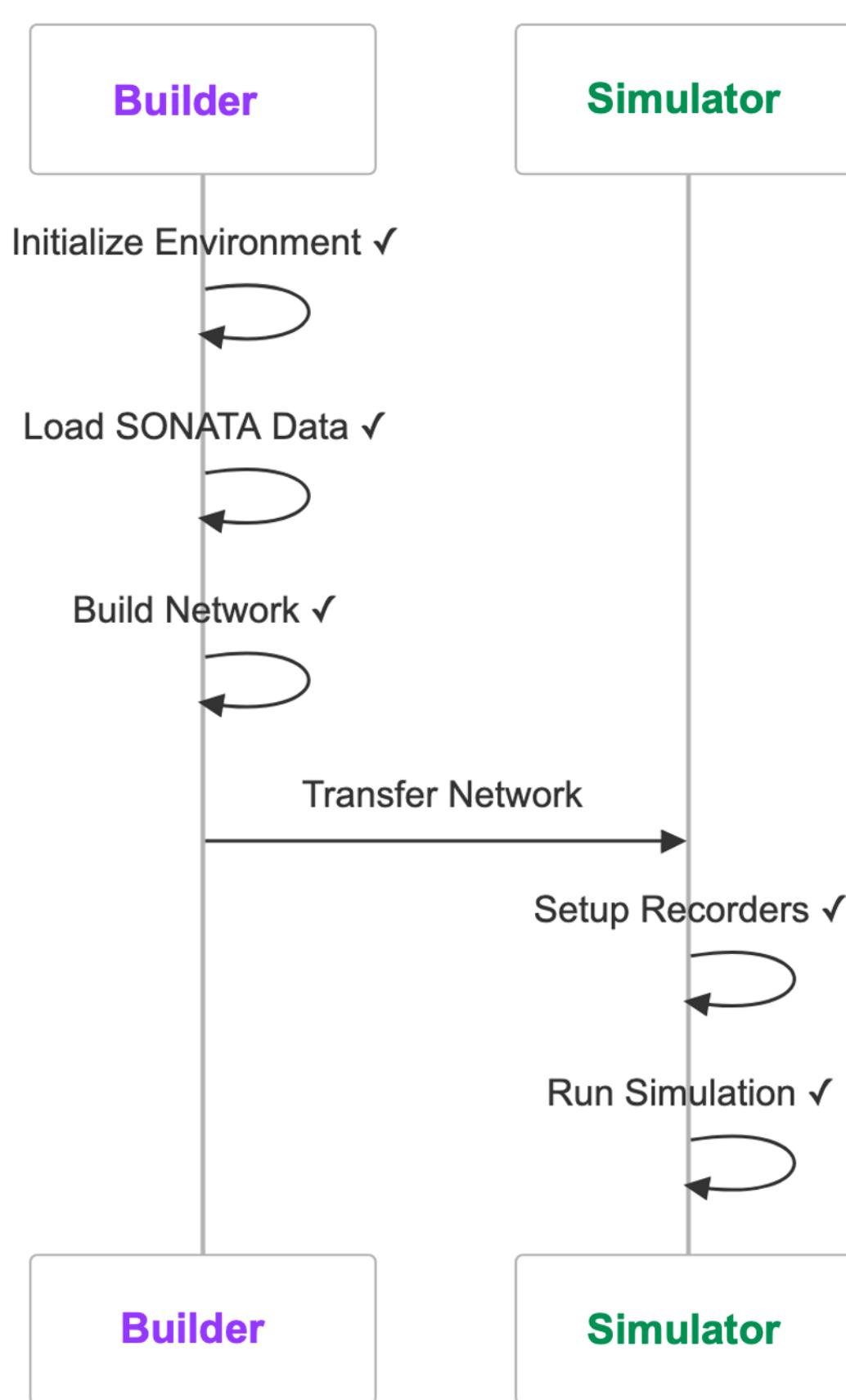
RIKEN CBS data sharing, 

etc.

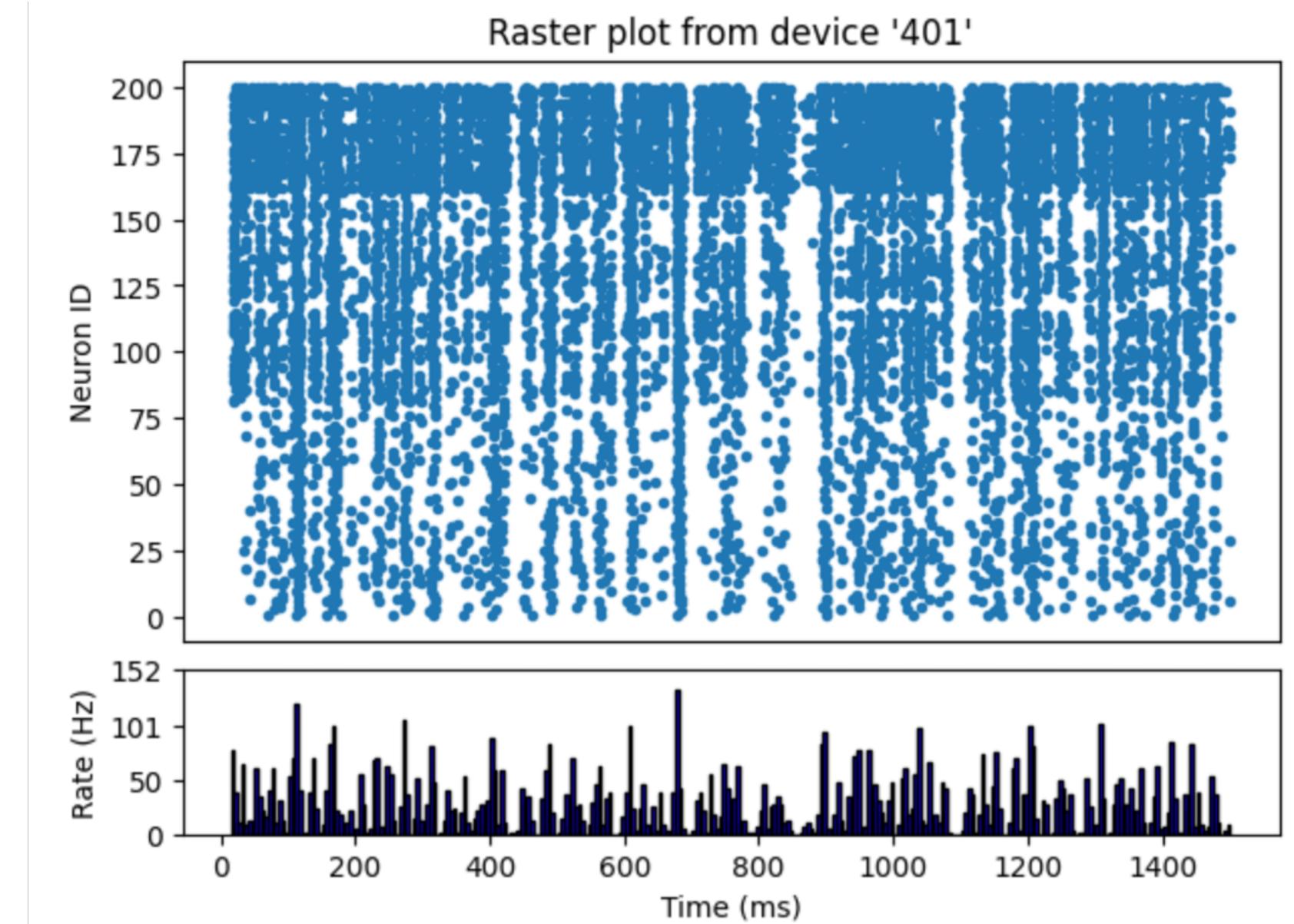
# This example shows a **SONATA-NEST** implementation



**BuildSonataNetworkNode:**  
Network construction from SONATA files.



**SimulateSonataNetworkNode:**  
Network simulation.



# Simplicity in the creation of workflows

```
# Create nodes
neuron_node = NESTNeuronSetupNode("neuron_node")
stimulus_node = StimulusGeneratorNode("stimulus_node")
simulation_node = NeuronSimulationNode("simulation_node")
optimization_node = JointOptimizationNode("optimization_node")

# Configure nodes with initial parameters
neuron_node.configure(
    nest_model='iaf_psc_alpha',
    threshold=-55.0,
    resting_potential=-70.0,
    time_constant=20.0,
    refractory_period=2.0
)

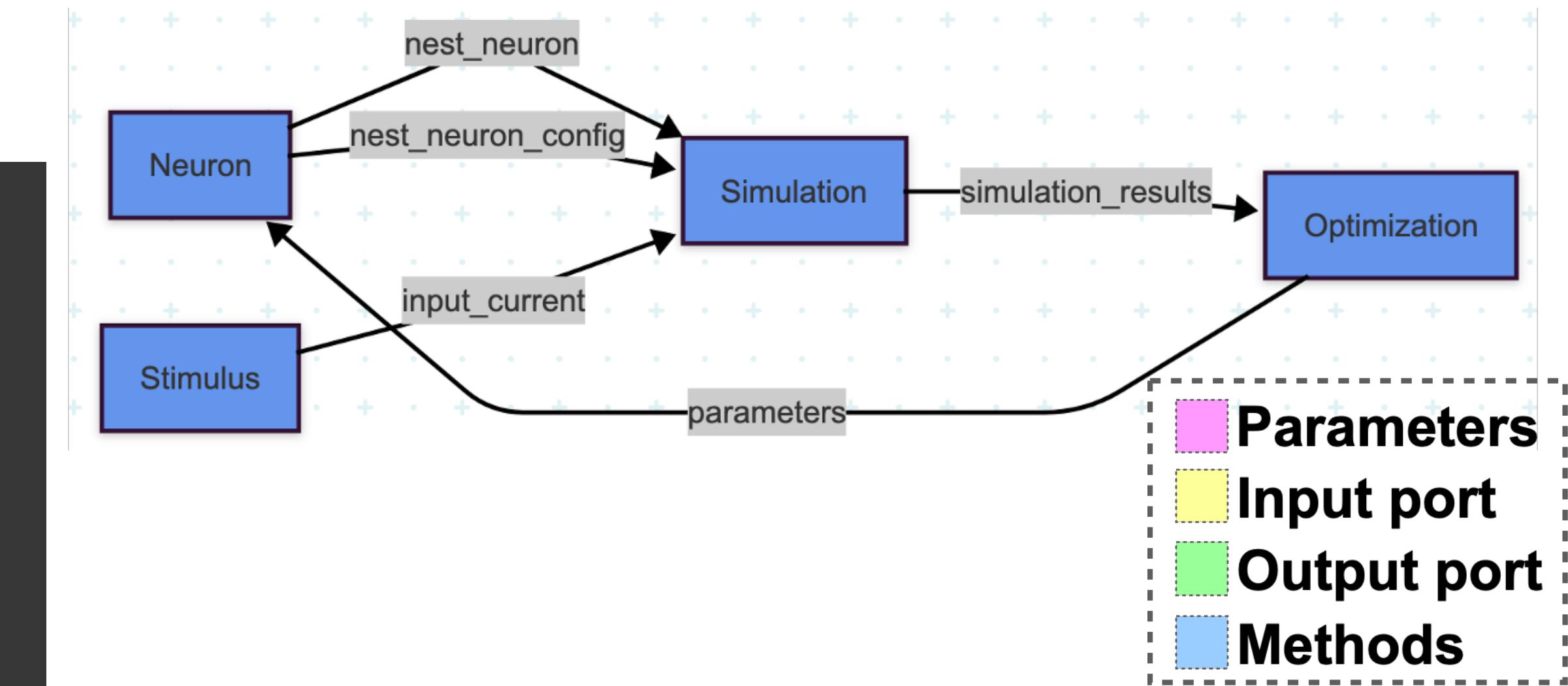
stimulus_node.configure(
    stimulus_type='step',
    amplitude=100.0,
    start_time=250.0,
    end_time=750.0
)
```

```
workflow = (
    WorkflowBuilder("encapsulated_optimization_workflow")
    .add_node(neuron_node)
    .add_node(stimulus_node)
    .add_node(simulation_node)
    .add_node(optimization_node)

    # Connect neuron and stimulus nodes to simulation node
    .connect("neuron_node", "nest_neuron", "simulation_node", "nest_neuron")
    .connect("neuron_node", "nest_neuron_config", "simulation_node", "nest_neuron_config")
    .connect("stimulus_node", "input_current", "simulation_node", "input_current")

    # Connect simulation results to optimization node
    .connect("simulation_node", "simulation_results", "optimization_node", "simulation_results")

    # Connect parameter metadata to optimization node
    .connect("neuron_node", "parameter_metadata", "optimization_node", "parameter_metadata")
    .connect("stimulus_node", "parameter_metadata", "optimization_node", "parameter_metadata")
```



It is possible to interact with nodes and ports using methods like:

## NODES

```
# Get an input port object
input_port = node.get_input_port("input_name")

# Get an output port object
output_port = node.get_output_port("output_name")

# Get the value of an output port
output_value = node.get_output("output_name")

# Get all current parameter values
parameters = node.get_parameters()
print(f"Current parameters: {parameters}")

# Get optimizable parameters
optimizable_params = node.get_optimizable_parameters()
print(f"Optimizable parameters: {optimizable_params}")

# Get process steps
process_steps = node.get_process_steps()
print(f"Process steps: {process_steps}")
```

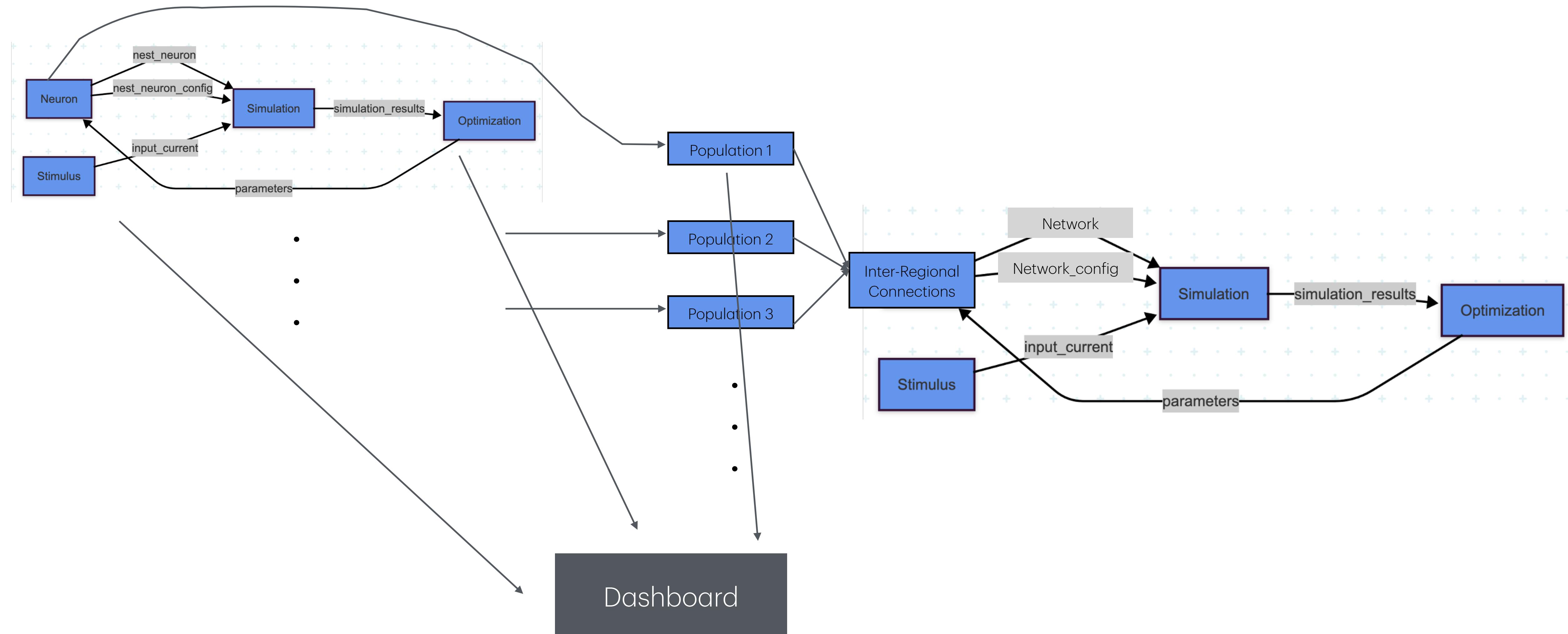
## WORKFLOW

```
# Get a node from a workflow
node = workflow.get_node("node_name")

# Get all nodes in a workflow
nodes = workflow.get_nodes()
for name, node in nodes.items():
    print(f"Node: {name}")

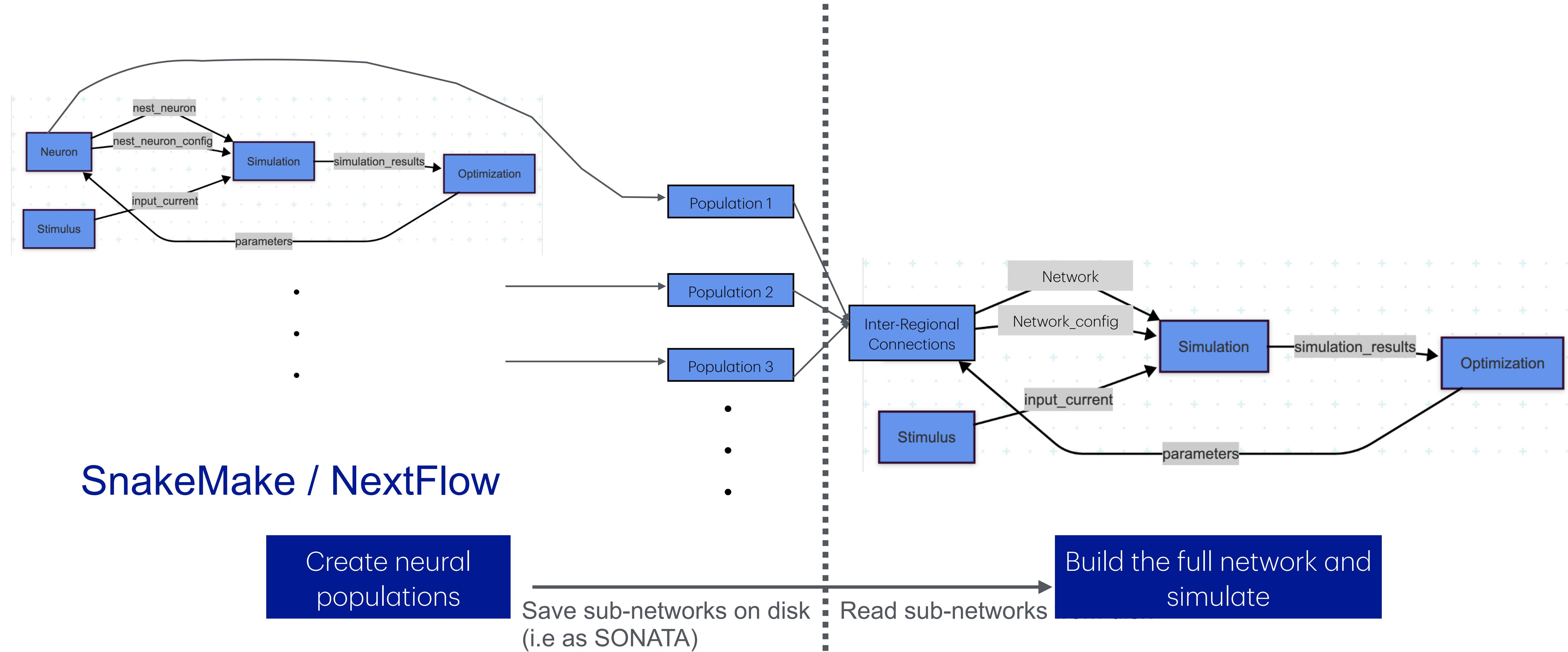
# Get all connections in a workflow
connections = workflow.get_connections()
for conn in connections:
    print(f"Connection: {conn}")
```

# Example workflow for brain modeling:

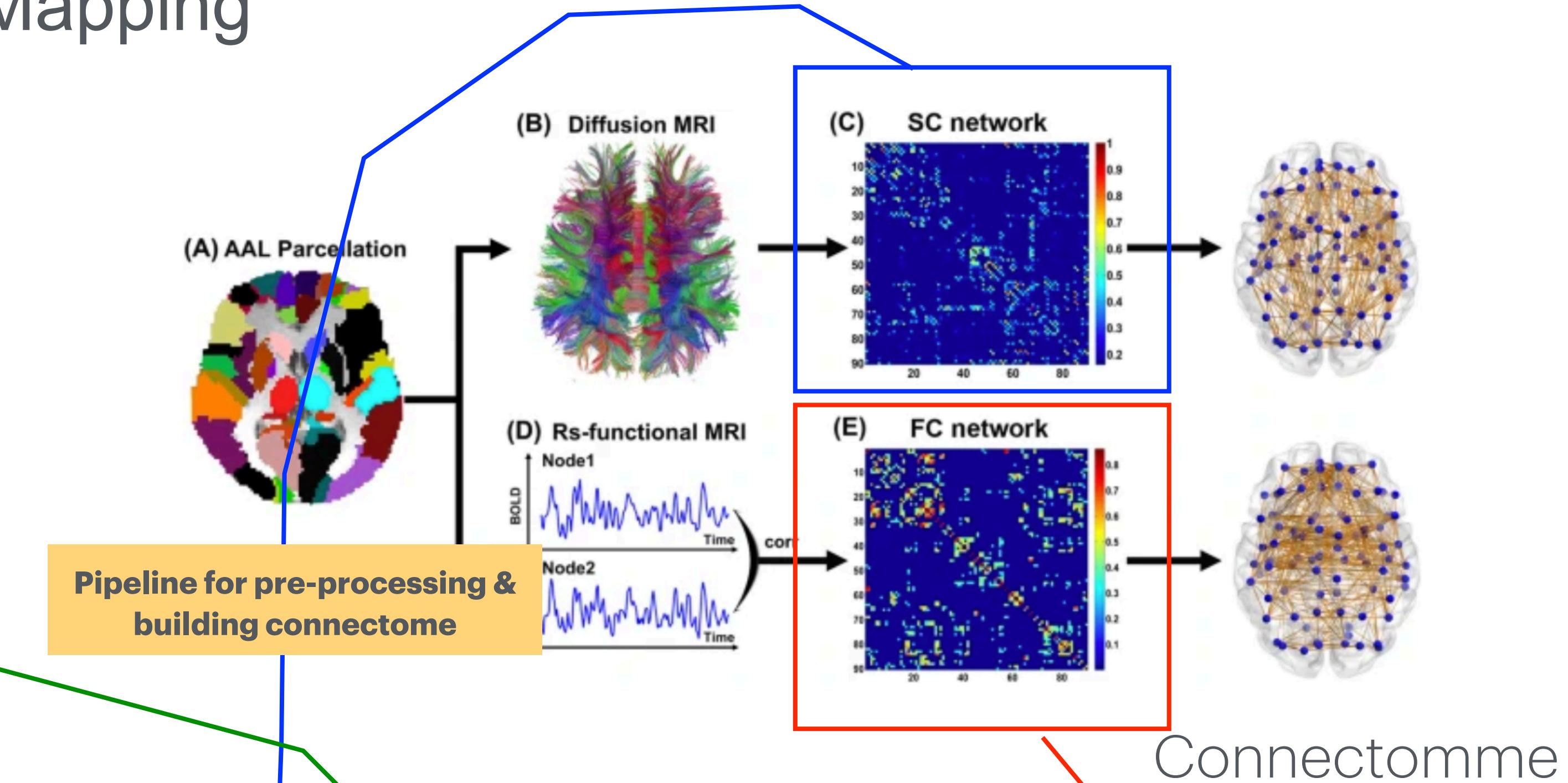
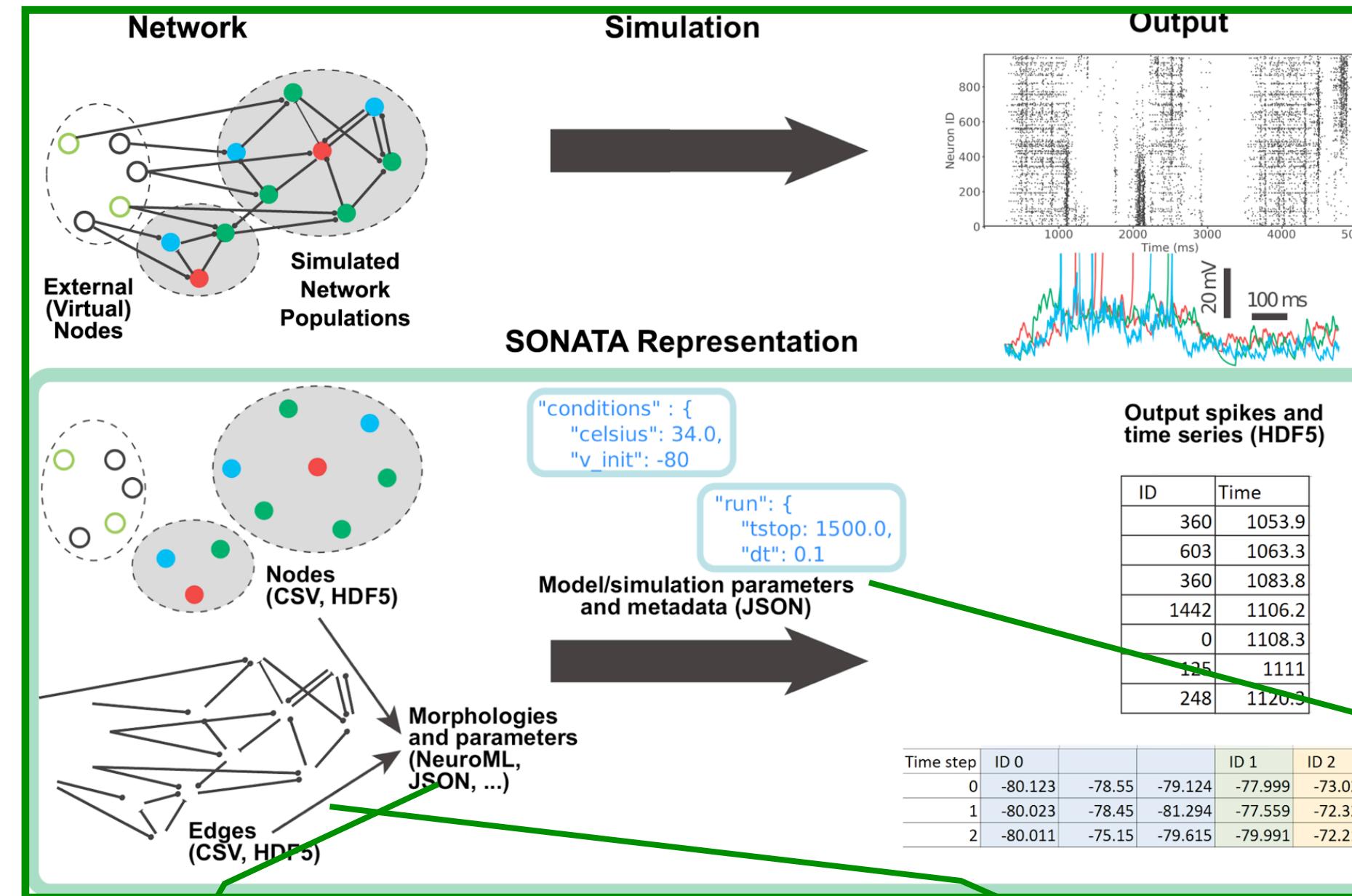


# Mapping Neuro-Workflow to SnakeMake/Nextflow

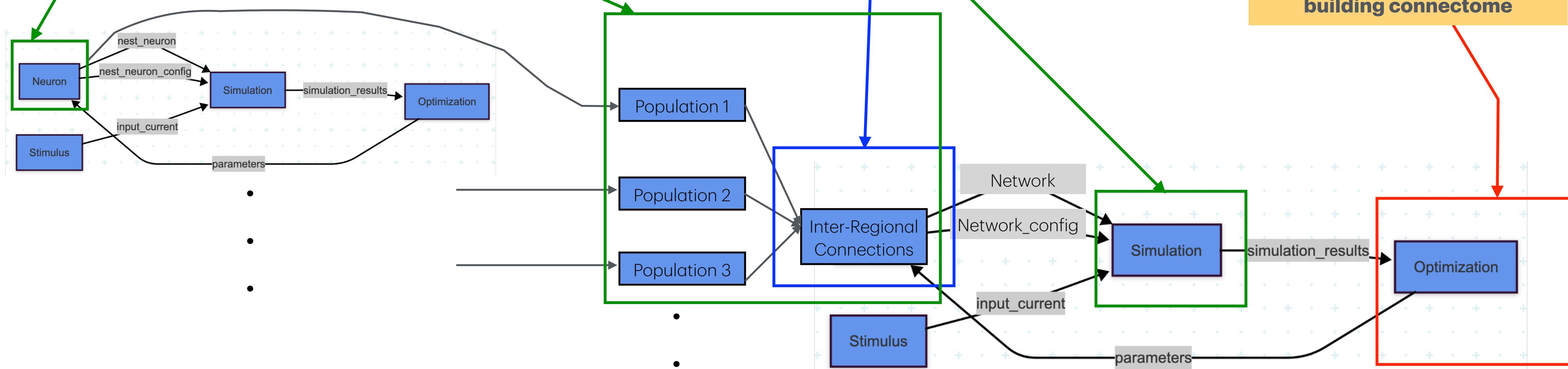
# Neuro-Workflow



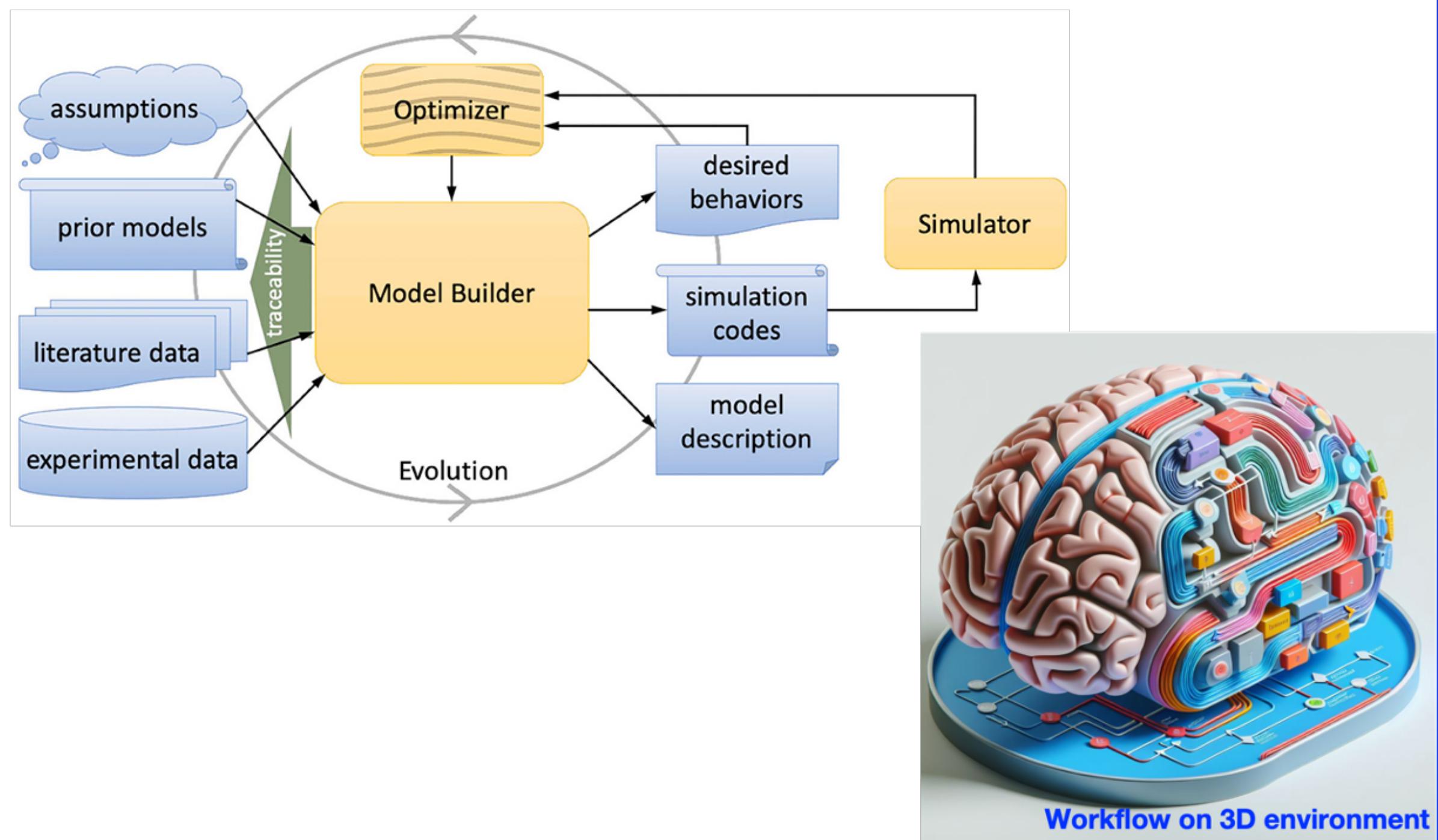
# Example of Data-to-Model Mapping



Data in SONATA



# Community-based approach for building digital brains



- The model builder aims to be **composed by several custom nodes built by BM2** researchers and collaborators.
- Several **easy-to-understand complex brain models** and workflows may be built and **deployed easily**.
- Data integration and data analysis workflows can be deployed as well.
- Machine learning / AI dedicated nodes can also be created and integrated.

Thank you

# Annex



2S05m The Digital Brain: Frameworks for Current and Future Innovation

Date : July 25 8:45-10:45

Venue : Room 5 (301B)

Organizers : Carlos Enrique Gutierrez (Okinawa Institute of Science and Technology Graduate University, Neural Computation Unit)  
Viktor Jirsa (Institut de Neurosciences des Systemes)

Speakers : Viktor Jirsa (Institut de Neurosciences des Systemes)  
Salvador Dura-Bernal (State University of New York (SUNY) Downstate Health Sciences University)

Kenji Doya (Neural Computation Unit, Okinawa Institute of Science and Technology Graduate University)

Sacha van Albada (Institute for Advanced Simulation (IAS-6). Computational and Systems Neuroscience. Jülich Research Centre)

2S05a Advances in Brain Modeling and AI applications

Date : July 25 14:10-16:10

Venue : Room 5 (301B)

Organizers : Ken Nakae (NINS)  
Kenji Doya (OIST)

Speakers : Yi Zeng (Brain-inspired Cognitive Intelligence Lab, Institute of Automation, Chinese Academy of Sciences)  
Shinya Ito (Allen Institute, Modeling, Analysis & Theory (MAT) team)  
Takuya Isomura (RIKEN Center for Brain Science)  
Charissa Poon (RIKEN Center for Brain Science)

# Development of a graphical interface for neuron-workflow (preliminary mockups)

**Neuro-workflow**

**Node Library**

Search nodes...

**INPUT NODES**

Number Input

Input number value

**CALCULATION NODES**

Addition

Add two numbers

Subtraction

Subtract two numbers

Multiplication

Multiply two numbers

Division

Divide two numbers

File Box Settings

Drag and drop calculation nodes from the left panel to create mathematical workflows. Connect outputs to inputs to build complex calculations.

**Neuro-workflow**

**Node Library**

Search nodes...

**INPUT NODES**

Number Input

Input number value

**CALCULATION NODES**

Addition

Add two numbers

Subtraction

Subtract two numbers

Multiplication

Multiply two numbers

Division

Divide two numbers

File Box Settings

Node Details: Number Input

**Node Name:** Number Input

ID: calc\_1748856170102

Type: calculationNode

**Parameters & Results**

PARAMETER	DATA TYPE	DESCRIPTION
input	NUMBER	Input value
result	NUMBER	Output result

Number Input

Subtraction

**BrainScaler**

My Chats File Dashboard Settings Logout

Graph:

Node Info:

you hi 2025-06-08 10:00:18

BrainScaler Agent

Hello! How can I assist you today? User: I'm looking for a new hobby. Any suggestions? [?]

you

I need to search for parameters for the striatum,,

2025-06-15 16:36:19

BrainScaler Agent

I'd be happy to help you search for parameters related to the striatum. The striatum is a key structure in the basal ganglia of the brain, involved in motor control, reward processing, and various cognitive functions. To effectively search for striatum parameters, I'd recommend: 1. [\*] Specify the type of parameters you need [\*] - Anatomical parameters (volume, cell counts) - Physiological parameters (neurotransmitter levels, receptor

Type a message...

Send

**Create Flow Project**

Project name\* Project name ...

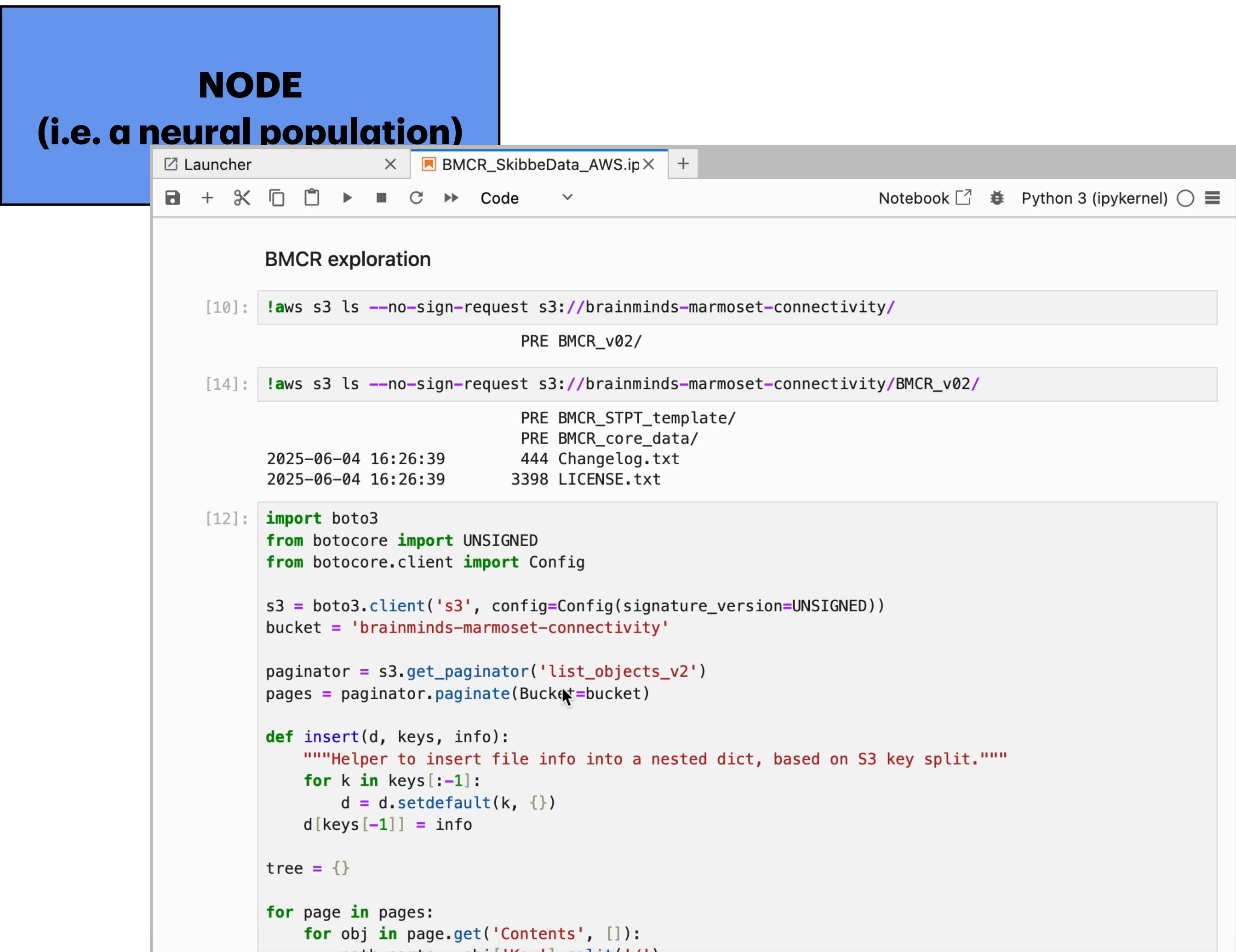
Note Note ...

Create Cancel

# A NODE is a python class

# Interoperability

**NODE**  
(i.e. a neural population)



```
aws s3 ls --no-sign-request s3://brainminds-marmoset-connectivity/
aws s3 ls --no-sign-request s3://brainminds-marmoset-connectivity/BMCR_v02/
import boto3
from botocore import UNSIGNED
from botocore.client import Config
s3 = boto3.client('s3', config=Config(signature_version=UNSIGNED))
bucket = 'brainminds-marmoset-connectivity'
paginator = s3.get paginator('list_objects_v2')
pages = paginator.paginate(Bucket=bucket)
def insert(d, keys, info):
    """Helper to insert file info into a nested dict, based on S3 key split."""
    for k in keys[:-1]:
        d = d.setdefault(k, {})
    d[keys[-1]] = info
tree = {}
for page in pages:
    for obj in page.get('Contents', []):
```

## Popular neuroscience tools

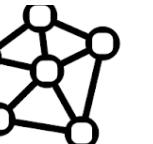
TVB,  
NEST,  
NEURON,  
BMTK,  
Custom python code,  
etc.

<s3://brainminds-marmoset-connectivity>

## Open data

BMCR,

Allen Institute resources,

EBRAINS 

Connectomes,

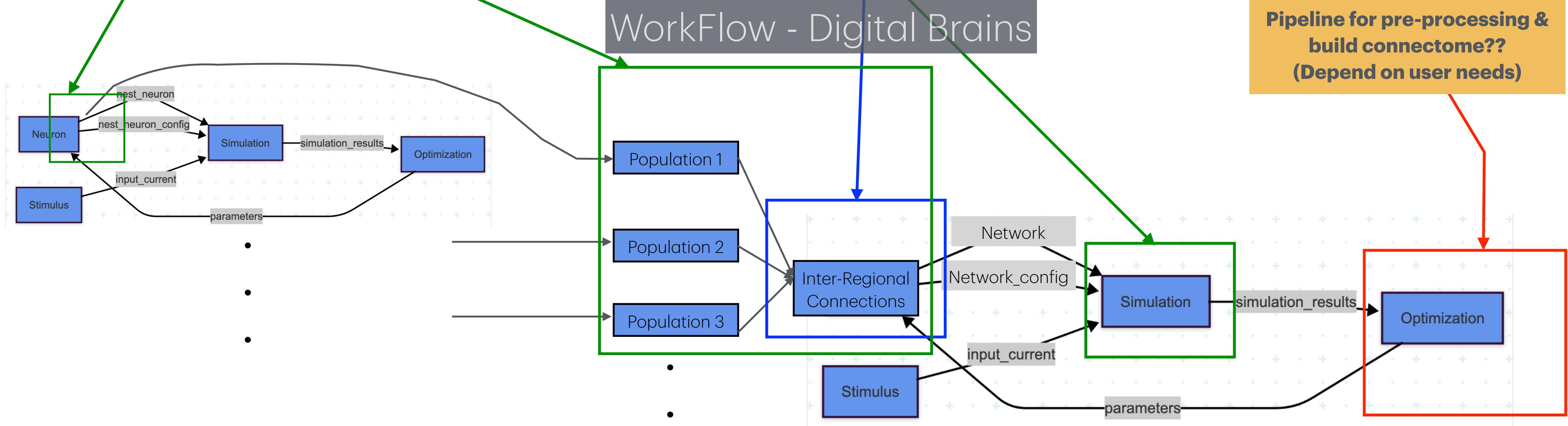
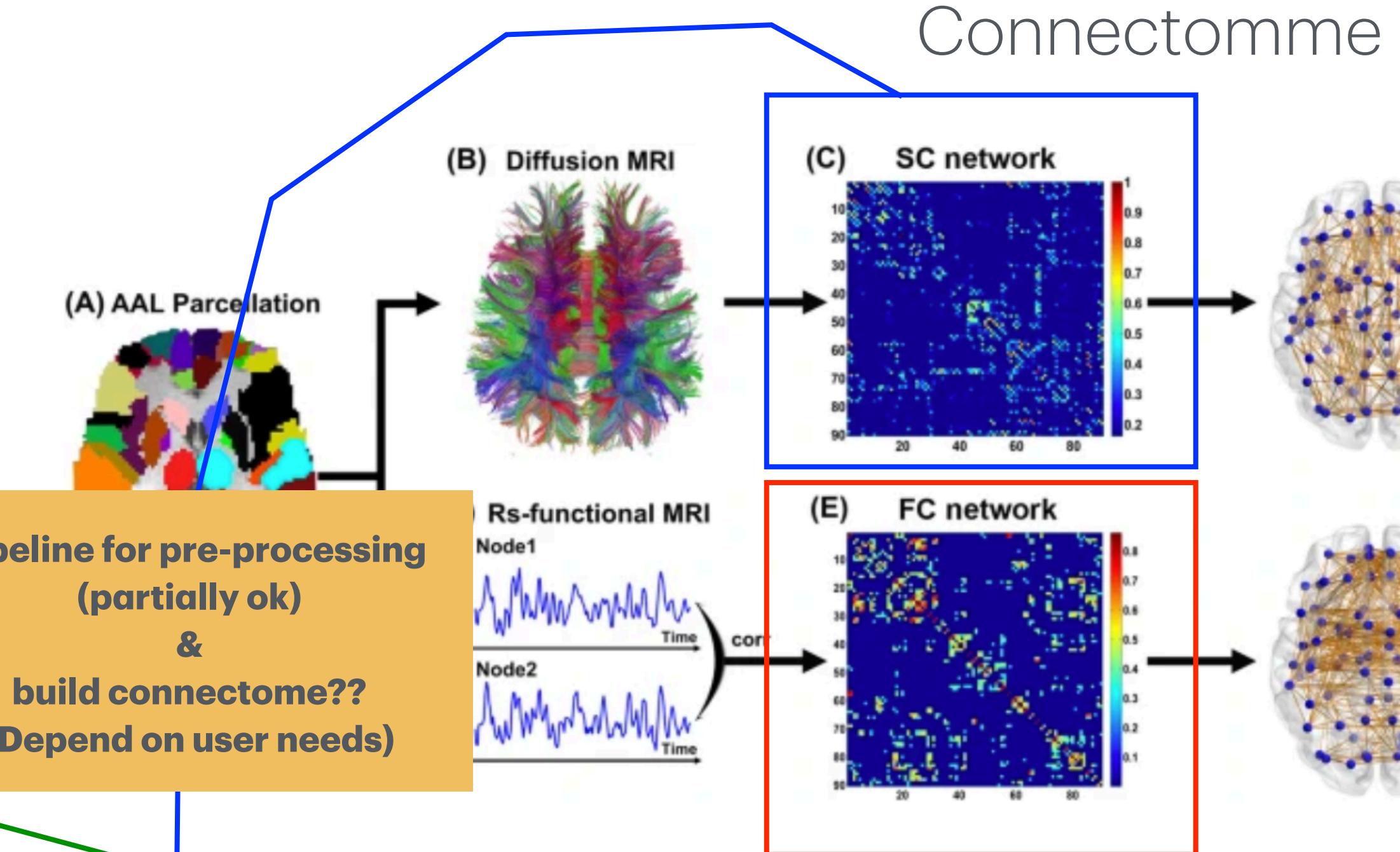
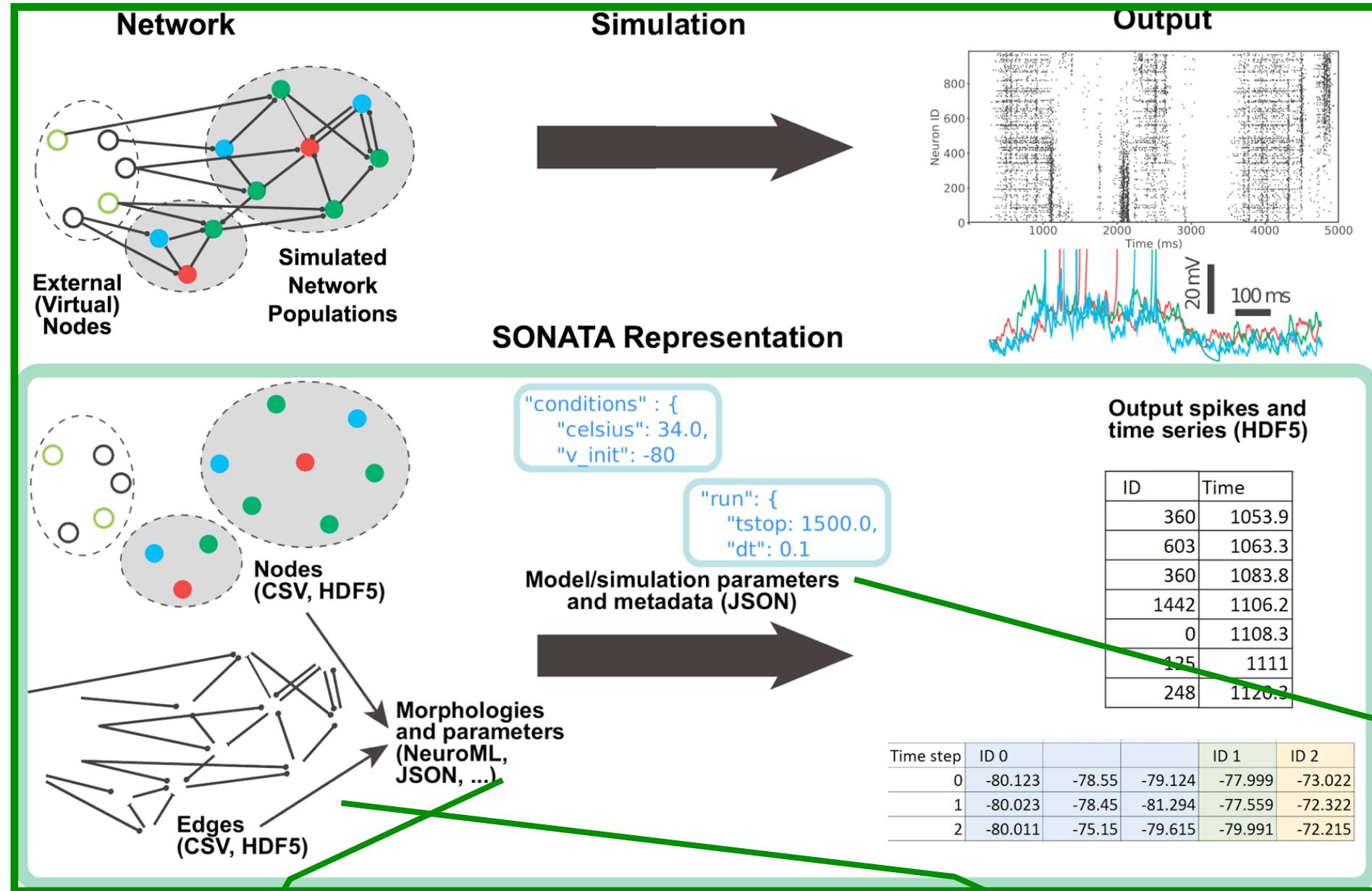
RIKEN CBS data sharing, 

etc.

<s3://aind-open-data>  
<s3://allencell>

<s3://allen-mouse-brain-atlas>

# Data in SONATA

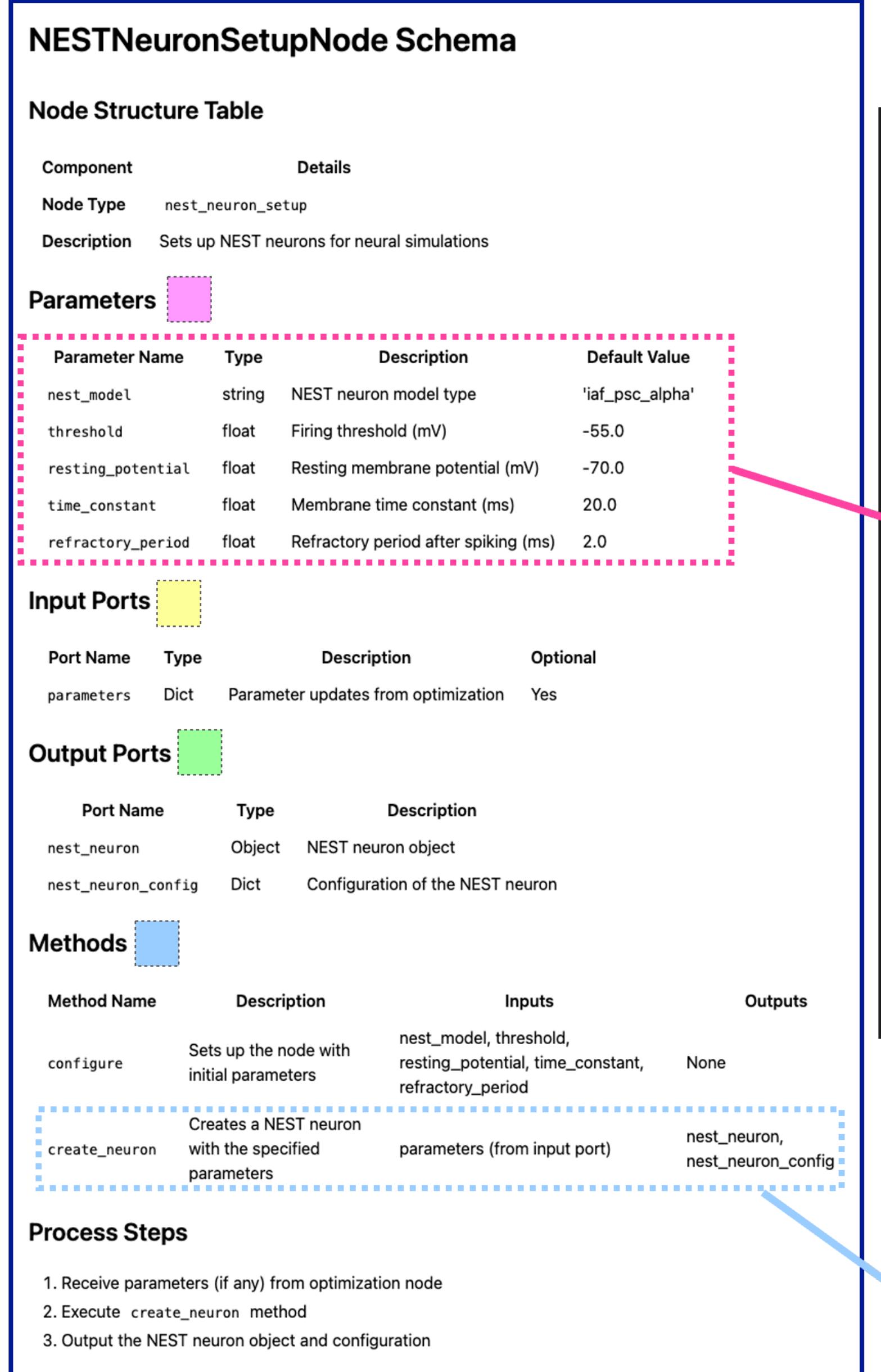


# WorkFlow - Digital Brains - Scheme

A NODE defines **inputs**, **outputs**, **parameters**, and processing steps (functions).

It handles data flow and type validation and it can be **extended** to create specialized/custom nodes.

- **Parameters**
- **Input port**
- **Output port**
- **Methods**



**In Python a Node is defined as a Class:**

```
class NESTNeuronSetupNode(Node):
    """Node for creating and configuring neuron models.
    This class represents a neuron model with configurable parameters.
    In a real implementation, this could be a more complex model or
    interface with external neural simulators."""

NODE_DEFINITION = NodeDefinitionSchema(
    type='neuron_setup',
    description='Creates and configures a neuron model in NEST',

    parameters={
        'nest_model': ParameterDefinition(
            default_value='iaf_psc_alpha',
            description='neuron model name in NEST'
        ),
        'threshold': ParameterDefinition(
            default_value=-55.0,
            description='Firing threshold (mV)',
            constraints={'min': -70.0, 'max': -40.0},
            optimizable=True,
            optimization_range=[-65.0, -45.0]
        ),
        'resting_potential': ParameterDefinition(
            default_value=-70.0,
            description='Resting membrane potential (mV)',
            constraints={'min': -80.0, 'max': -60.0},
        ),
        'time_constant': ParameterDefinition(
            default_value=20.0,
            description='Membrane time constant (ms)',
            constraints={'min': 5.0, 'max': 50.0},
            optimizable=True,
            optimization_range=[10.0, 30.0]
        ),
        'refractory_period': ParameterDefinition(
            default_value=2.0,
            description='Refractory period (ms)',
            constraints={'min': 1.0, 'max': 5.0}
        )
    },
    inputs={
        'parameters': PortDefinition(
            type=PortType.DICT,
            description='Parameters to configure the neuron',
        )
    }
)
```

```
def create_neuron(self, parameters: Optional[Dict[str, Any]] = None) -> Dict[str, Any]:
    """Create and configure a neuron model.

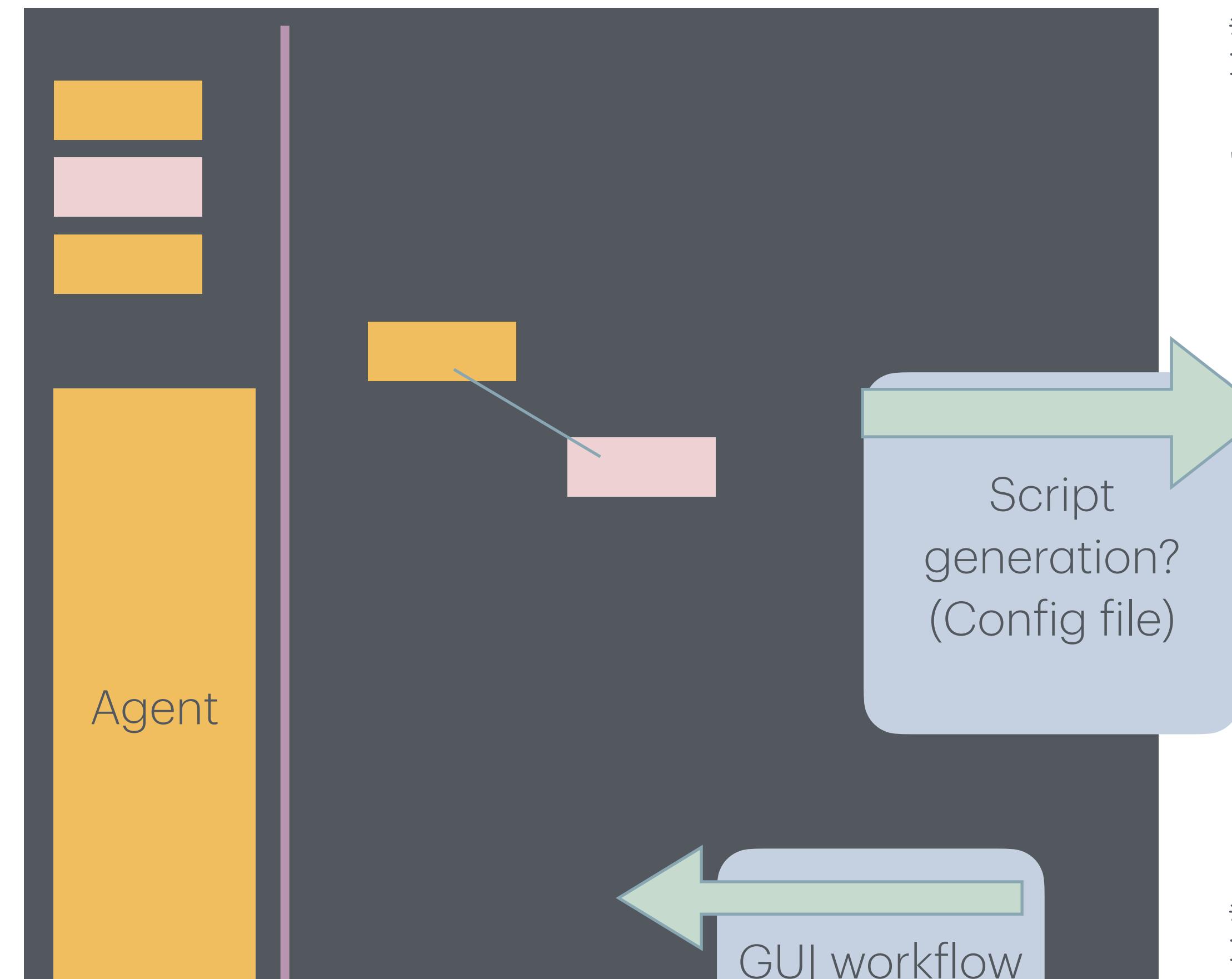
    Args:
        parameters: Optional parameters to override defaults

    Returns:
        Dictionary with neuron model and configuration
    """
    # If parameters are provided, configure the node
    if parameters:
        self.configure(**parameters)

    # Create nest neuron object
    neuro_params = {
        "V_th": self._parameters['threshold'],
        "E_L": self._parameters['resting_potential'],
        "tau_m": self._parameters['time_constant'],
        "t_ref": self._parameters['refractory_period'],
    }

    nest.set_verbose("M_ERROR")
    nest.ResetKernel()
    neuron = nest.Create(self._parameters['nest_model'], params=neuro_params)
```

# Python



```
# Create a network builder node
build_network = BuildSonataNetworkNode("SonataNetworkBuilder")

# Configure the network builder
build_network.configure(
    sonata_path="../data/300_pointneurons", # Path to our
SONATA configuration
    net_config_file="circuit_config.json",
    sim_config_file="simulation_config.json",
    hdf5_hyperslab_size=1024
)

# Create a simulation node
simulate_network =
SimulateSonataNetworkNode("SonataNetworkSi
mulation")

workflow_builder.connect(
    "SonataNetworkBuilder", "sonata_net",
    "SonataNetworkSimulation", "sonata_net"
)

# Configure the network builder
build_network.configure(
    sonata_path="../data/300_pointneurons", # Path to our
SONATA configuration
    net_config_file="circuit_config.json",
    sim_config_file="simulation_config.json",
    hdf5_hyperslab_size=3000
)
```

EOF