

# DotMotif: Subgraph isomorphisms on large brain graphs

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## ABSTRACT

Recent advances in neuroscience and bioimaging have enabled scientists to explore brain structure at the level of individual nanoscale synaptic connections. This measure of connectivity, when represented as a graph with neurons as nodes and synapses as directed edges, can be large and complex, presenting significant barriers to searching for structure and testing neuralcircuit hypotheses. We leverage graph database and analysis libraries to provide an easy-to-use grammar suitable for rapidly constructing queries and searching for subgraph isomorphisms, or "motifs." This abstracts many of the computer science and graph theory challenges associated with nanoscale connectomics and allows neuroscientists to quickly achieve reproducible findings.

Our approach, dubbed "DotMotif," simplifies identification of basic as well as complex neural connectivity structures relevant to the systems-neuroscience community. We contextualize these results and demonstrate efficiently that the found motifs are unlikely to have occurred by chance; we also demonstrate the versatility of our approach through the exploration of errorful graphs. All of our tools are released open source to empower other scientists to use and extend these methods.

### BACKGROUND

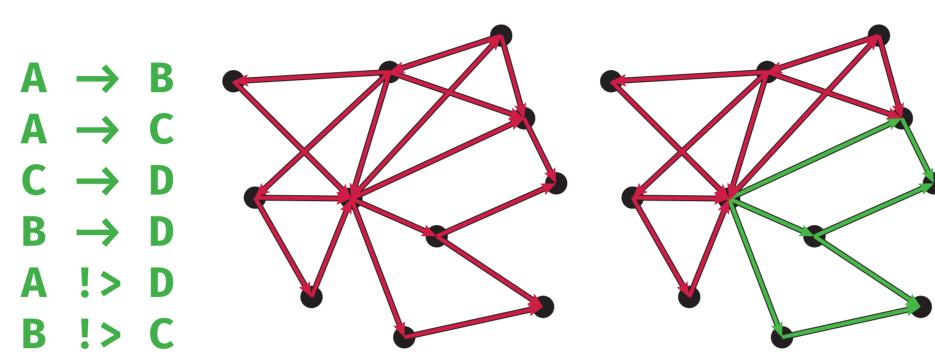
Nanoscale connectomes:

- Neurons are nodes
- Synapses are directed edges

This abstraction enables use of specialized graph analysis software.

Subgraph isomorphism identification: hypothetical small graph is searched for and identified in a larger complete graph.

One common and speedy implementation of this task is VF2 (Cordella 2004).



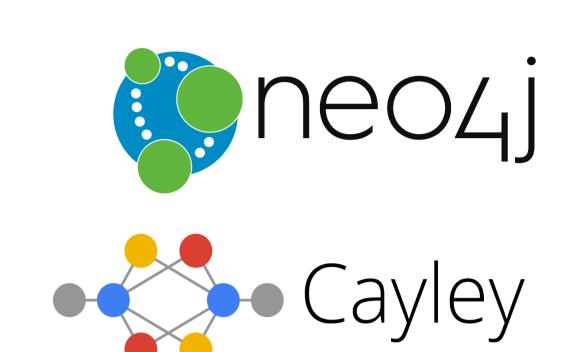
Subgraph isomorphism task:

- Common to industry domains such as e-commerce or search engines
- Graph datastore technologies have been developed to handle this task on very large (billion-node) graphs

Identifying brain motifs in large brain graphs can be rephrased as a subgraph isomorphism task: Graph databases can then be used to efficiently perform connectomics-flavored queries.

Weaknesses of these tools:

- Complex query syntax
- No error-checking prior to execution
- Nontrivial data ingest/export
- Requires tool familiarity/expertise



Amazon Neptune JanusGraph OrientDB

### METHODS

#### DOTMOTIF DOMAIN-SPECIFIC LANGUAGE

We propose a graph query syntax, the ".motif" format. This syntax can be used as an alternative to CSV or handcurated query design to formulate questions which are then compiled into an intermediate format.

**EDGES**  $A \rightarrow B$ **B!>A C--D**  $D \diamondsuit E$ E !! F

**EDGE ATTRIBUTES**  $A \rightarrow B$  [type=Glu,x>450] **NODE ATTRIBUTES** A.radius > 12

Our Python implementation includes syntax highlighting for major code editors.

#### **MACROS** inhibit\_feedback(A, B, C) { C.type='inhibitory'

inhibit\_feedback(x, y, z)

#### DOTMOTIF/CYPHER **COMPARISON**

# One-way edge: uniedge(A, B) { B !> A unitri(A, B, C) unitri(x, y, z)

e:Neuron)-[e\_g:SYN]→(g:Neuron) AND NOT unitri(e, f, g)

#### **VALIDATION & EXECUTION**

Common mistakes are easily caught at parse/compile time using the dotmotif.validators submodule. Validators are used to check both for query formation errors as well as biologically implausible motif components:

**IMPOSSIBLE QUERY** 

 $A \rightarrow B$ A !> B

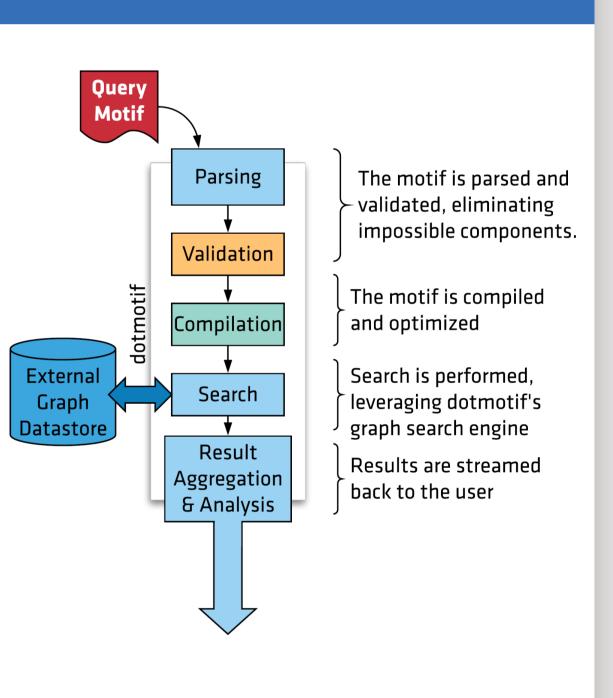
**BIOLOGICALLY IMPLAUSIBLE** A → B [type=inhibitory]  $A \rightarrow B$  [type=excitatory]

After validation, the query is compiled into an intermediate format, which can then be executed on a large search graph using a variety of graph datastore technologies, such as networkx, Neo4j, Cayley, Neptune, etc.

#### INFRASTRUCTURE & INTERPRETATION

DotMotif provisions graph datastores and handles data ingest/export to common data standards:

- Reduces query syntax complexity
- Enables query compilation and optimization
- Standardizes in-memory graph queries for use with arbitrary DB
- Provisions graph database Docker containers where needed
- Performs data ingest
- Sanitizes and standardizes outputs for ease of use



### RESULTS

### TAKEMURA ET AL (eLIFE 2017) CASE STUDY

This paper identified the circuitry responsible for "ON" motion response in the fruit fly visual system. The circuit spans multiple brain regions and involves multiple cell types whose organizations and inputs onto motionsensing cells in the lubula.

### MOTIF CONSTRUCTION

Original motif design from reported circuit:

 $L1 \rightarrow Mi1$  $L1 \rightarrow Tm3$  $L3 \rightarrow Mi9$  $Mi1 \rightarrow T4$  $Tm3 \rightarrow T4$  $Mi9 \rightarrow T4$ Tm9  $Tm9 \rightarrow T5$  $L2 \rightarrow Tm1$ 

### CONDITIONS

Can add conditions to improve query specificity when such data are available T5.name contains "T5" T4.z > 900

**EXCLUDED CONNECTIONS** 

file (along with constraints and executor parameters) to

Can specify connections to exclude: L1 !> T4 L3 !> T4 Tm2

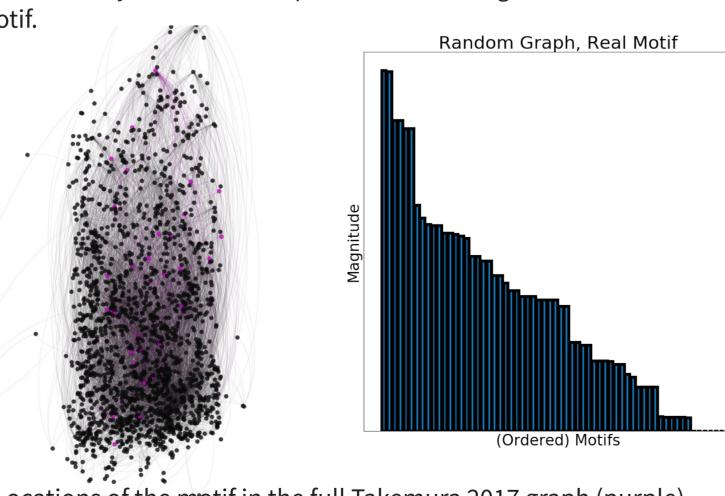
 $Tm1 \rightarrow$  $\bullet$   $\bullet$   $\bullet$ 

 $Tm2 \rightarrow T5$ After construction, can render, execute, or store in .motif

share with others or package with publication.

1.75 The motif identified in the paper. Connections from photoreceptors to the laminar layer and from lobular neurons are not included in this search query.

Frequency of permuted versions of the motifidentified in Takemura 2017. Permutations here are variations in edge-direction of the published "ON" motion selectivity motif. X axis represents increasing level of noise added to the motif



Left: Locations of the motif in the full Takemura 2017 graph (purple). Right: Frequency of permuted versions of the motifidentified in Erdös-Rényi random graph of the same size and edge density. This peak is qualitatively less pronounced and the distribution has a shorter tail.

### PUBLICATION & REPRODUCIBILITY

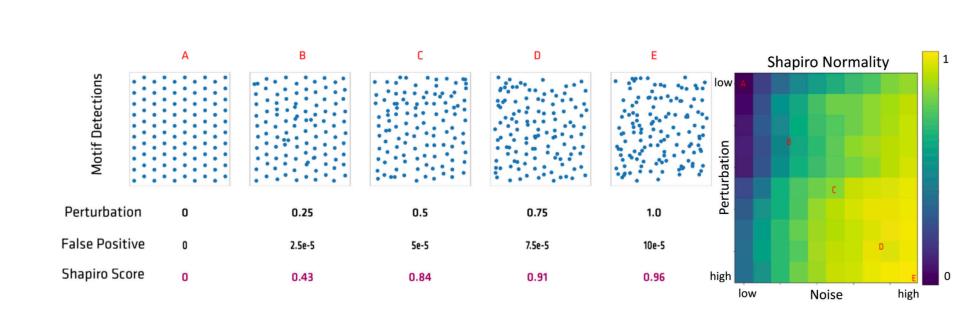
.motif file format includes:

- Motif graph structure, as well as constraints, metadata, and comments
- Parameters used to construct the search query • Version and release information for the codebase used to
- generate the file Provenance metadata (where available) including date of
- creation, user/author name Checksum for validation

Immutable file can then be shared or published.

### SPATIAL MOTIF DISTRIBUTION

DotMotif includes a suite of periodicity measures for analyzing outputs of motif searches. Below, synthetic simulation data are perturbed and tested for periodicity using a simple Shapiro normality test. These measures may be useful for some scientific questions that expect repeated substructure.



### STATISTICAL SIGNIFICANCE TEST

Once motifs are identified, researchers may wish to investigate local structure directly or to determine if motifs occur more likely than chance. Some possible directions for testing significance include:

- Permutation tests
- Comparison with theoretical results Your idea here?

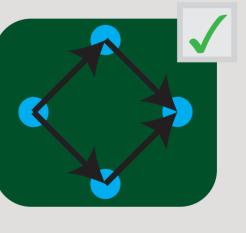
### **TOOL COMPATIBILITY**

DotMotif imports and exports to major graph framework formats in Python as well as on disk (graphml, CSV, etc), and simplifies graph ingest to graph databases like Cayley or Neo4j.

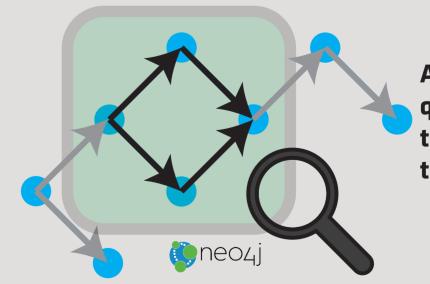
DotMotif is compatible with the Janelia NeuPrint data format, and the databases can be used interchangeably.



A query is submitted in .motif format.



The query is validated (is the structure possible? Is the structure biologically feasible?) and compiled into an intermediate data format.



A search is performed, here using a Neo4j query executor. Responses are returned to the user as a pandas dataframe, with pointers to the original "haystack" graph.

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