

PORGY: A Visual Graph Rewriting Environment for Complex Systems

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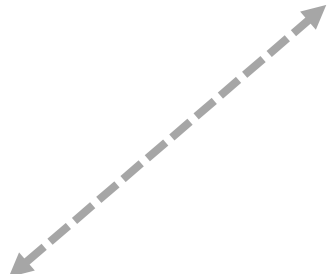
Visu 2012, 25/09/2012,
Telecom ParisTech



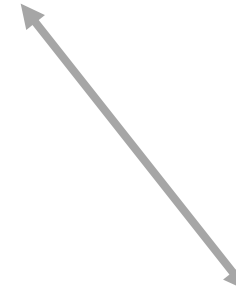
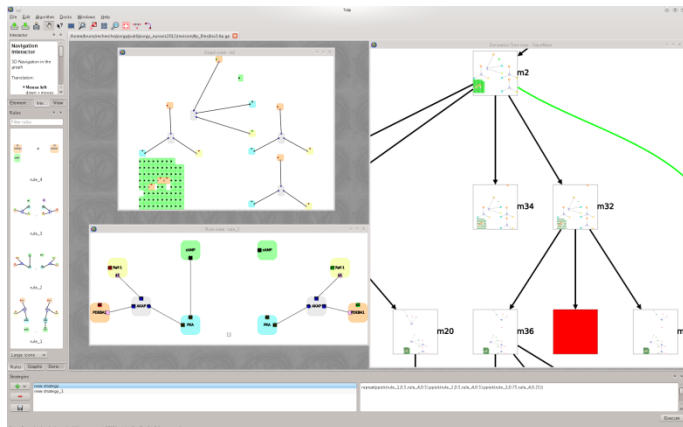
Modeling Complex Systems



Domain experts



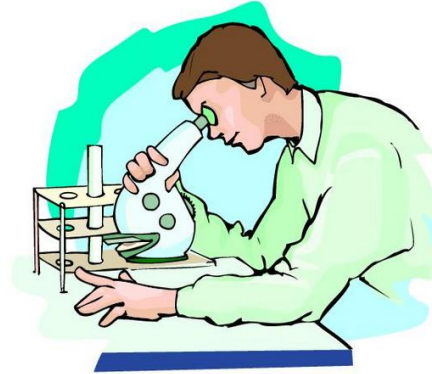
Visualization



Modeling experts

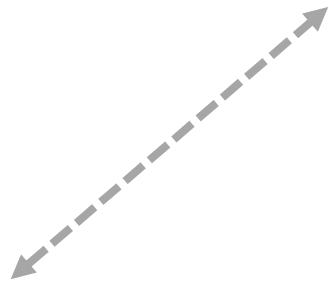


Modeling Complex Systems

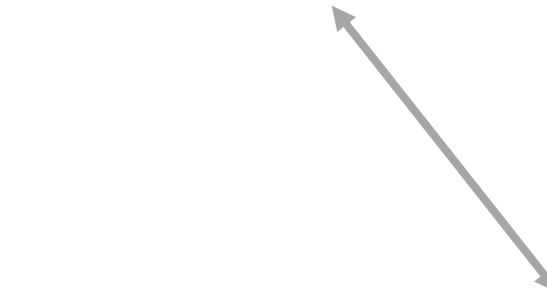
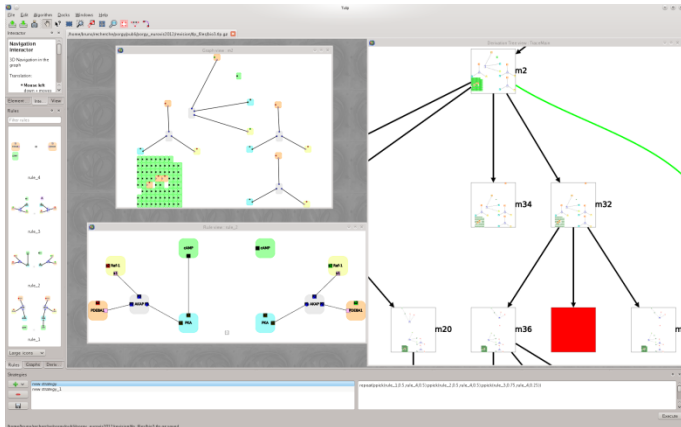


Biologists

See video 1



Visualization



Graph rewriting
experts

Modeling Complex Systems



- Overall goal: understand role of pathway *interaction* in the regulation of cell proliferation, transformation and survival
- More specific goals:
 - Explain the overall dynamics using a small set of rules prescribing how molecules bind
 - Assess the validity of the model by showing how system parameters obey expected ‘laws’

Modeling Complex Systems

- In simple terms: model design and validation can be seen as a « *what if ?* » game
 - *What if* we have this rule governing how molecule of type A interacts
 - *What if* each rule R only applies with probability p ?
 - *What if* ... ?

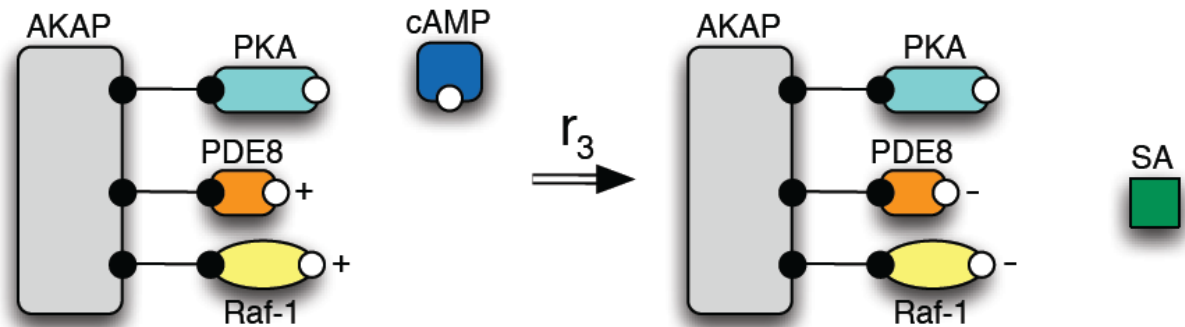


See video 2

Modeling Complex Systems



- The method:
 - Design simple binding rules

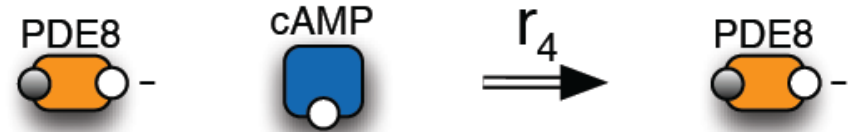


- Run simulations, perform measurements
- Adapt (change) rules
- Keep track of past simulations

Modeling Complex Systems



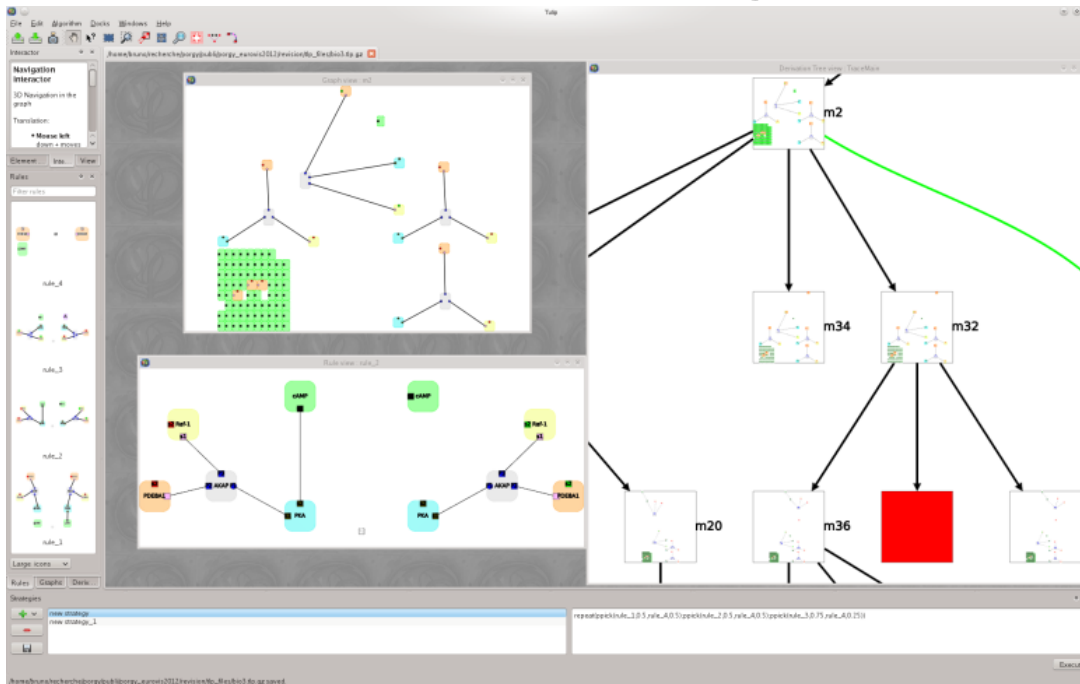
- The formalism:
 - Model molecules as graphs



- Binding rules become local graph transformations
- The whole thing becomes a Graph Rewriting System (GRS)

Modeling Complex Systems

- The challenge:
 - Design a visual environment to support rule-based modeling

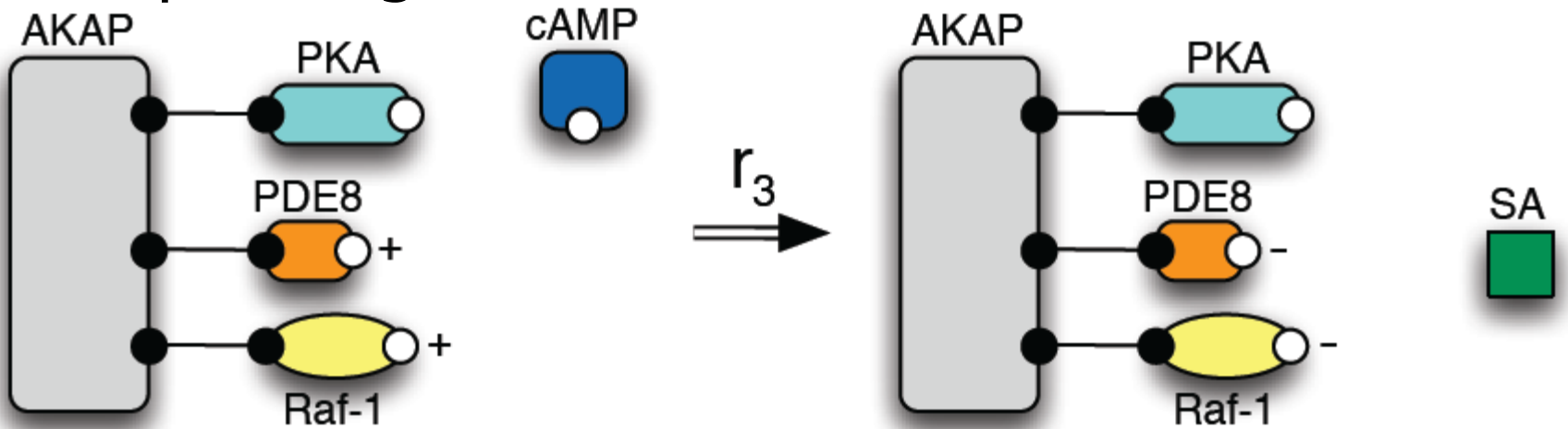


Graph rewriting systems

- GRS have a long history in theoretical computer science
 - Powerful graphical computation paradigm
 - GRS formal languages [Progress (Schür et al. 1997), Fujaba (Nickel et al. 2000), GP (Plump 2009), ...]
- Growing number of applications
 - Security policies, model driven software engineering, biomolecular interactions

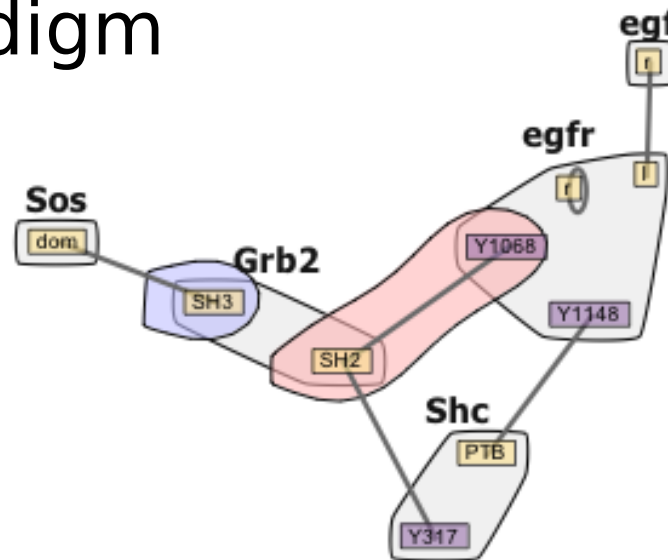
Graph rewriting systems

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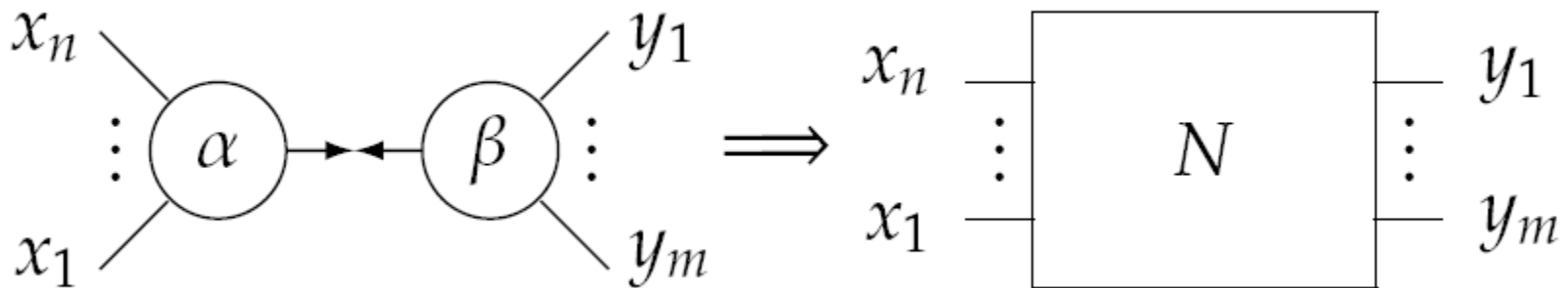
Graph rewriting systems

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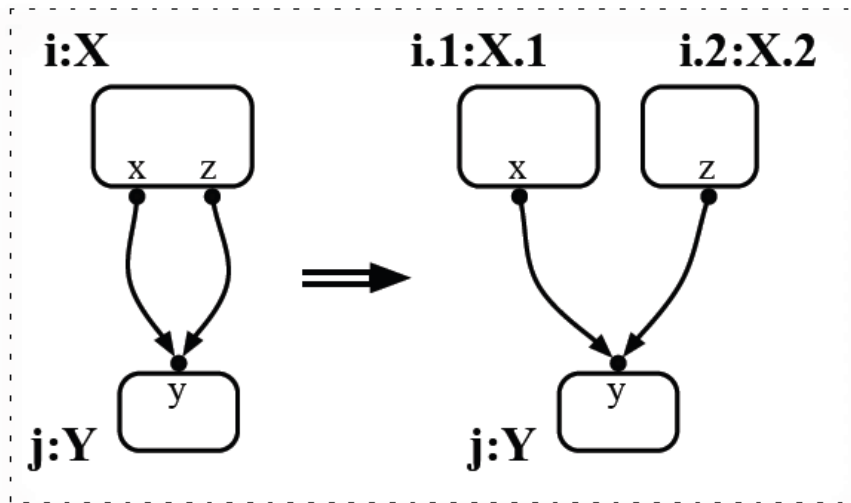
Graph rewriting systems

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Graph rewriting systems

- GRS have a long history in theoretical computer science
 - Powerful graphical computation paradigm



Supporting rule-based modeling

The screenshot displays the Tulp software interface, which is used for rule-based modeling. The interface is divided into several panels:

- Navigation Interactor:** Located on the left, it provides 3D navigation controls for the graph, including a translation section with a mouse icon and instructions: "Mouse left" and "down + moves".
- Rules:** A panel below the interactor showing a list of rules (rule_1, rule_2, rule_3, rule_4) with small graphical icons representing each rule.
- Graph view (m2):** The central workspace showing a network graph with nodes and edges. A large green grid is overlaid on the left side of the graph.
- Rule view (rule_1):** A detailed view of a specific rule, showing the transformation of a network state. The left side shows the initial state with nodes like PKA, AKAP, and PDEB1. The right side shows the resulting state after the rule is applied, with nodes like Ref-1 and cAMP.
- Derivation Tree view (TraceMain):** A tree structure on the right showing the sequence of model states (m2, m34, m32, m20, m36, m) generated from the initial model. A green arrow points from the root node m2 to m32, and a red square highlights a node in the tree.
- Strategies:** A panel at the bottom showing a list of strategies and a code editor with the following code:

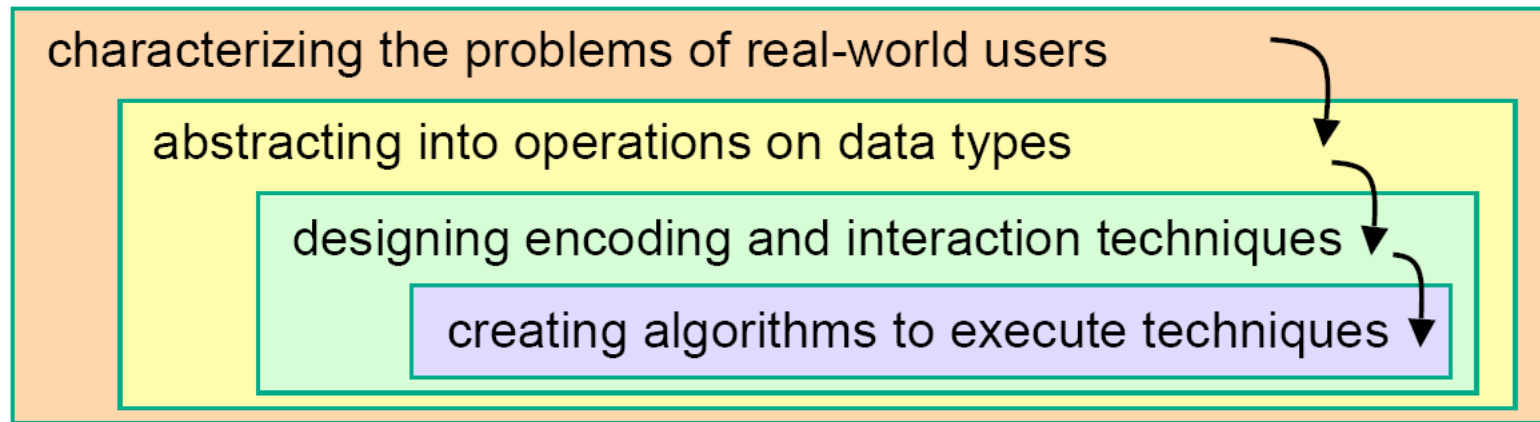
```
repeat(ppick(rule_1,0.5,rule_4,0.5);ppick(rule_2,0.5,rule_4,0.5);ppick(rule_3,0.75,rule_4,0.25))
```

The status bar at the bottom indicates the file path: `/home/bruno/recherche/porgy/publi/porgy_eurovis2012/revision/ftp_files/bio3.tlp.gz.saved`.

Visualization system design

- Adopt a methodology according to

T. MUNZNER: **A nested process model for visualization design and validation.**
IEEE Trans. on Visualization and Computer Graphics 15, 6 (2009), 921–928



3-year project

Biologists (O. Andrei), GRS experts (Fernandez, Kirchner)

Visualization system design

M SYSTEM MODELING	G GRAPH REWRITING QUESTIONS	R TASK ABSTRACTIONS DESIGN REQUIREMENTS	A VISUAL / INTERACTION / ALGORITHMS
M1 Design elementary molecular interactions	G1 Design the ruleset and the initial graph G_0	R1 Build/Edit G_0 /rules	A1 Support port graph editing
M2 Define an evolution scenario	G2 Define a rewriting strategy	R2 Build/Edit a rewriting strategy (e.g., reg. exp.)	A2 Drag and drop graphical entities between different views
M3 Observe / Study system evolution	G3 Iterate rule applications G4 Visualize their effects	R3 Grab a strategy or rule and trigger a computation R4 Replay rule applications	A3 Compute subgraph isomorphism A4 Show graph transformations (Animations / Small multiples)
M4 Keep track of computations / Allow backtracking to check, adjust and/or modify model	G5 Check for convergence or termination/premature end of computation G6 Eventually fix the ruleset	R5 Trigger computations from any node of the derivation tree R6 Show dead-end situations in the derivation tree	A5 Build and layout derivation tree A6 Tree drawing issues: grow branch from internal node, insure stability of layout
M5 Query for the presence of certain molecules at different stages M6 Study behavior of given parameters as system evolves M7 Alternate between parameter behavior and model	G7 Local inspection/query of graph items (nodes, edges, subgraphs) G8 Compute attributes or structural properties of graphs as rules are applied	R7 Select (group of) nodes R8 Test for the presence of identical groups of nodes R9 Plot parameter evolution R10 Synchronize the plot with the derivation tree R11 Allow selection of graph items from the plot	A7 Emphasize selected items wherever shown A8 Manage subgraph hierarchies A9 Compute subgraph isomorphism A10 Synchronize underlying data structures (coordinated views)
M8 Study model computational / structural properties	G9 Check for confluence of computation G10 Inquire about structure underlying ruleset	R12 Check whether graphs obtained from different rule sequences are the same R13 Check how/where graphs are the same on an alternate view	A11 Compute subgraph isomorphism A12 Build quotient graph from equivalence relation (isomorphism) between graphs A13 Maintain coherence with synchronized views

Visualization system design

System modeling

Define elementary molecule interactions

Define an evolution scenario

GRS questions

Define *rhs/lhs* subgraphs

Define a *rewriting strategy*

[Fernandez, Kirchner, Namet]

- System modeling tasks/questions correspond to 'pure' GRS questions
 - Therefore indicating that genericity is achievable

Visualization system design

System modeling

Heading towards model validation

Query for the presence of molecules

Study model parameters

GRS questions

Iterate rule applications

Local inspection of graph items

Compute graph structural properties (metrics)

Visualization system design

Task requirements

Build/Edit rules or graphs, rewriting strategy

Trigger computations

Show dead-end situations

Selection

View synchronization

Visual / interaction / Algorithms

Graph editing

Show graph transformations

Drag & drop entities between views

Subgraph isomorphism heuristics

More involved tasks

System modeling

Keep track of computations
Allow backtracking to check, adjust and/or modify model

Study model computational / structural properties

GRS questions

Check for convergence or termination / premature end of computation
Eventually fix the ruleset

Check for confluence of Computation

Inquire about structure of underlying ruleset

Keeping track of computation

System modeling

Keep track of computations
Allow backtracking to check, adjust and/or modify model

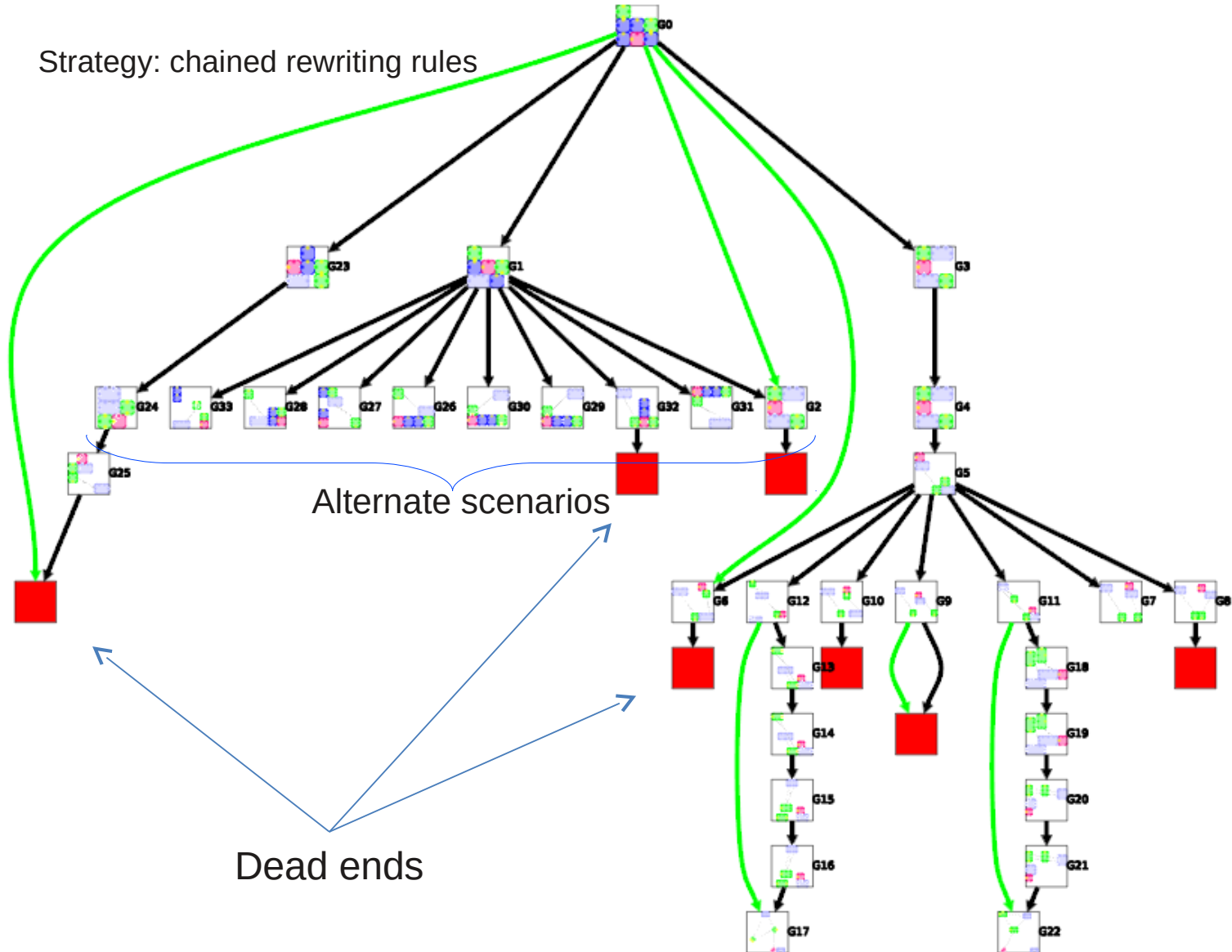
GRS questions

Check for *convergence* or termination / premature end of computation
Eventually fix the ruleset

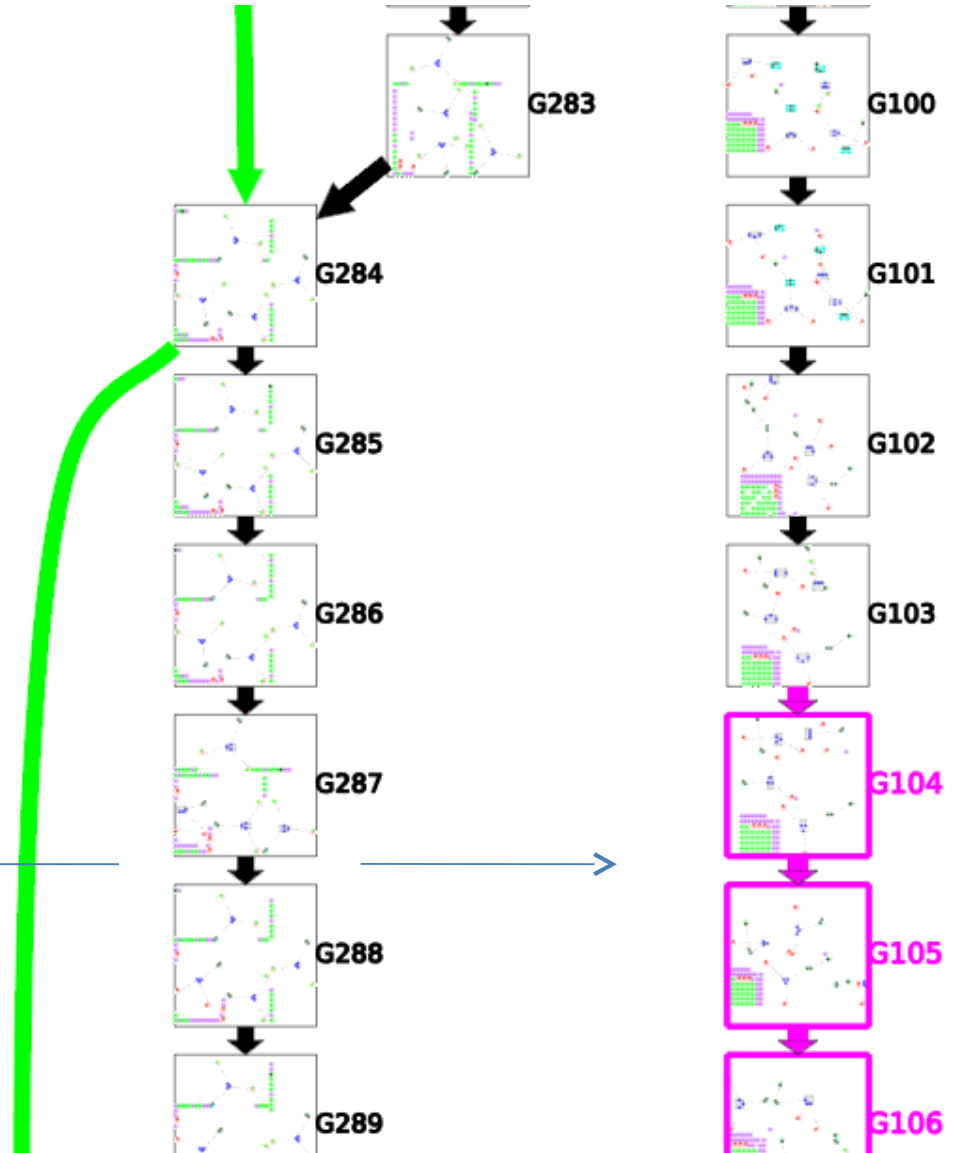
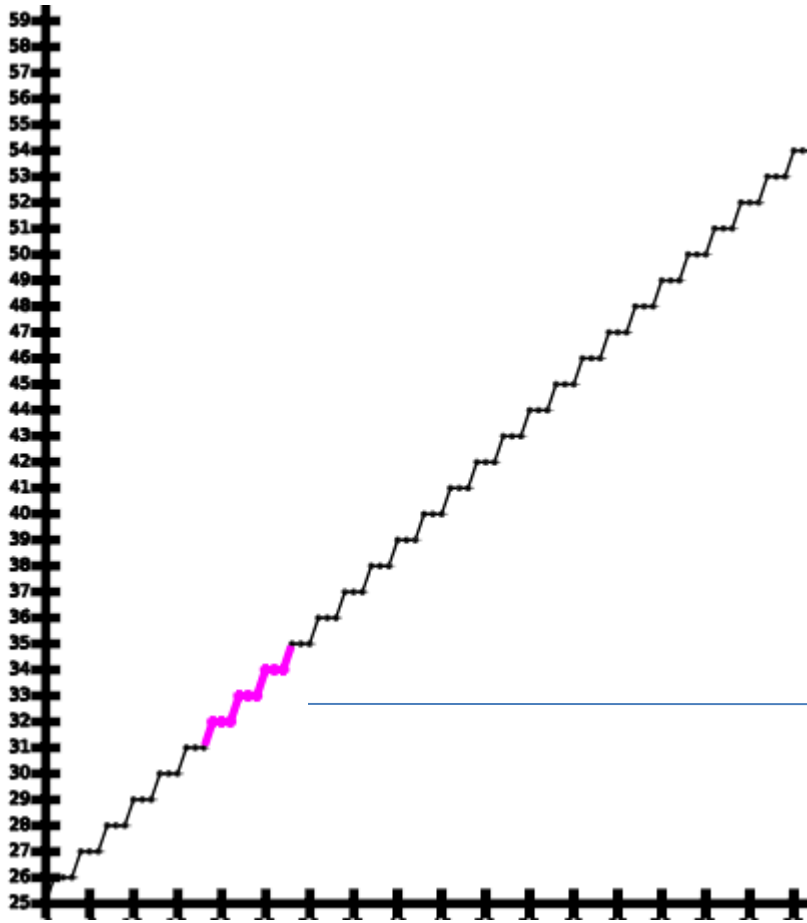
- Derivation *tree* as a history mechanism and data structure
 - Rule application is *non-deterministic*

Keeping track of computation

Strategy: chained rewriting rules



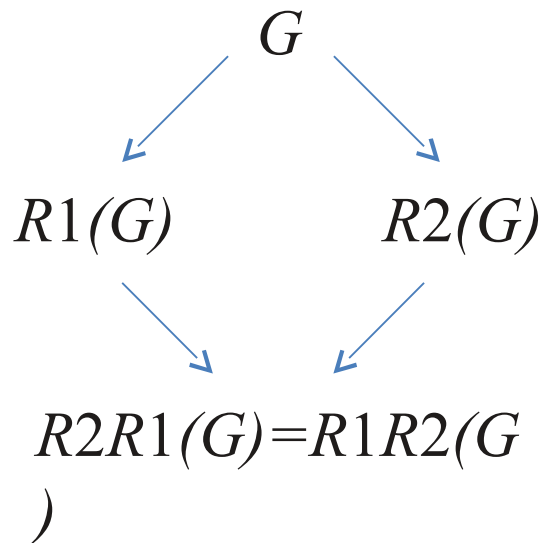
Track model parameter



More involved tasks

System modeling

Study model
computational
/ structural properties



Inquire about structure underlying ruleset

Check for *confluence* of Computation

Inquire about structure of underlying ruleset

- *Confluence* means rules 'commute'

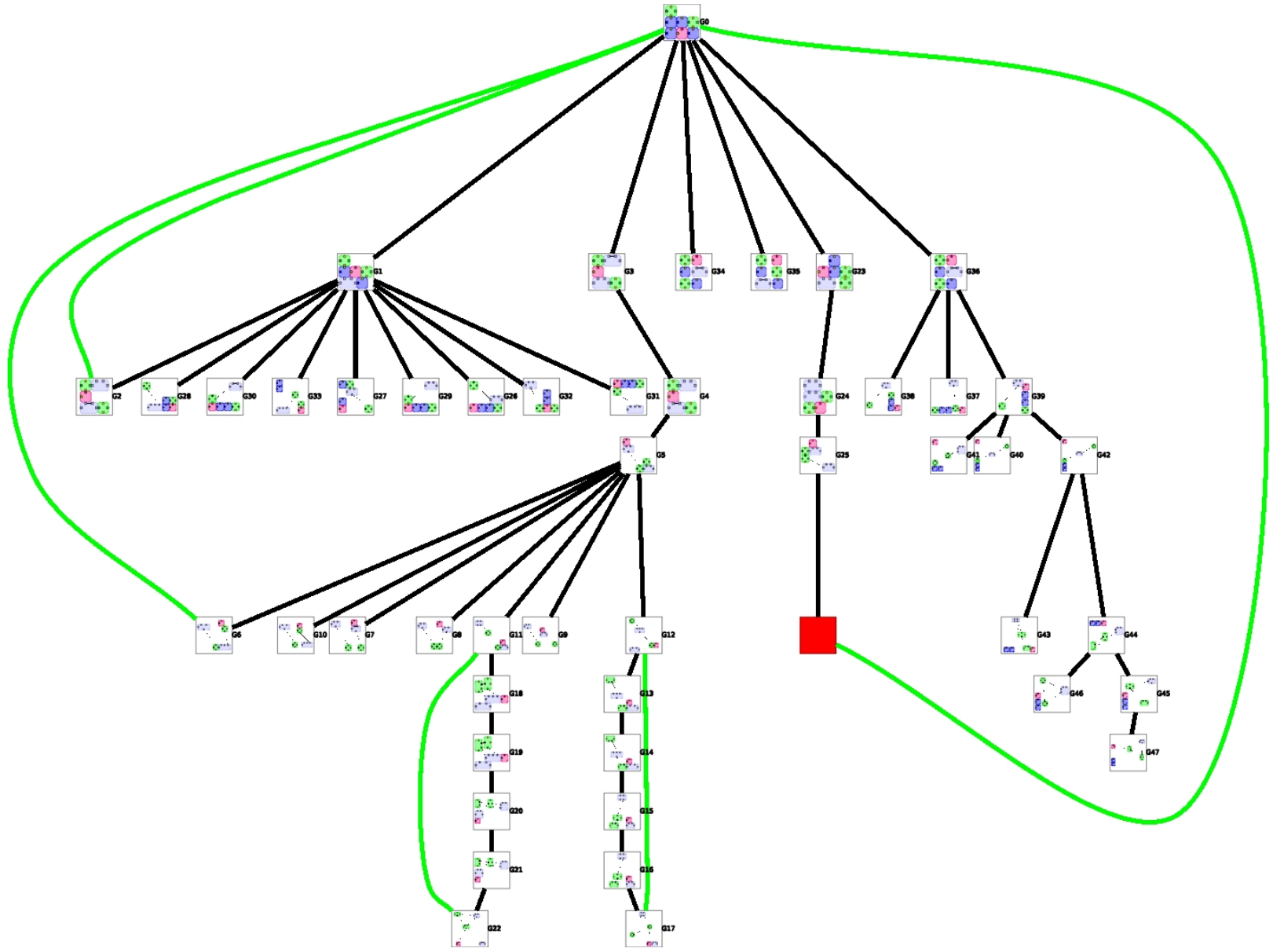
Confluence

- *Confluence* is heavy duty stuff – both conceptually and computationally
 - When combined with convergence it means « All roads lead to Rome »
 - Testing confluence requires identifying isomorphic copies of a graph

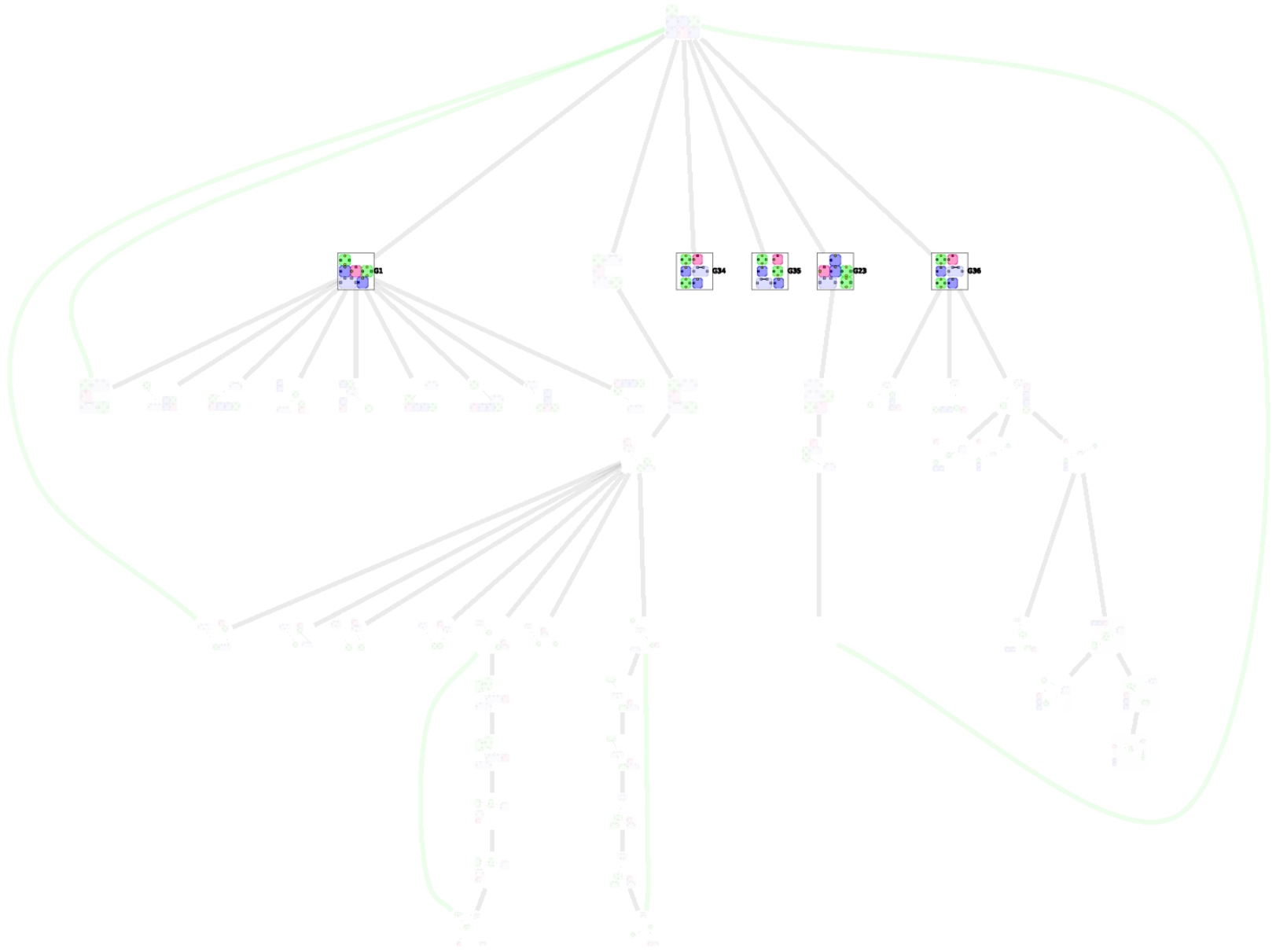
Confluence

- *Confluence* is heavy duty stuff – both conceptually and computationally
 - After identifying isomorphic copies, the derivation tree may be *folded* into a graph
 - Confluence is studied through pattern identification in the *folded* graph

Confluence



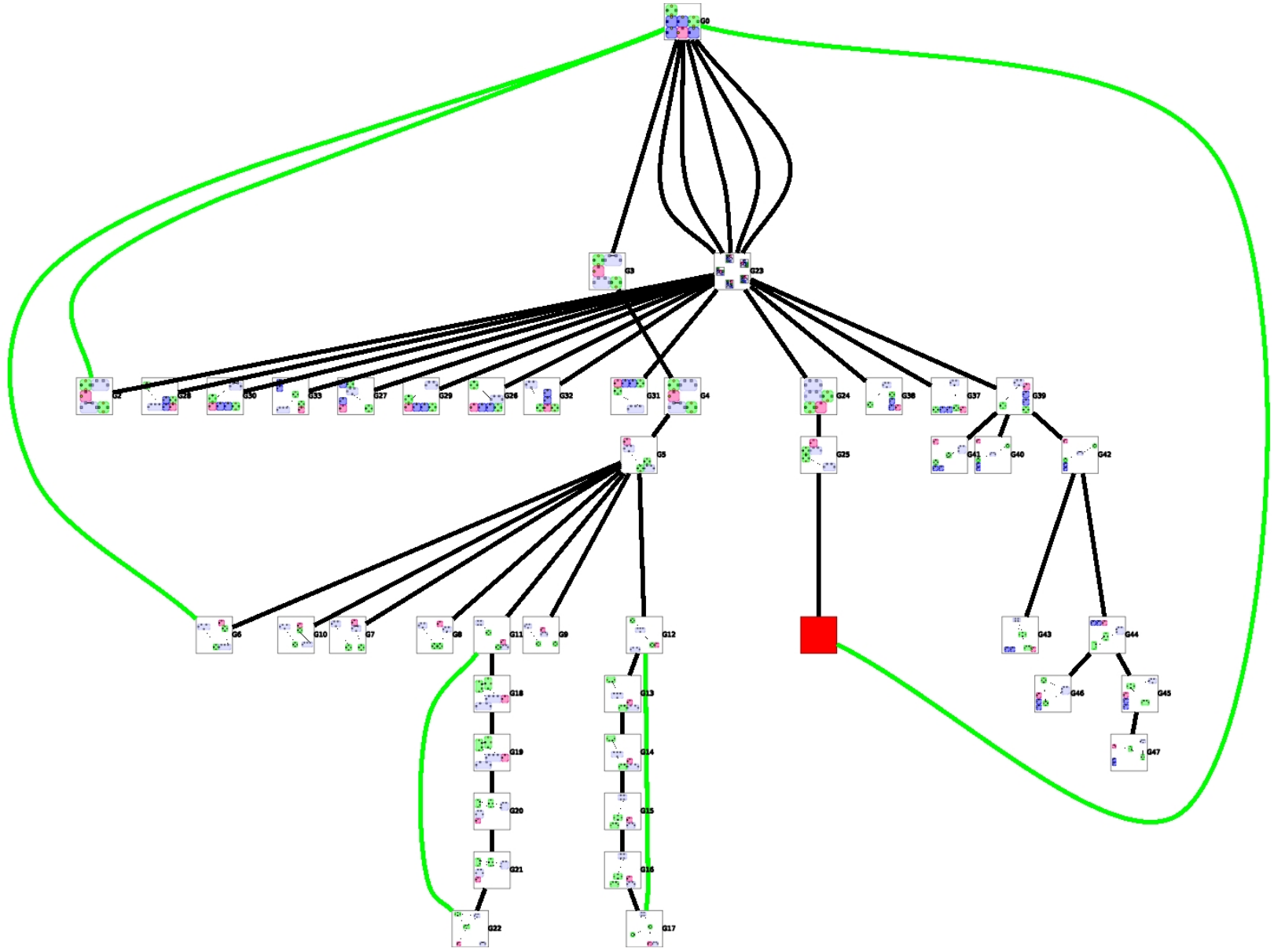
Confluence



Confluence



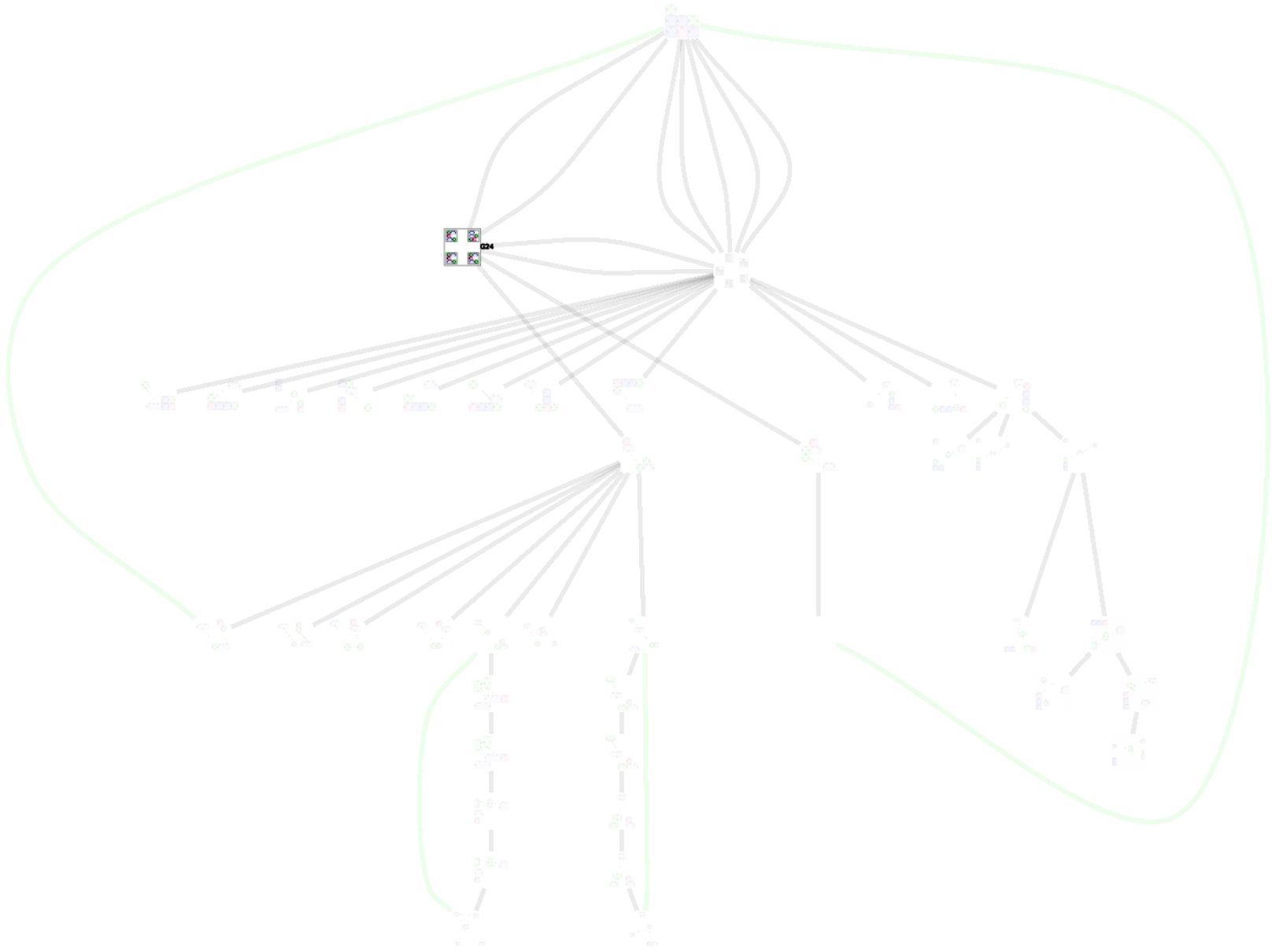
Confluence



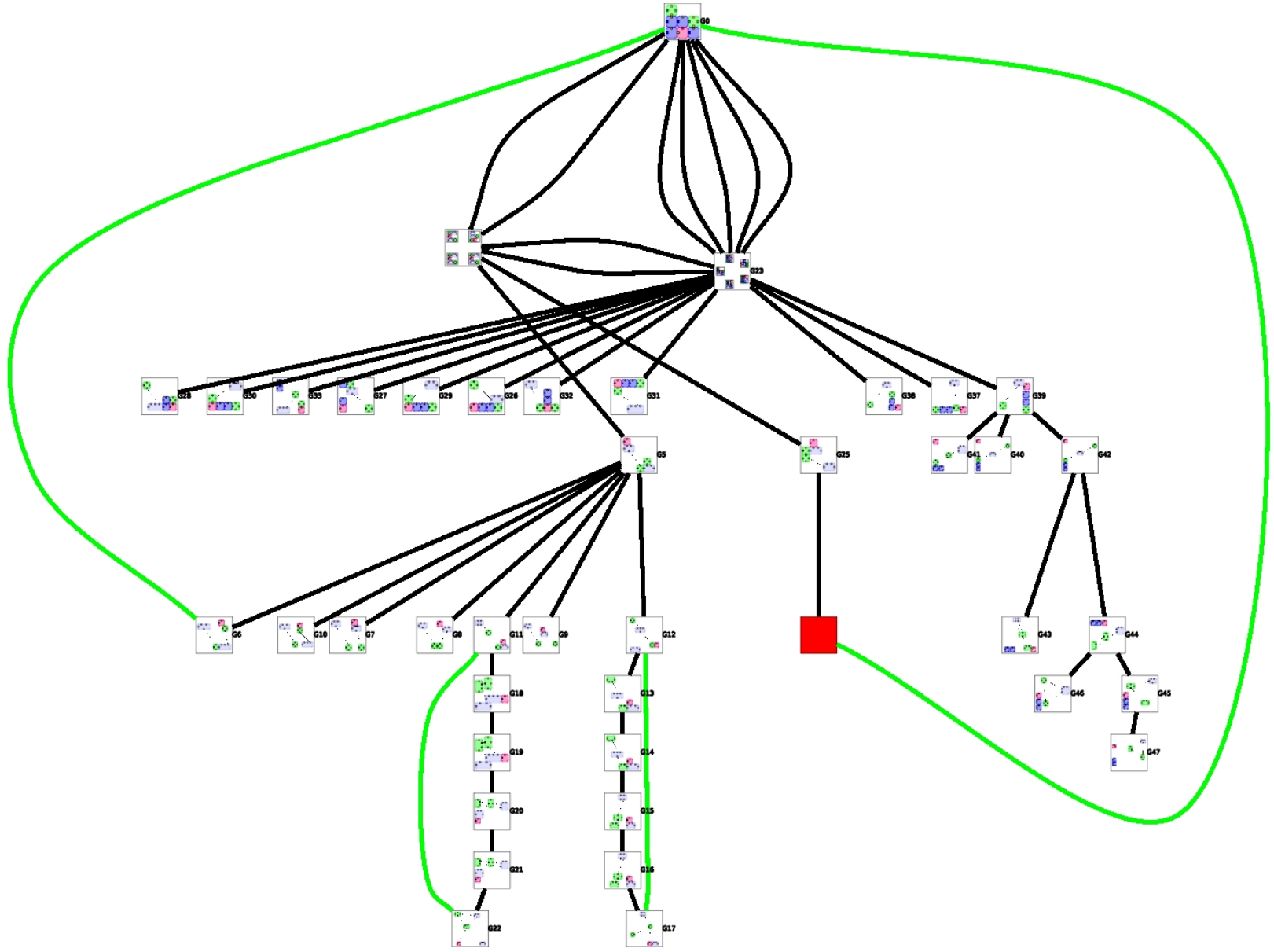
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Confluence



Confluence



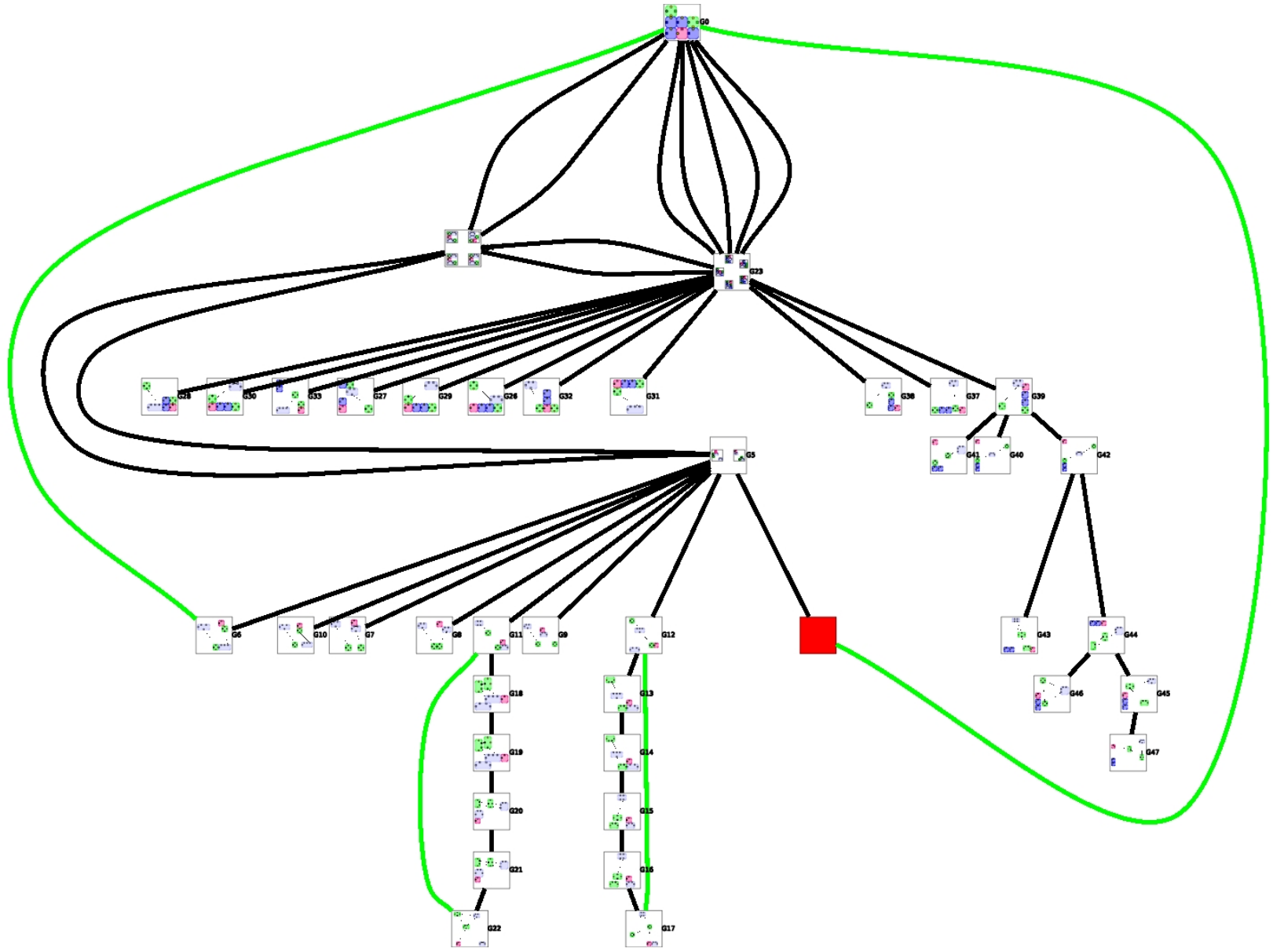
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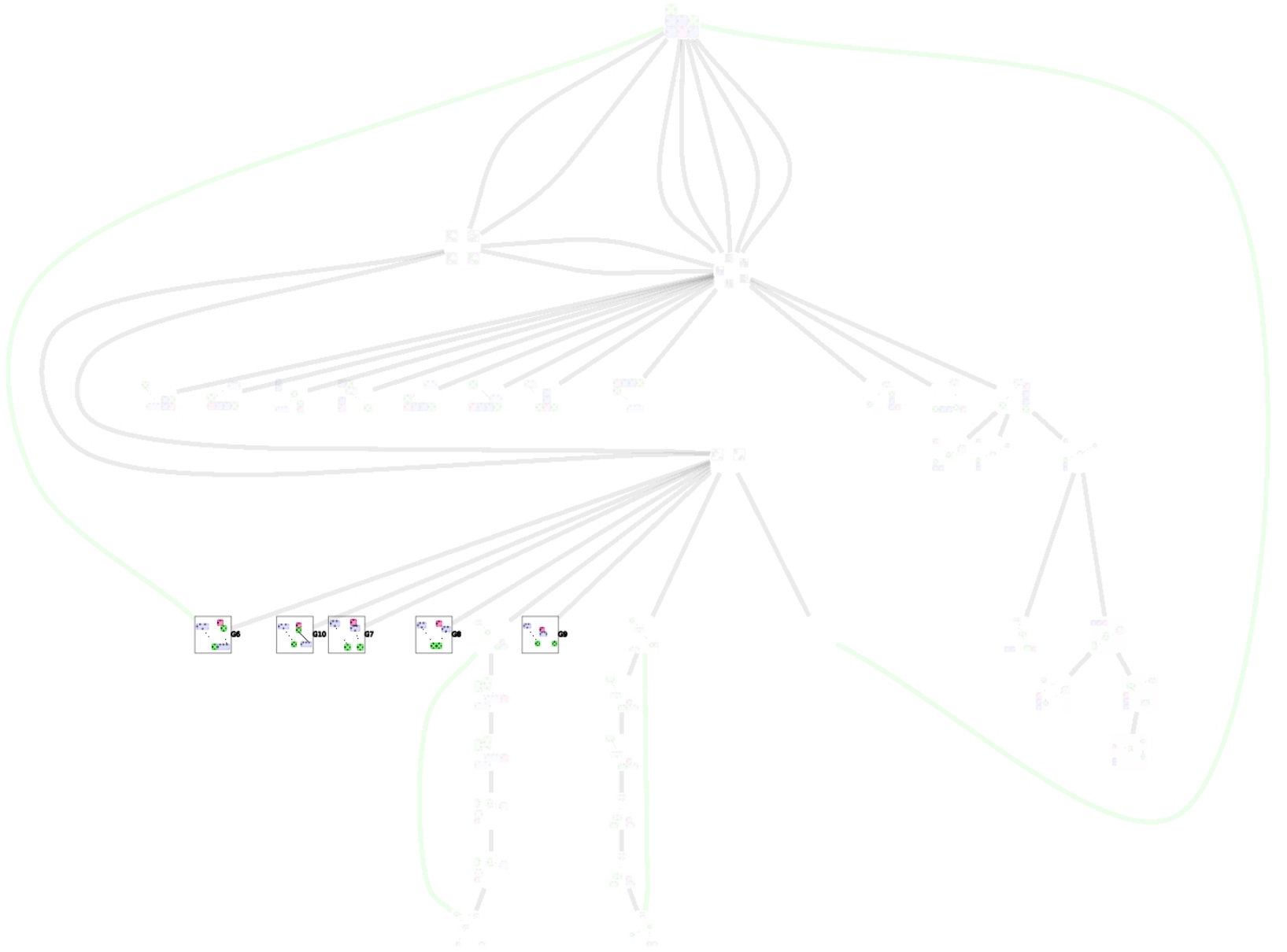
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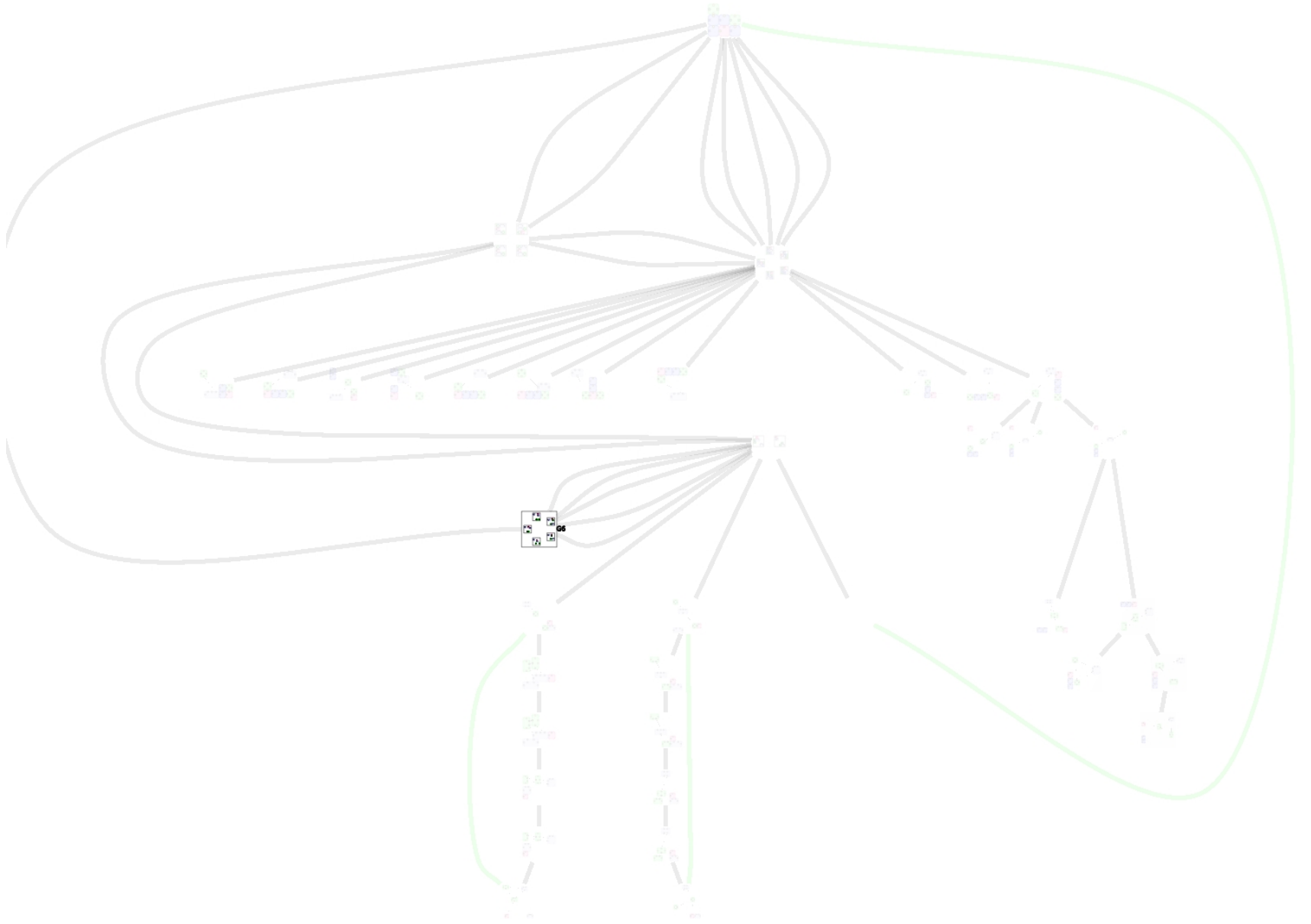
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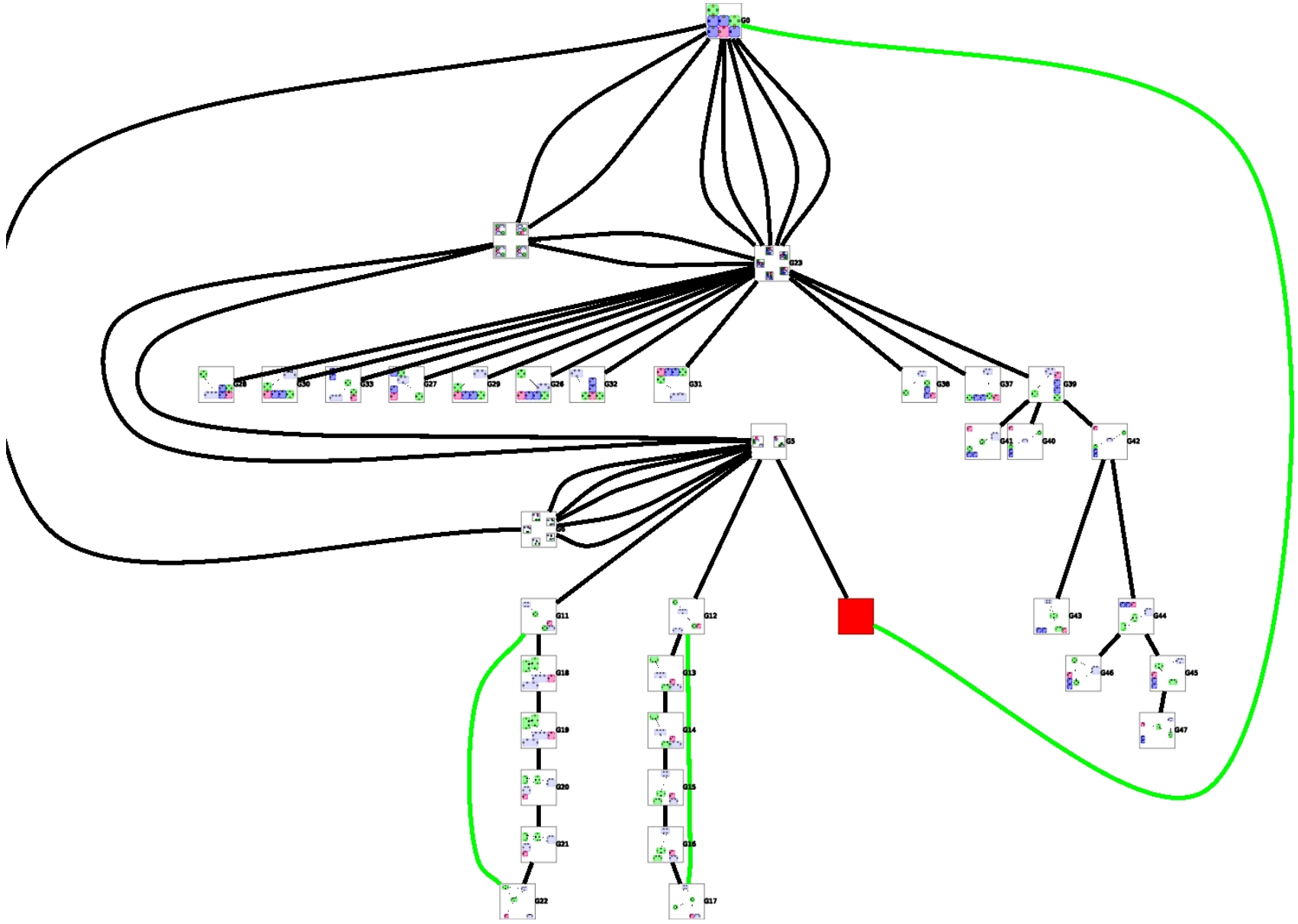
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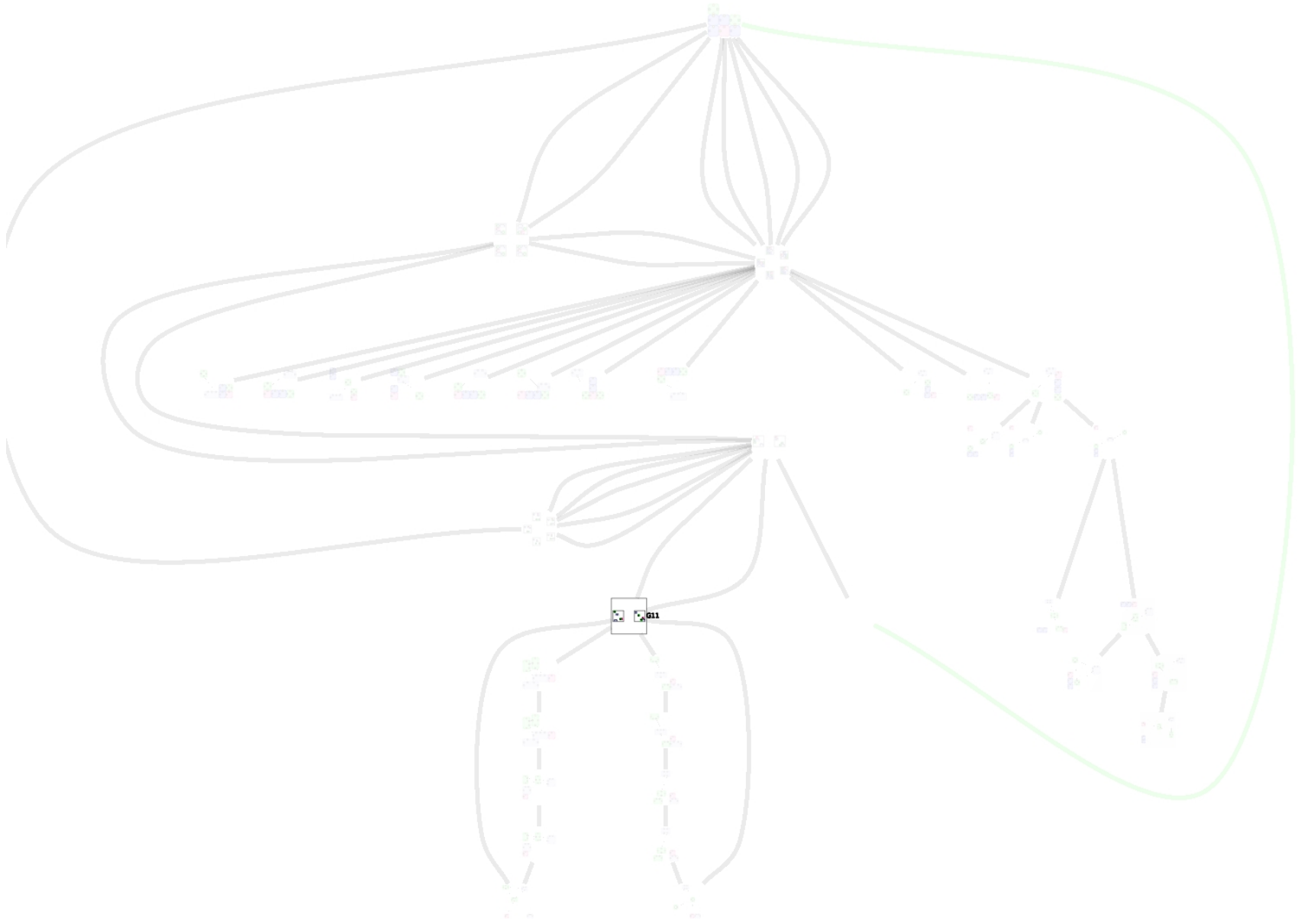
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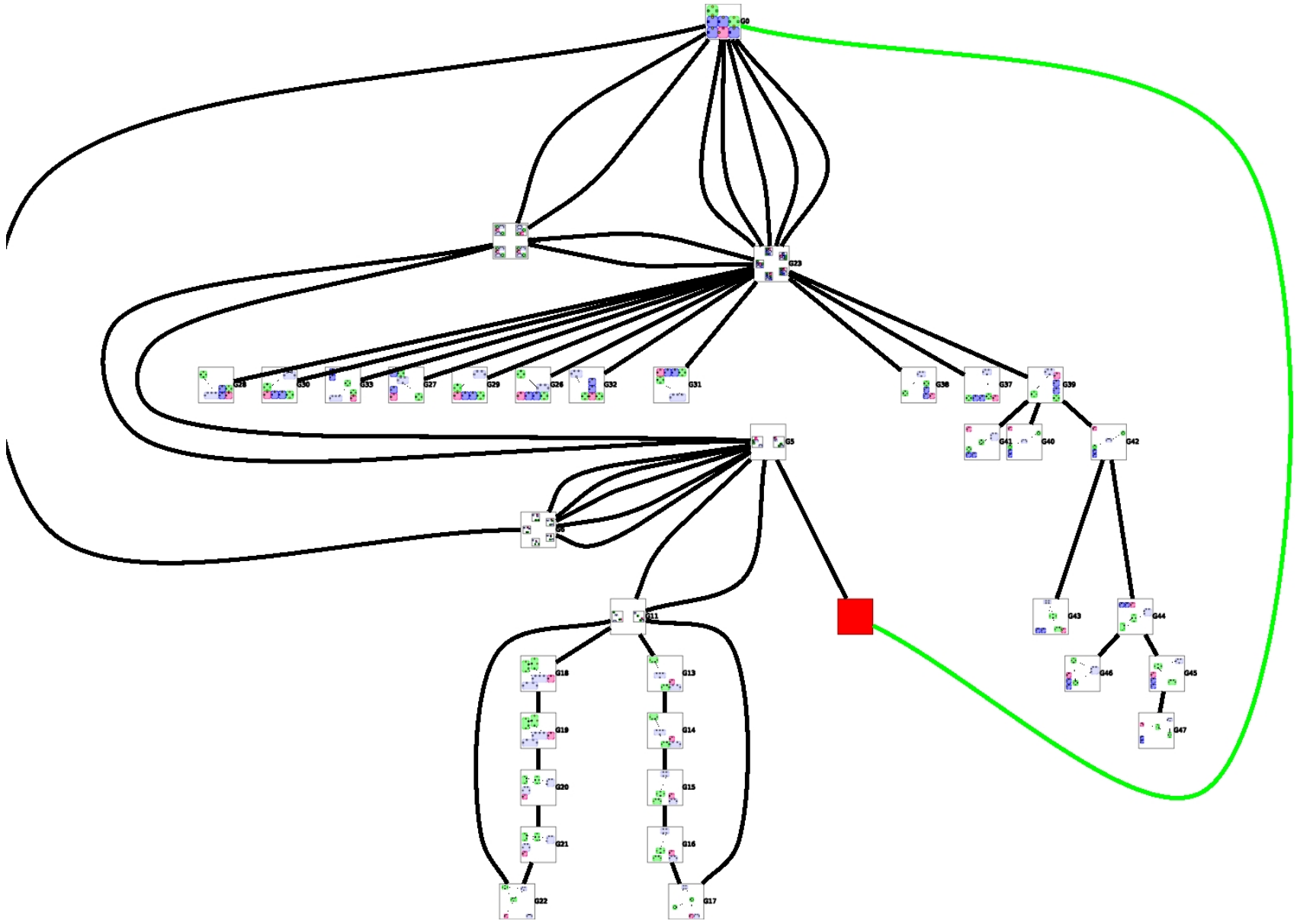
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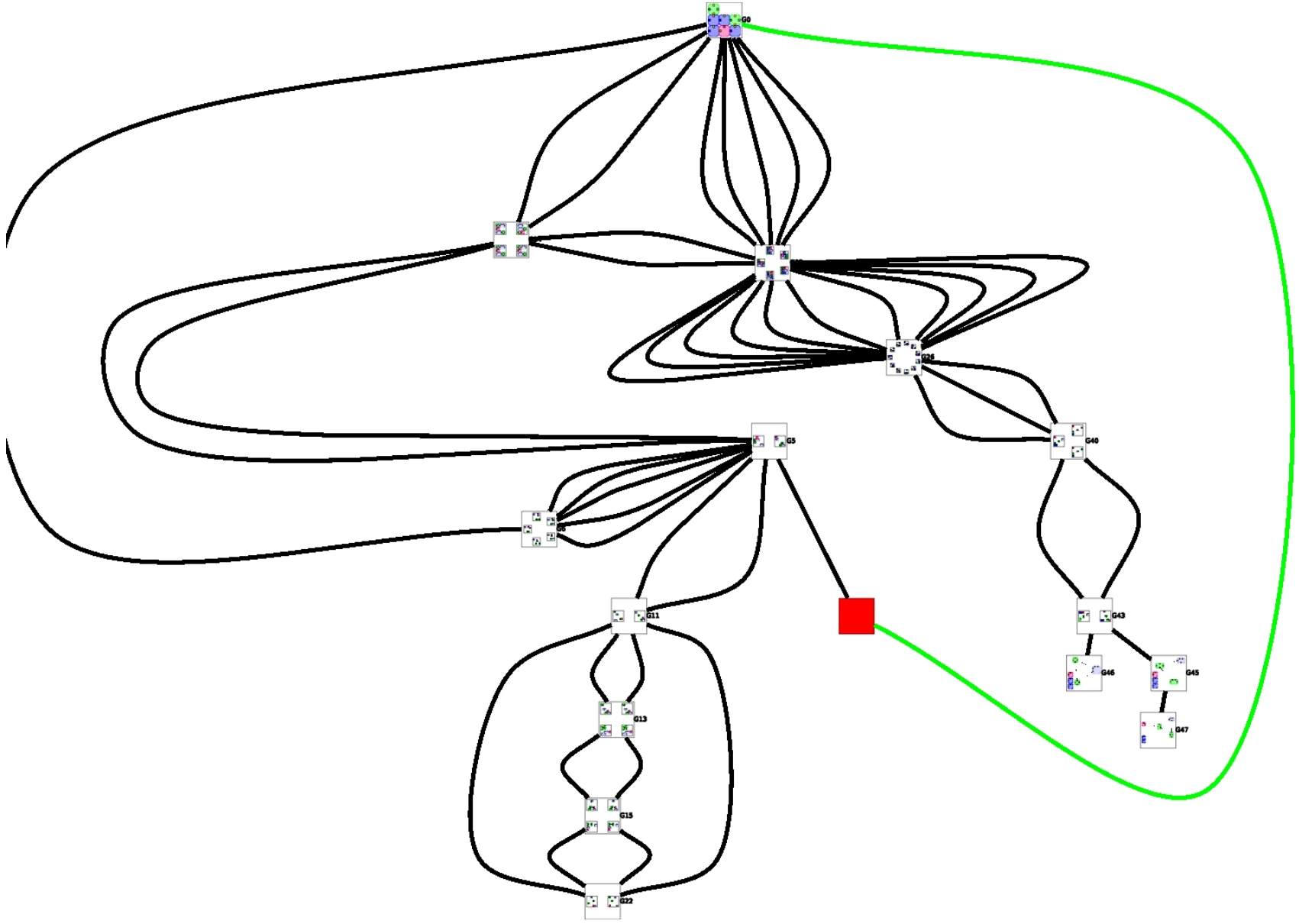
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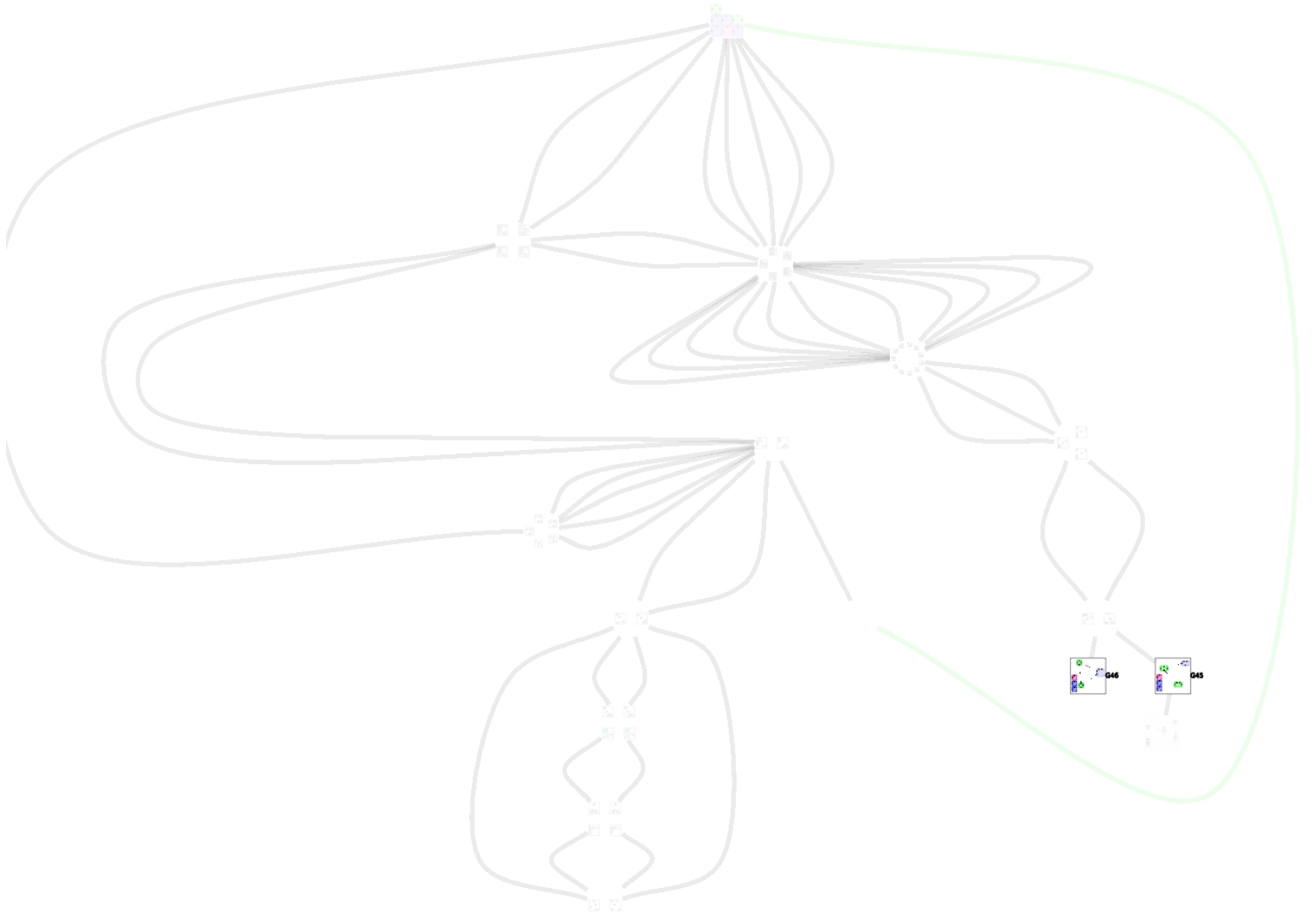
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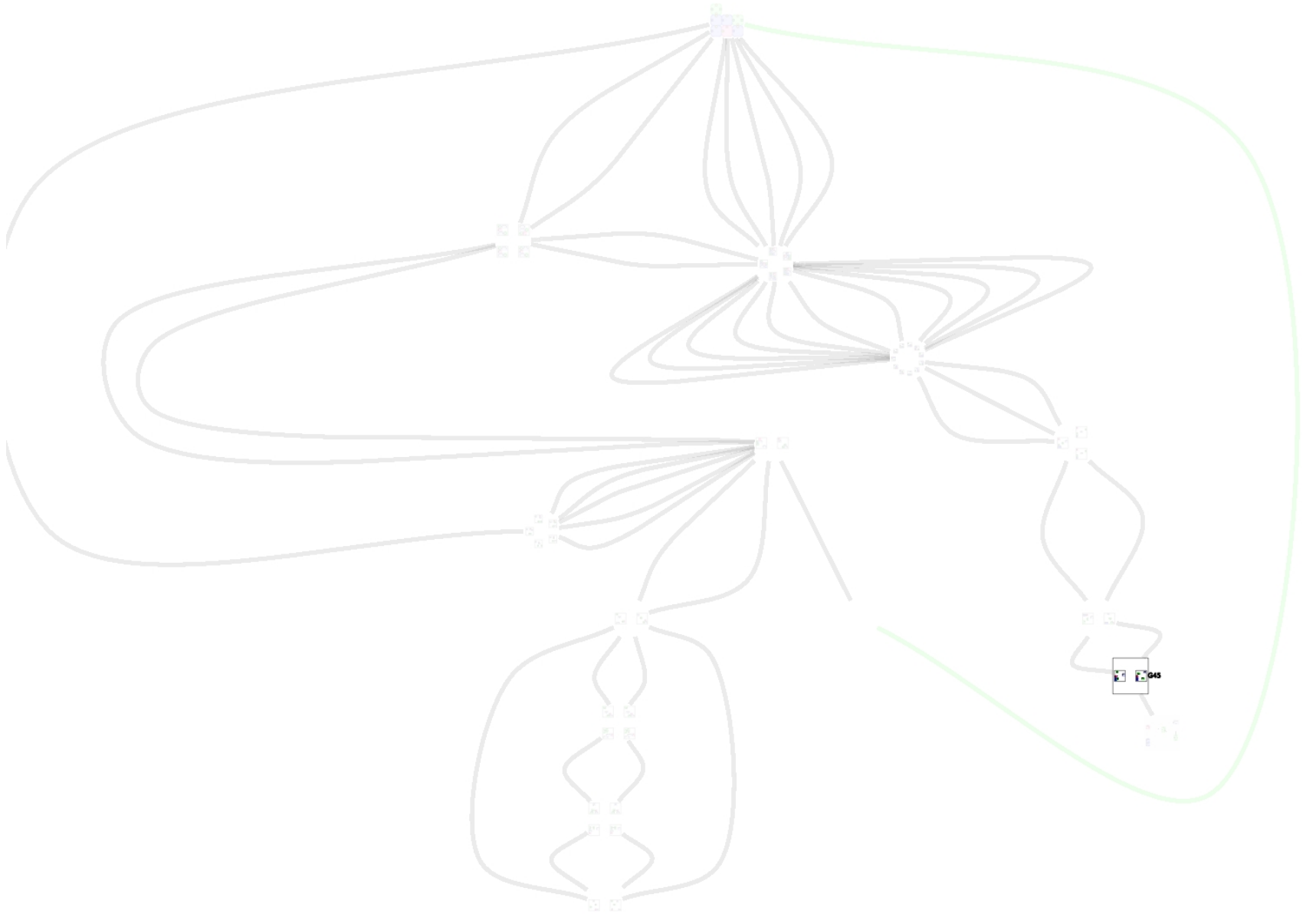
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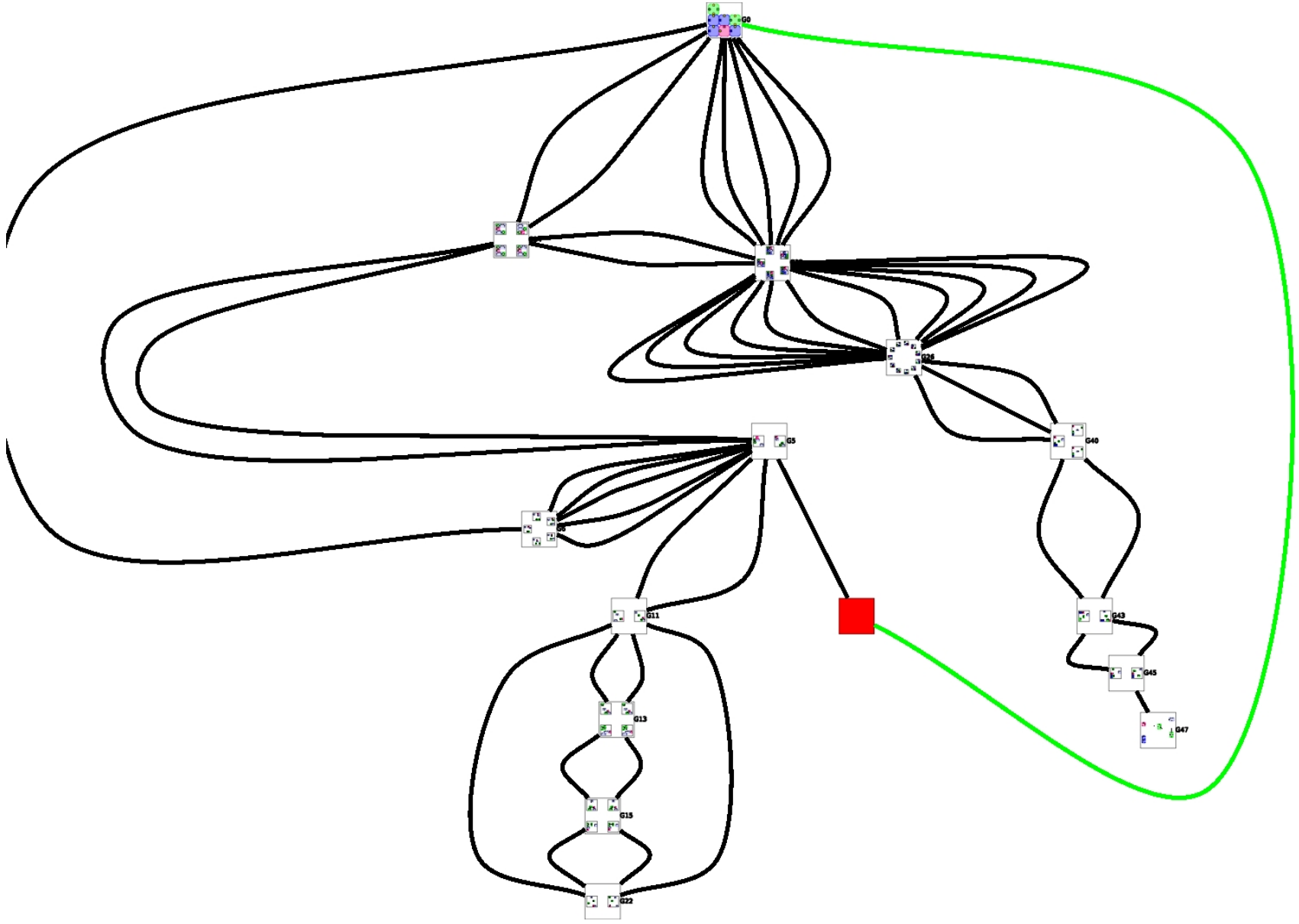
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Confluence



Confluence

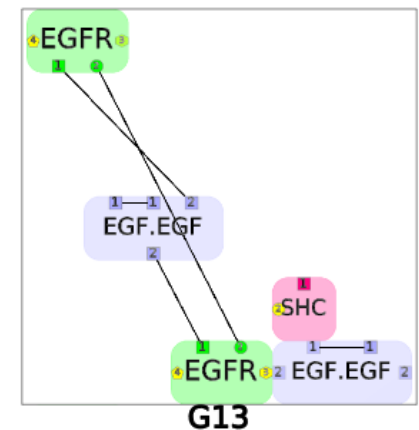
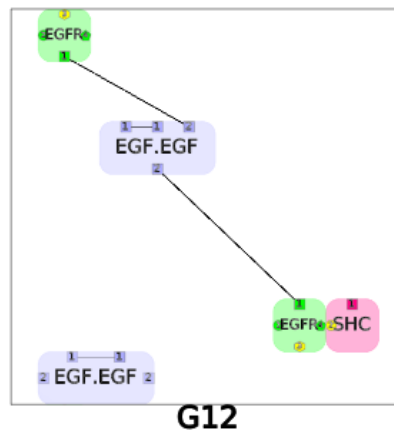
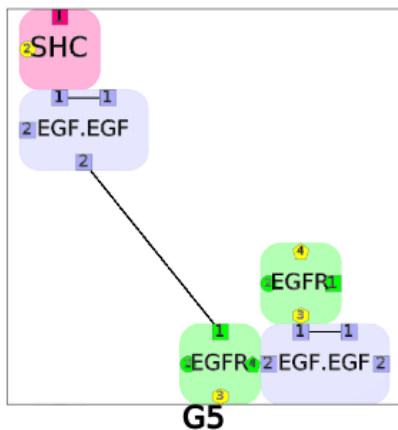
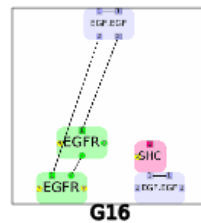
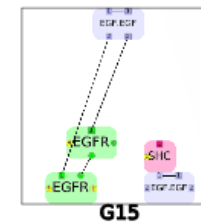
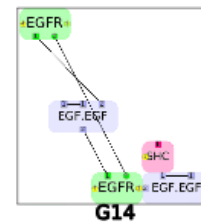
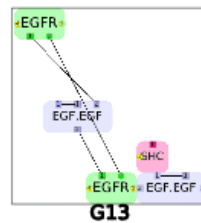
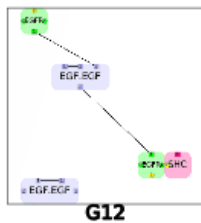
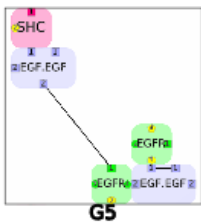


Visual encodings

- Node-link diagrams came as an obvious choice due to strong graphical conventions (from both user communities)
 - For graphs
 - For rules
- Similarly, the derivation tree is drawn using a classical top-down hierarchical layout

Visual encodings

- We introduced small multiples as an option to graph animation [Archambault et al. 2011]



Interaction

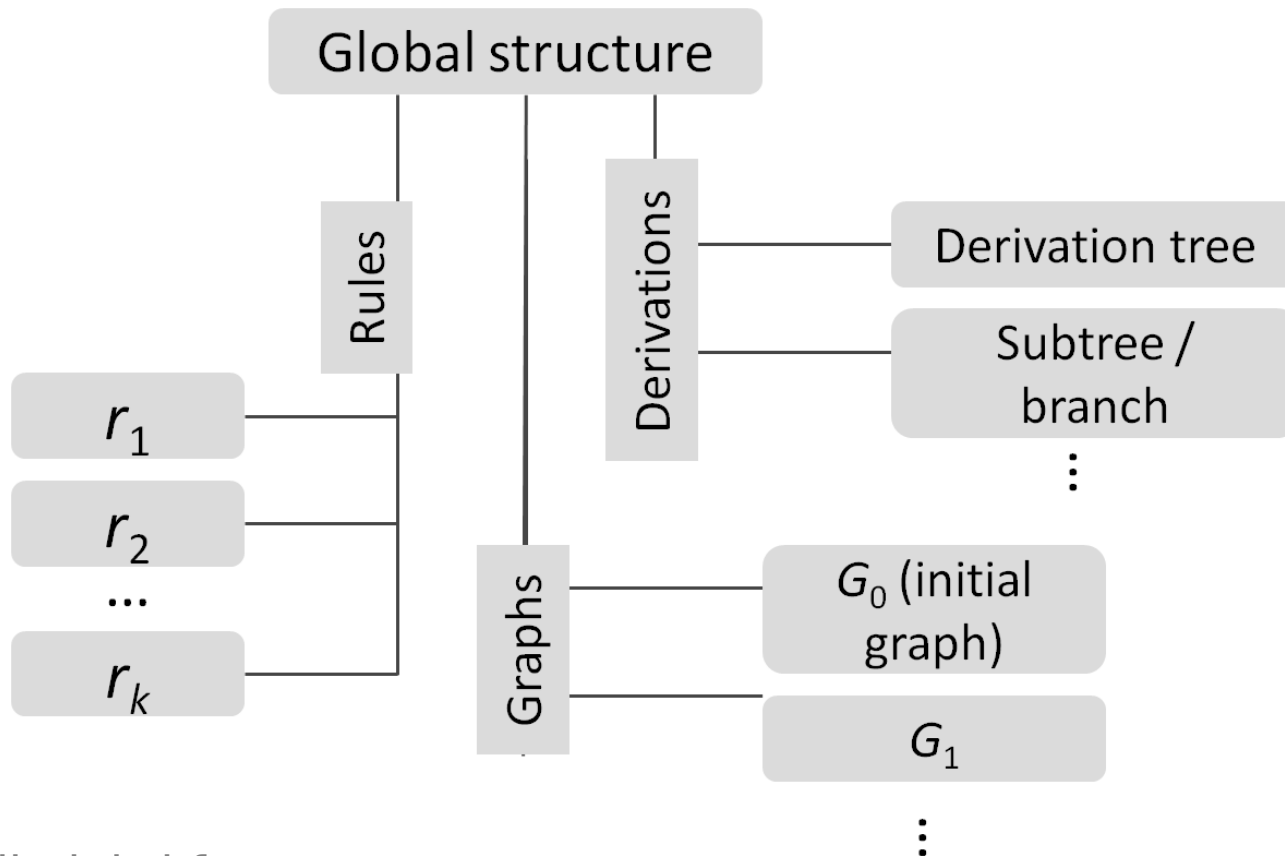
- Ease entities manipulation between views (drag & drop)
 - Rules / strategies dropped on graphs
- Tooltips to have a closer look at entites (rules, graphs) without having to instantiate views
 - For graphs
 - For rules
- Selection of entities *across* all views

Data structure

- Implementing the necessary underlying data structures is far from obvious
 - All graphs resulting from rule applications share a common pool of nodes and edges
 - Derivation tree: nodes contain graphs
 - Folded graph
 - Nodes in scatterplots *are* graphs – allows direct selection from/to derivation tree

Data structure

- Implementing the necessary underlying data structures is far from obvious



Discussion

- PORGY is quite unique in offering simulation steering using a derivation tree, as far as GRS are concerned
 - Compares to World Lines [Waser et al. 2010] in that respect
 - EGRF model was post-validated using combined GRS and parameter tracking
 - Visualization & Interaction vs text-based approaches
- The design of PORGY relies on long term user experience, based on Munzner's formal approach to viz design
 - Potential impact on both GRS and domain application communities

Future Work

- Layout stability issues
 - Difficult because incremental change take place over a hierarchy
 - The drawing of rules often relies on implicit assumptions: no universal layout for rules
- Extend model tracking to multiple parameters
- Graph folding
 - Scalability issues with subgraph isomorphism

Thanks



- Download the tool <http://tulip.labri.fr>
(search for Projects/PORGY)
- Ask for a live demo
- {Bruno.Pinaud, Guy.Melancon}@labri.fr