MiniClean: A Single-Machine System for Cleaning Big Graphs

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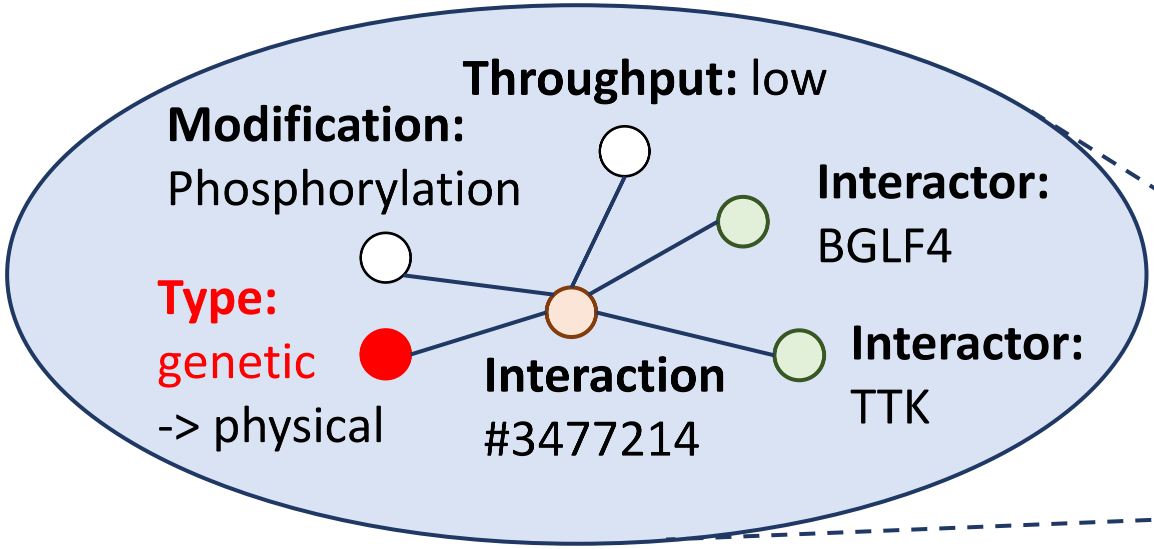
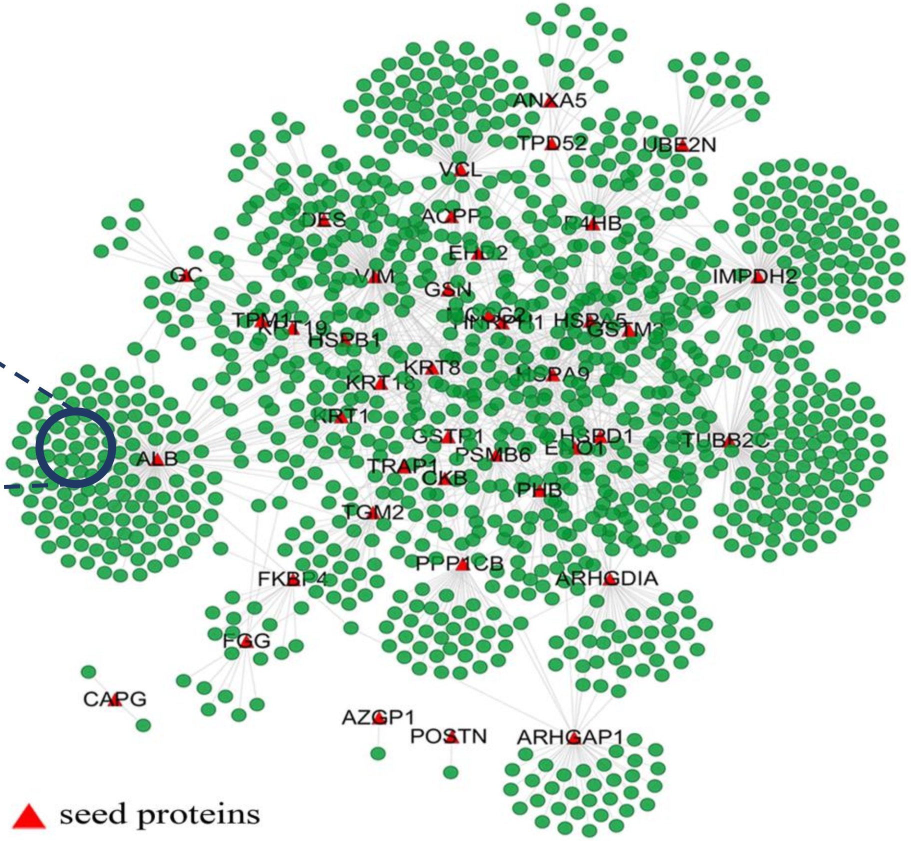
University of Edinburgh, Beihang University

- **Introduction**: 00’00 – 08’55
- **Live Demo**: 08’55 – 12’21
- **Evaluation**: 12’21 – 13’38

Graph Data Quality and Graph Applications



A mislabeled instance in BioGRID[2]



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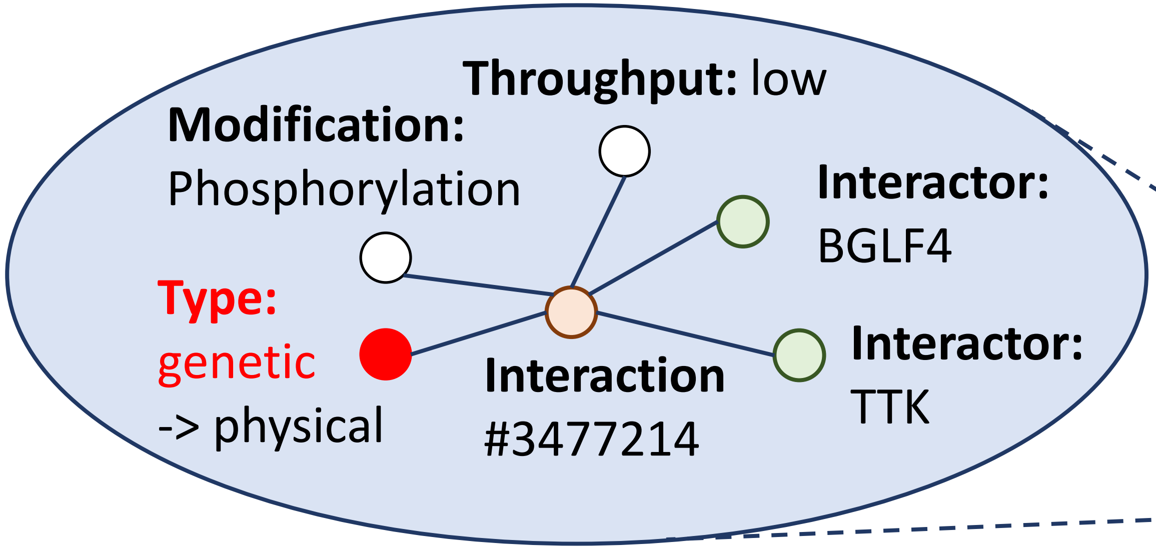

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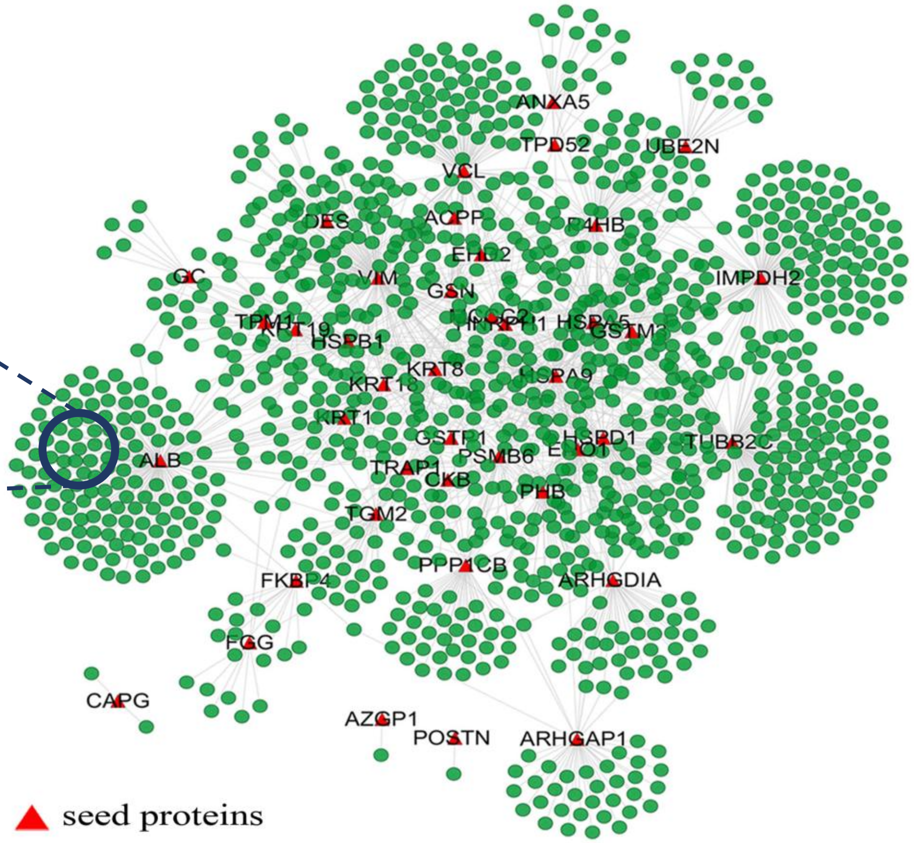

- *Errors (e.g., duplicates, conflicts) are common.*
- *Errors can misguide data-driven decision making.*

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Graph cleaning is crucial

Approaches to Graph Cleaning

- **Strawman 1**: ML models (e.g., Ditto, KGClean).
  - Transform graphs into embeddings.
  - Detect errors (duplicates/conflicts) via binary classification.
  - Predictions are probabilistic and hard to explain.
- **Strawman 2**: Logic rules.
  - Apply rules via pattern matching and predicate verification.
  - Deduce dependencies to detect and correct errors.
  - Difficult to find rules that cover all the cases.

Take advantage of both ML and logic reasoning

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- **Our Solution**: ML models + Logic rules.
  - $M_1(x_0, x_1) > \delta_1 \wedge X_1 \rightarrow x_4.\mathrm{val} = \mathrm{physical}$
  - $x_4.\mathrm{val} = \mathrm{genetic} \wedge X_2 \rightarrow M_2(x_0, x_3) > \delta_2$

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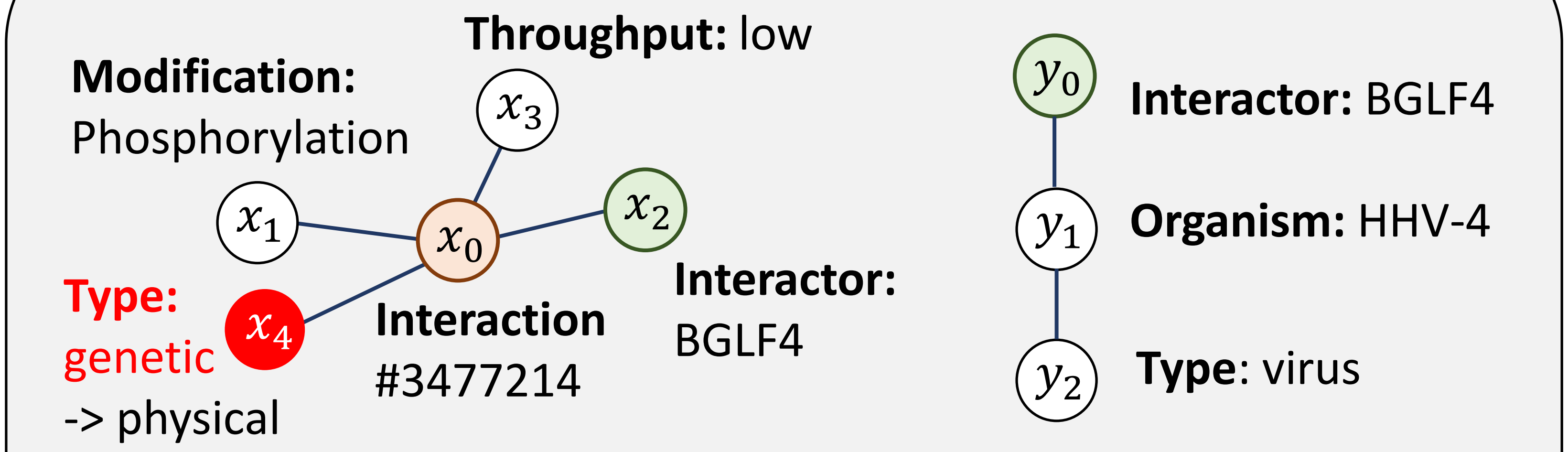
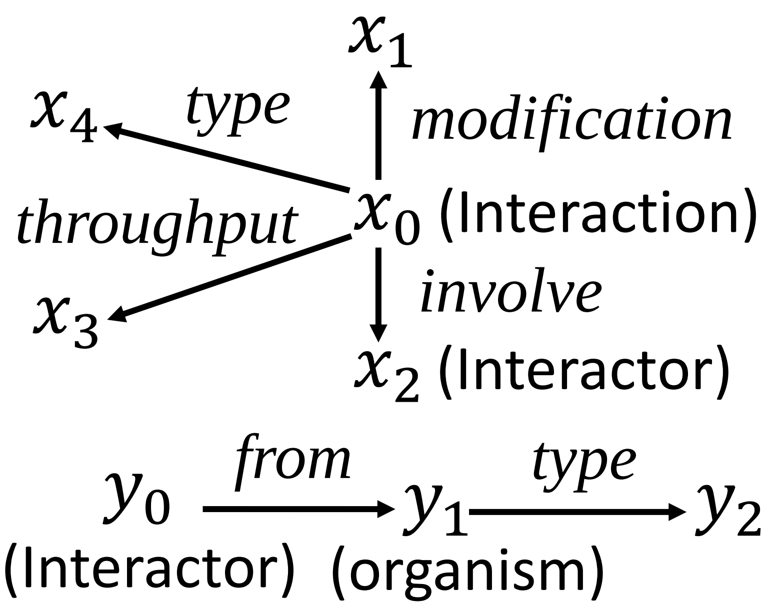
Approaches to Graph Cleaning



$$X_1 \coloneqq < x_2.\mathrm{id} = y_0.\mathrm{id} \wedge y_2.\mathrm{val} = \mathrm{virus} >$$



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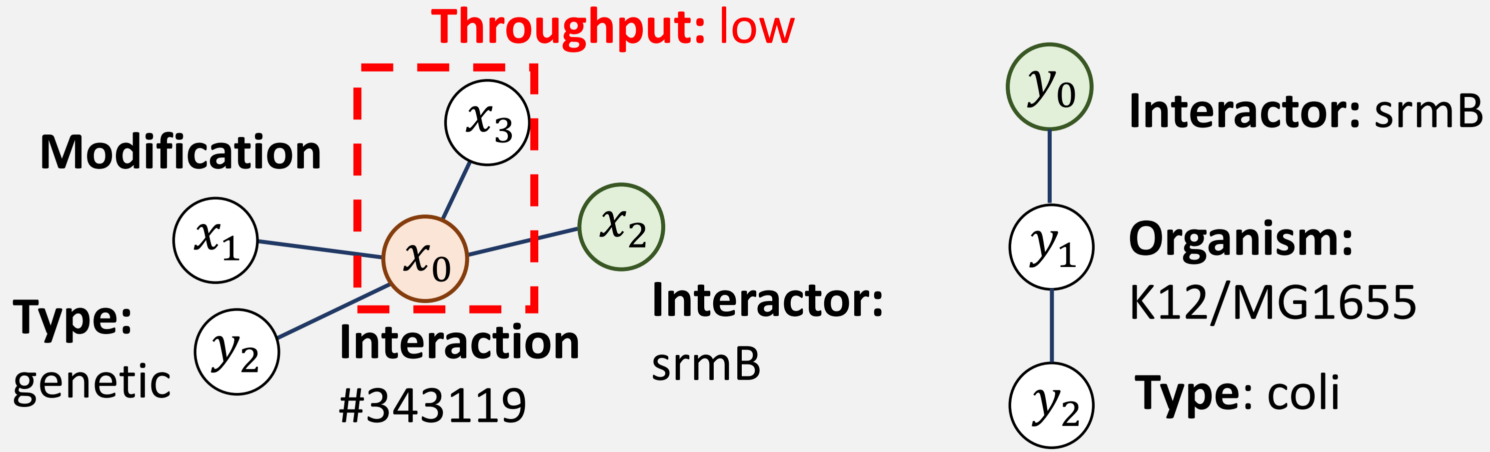

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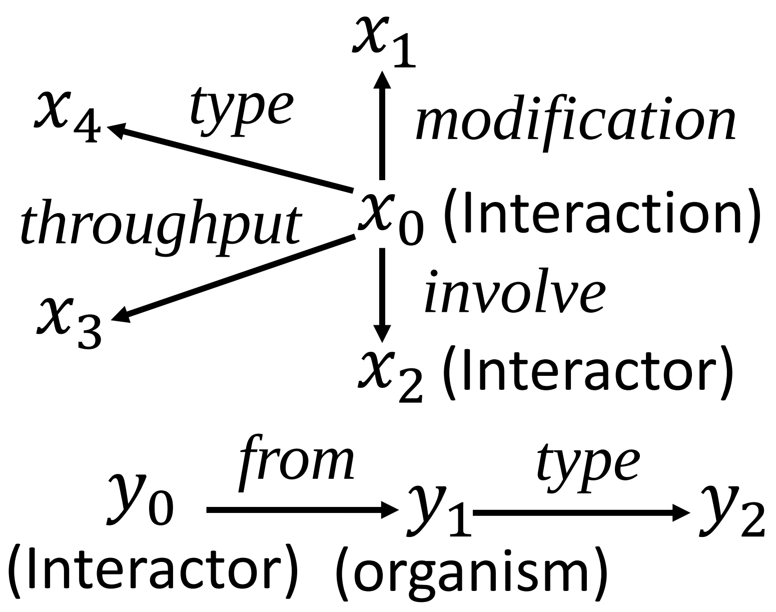

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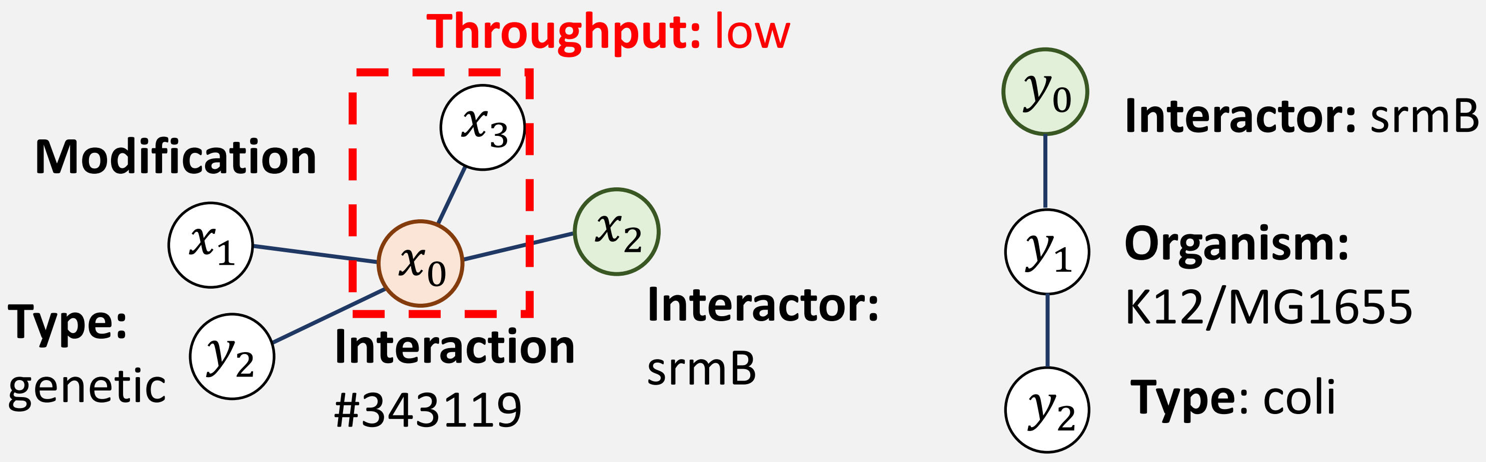

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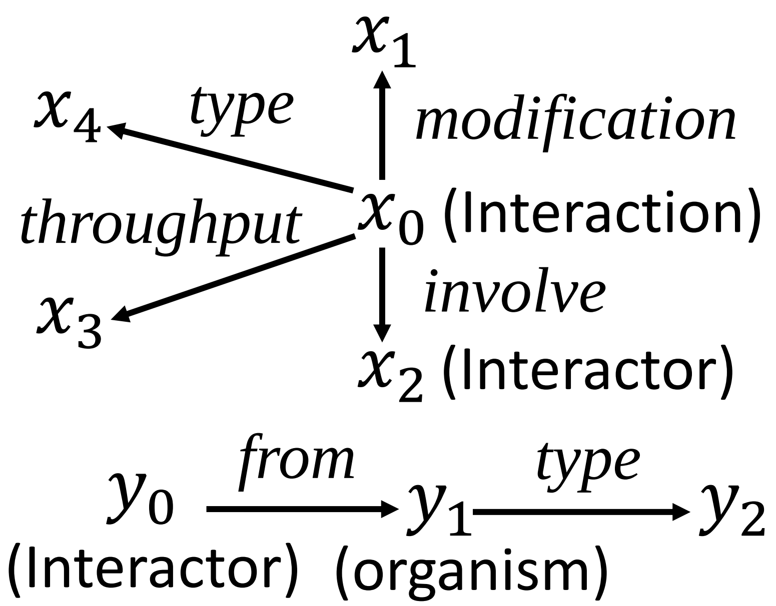

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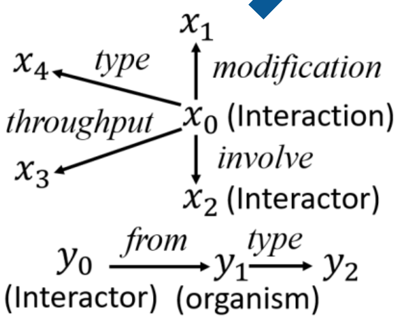
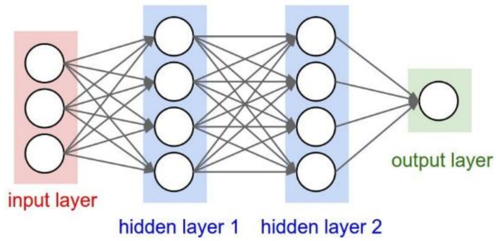
- *Generalizability (ML)*
- *Reliability (Logic)*
- *Explainability (Logic)*

Graph Cleaning Rules (GCRs)

$\mathcal{Q}[x_0, y_0](X \rightarrow p_0)$





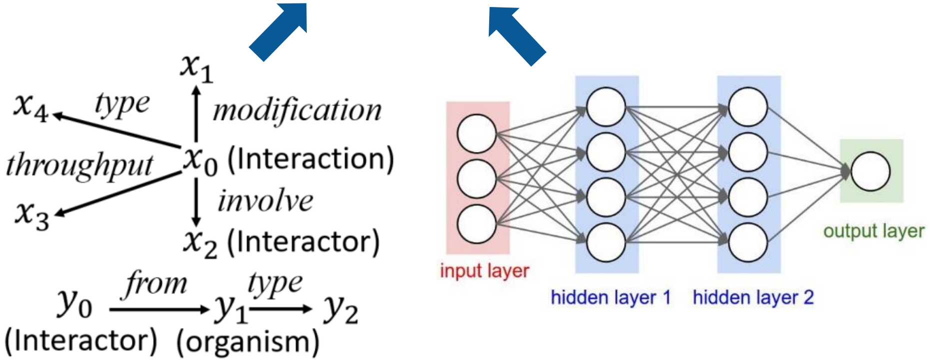
- ✓ $\mathcal{Q}[x_0, y_0]$: dual star pattern
- ✓ $X \rightarrow p_0$: dependency
- ✓ X: precondition (conjunction of predicates)
- ✓ p_0: consequence (predicate)

Dependency deduction:

- ML predicates $M(x.\bar{A}, y.\bar{B})$: for ML classification & regression
- Variable and constant predicates $x.A \oplus y.B, x.A \oplus c$: for value associations

Graph Cleaning Rules (GCRs)

$Q[x_0, y_0](X \to p_0)$



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Functionalities

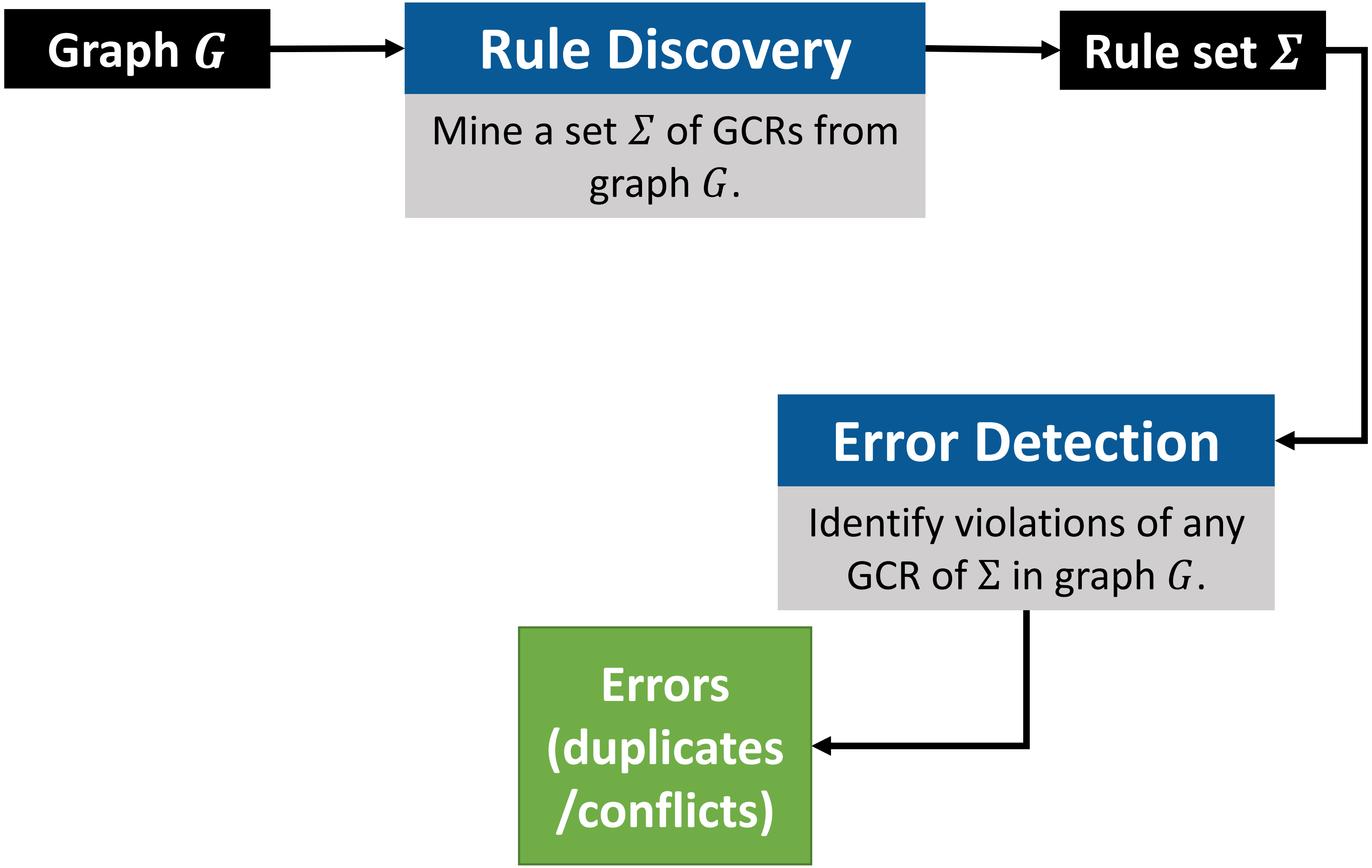
- ✓ *Conflict resolution*
- ✓ *Entity resolution*
- ✓ *ML explanation*

Cleaning with GCRs

Graph G → **Rule Discovery** → **Rule set Σ**

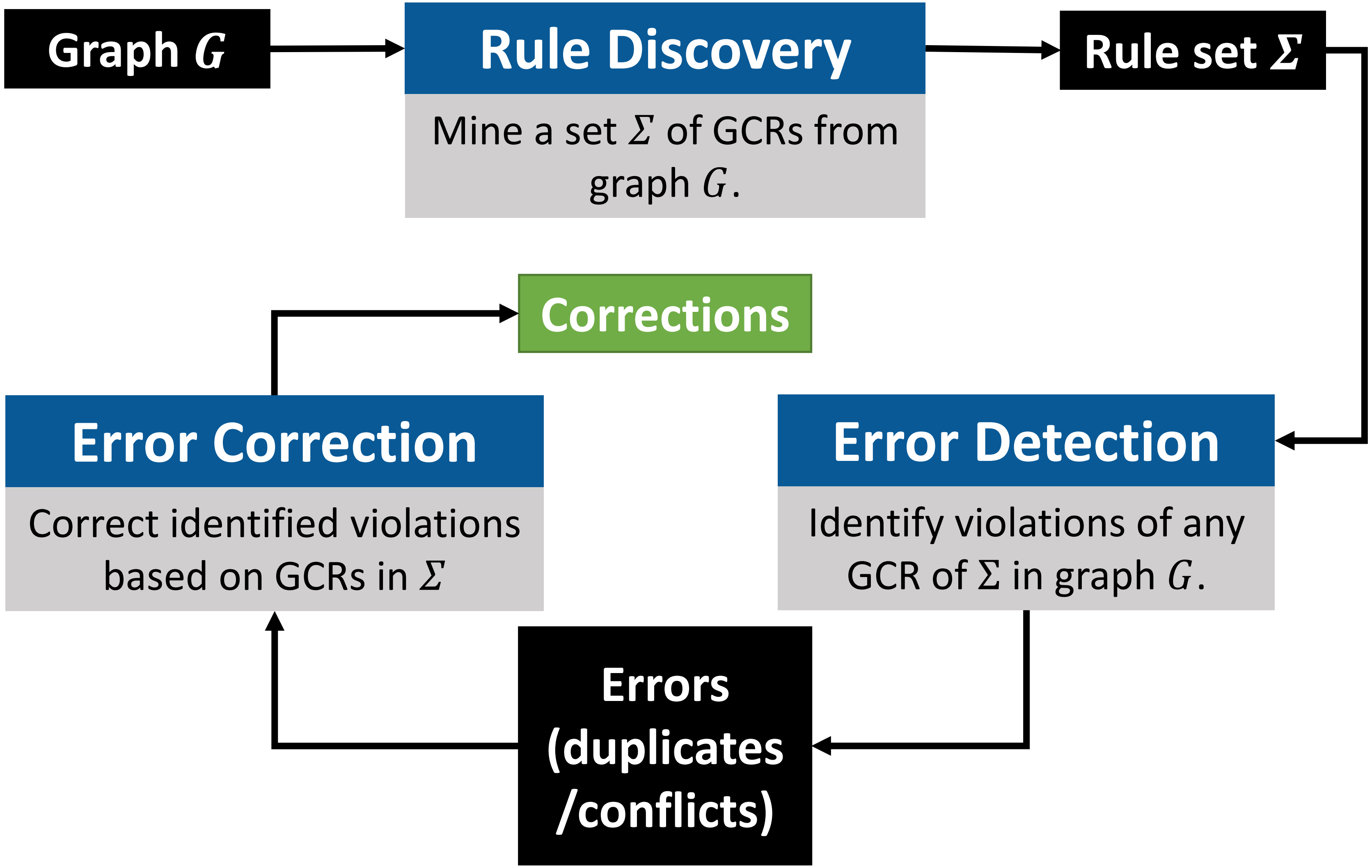
Mine a set Σ of GCRs from graph G.

Cleaning with GCRs



The workflow of graph cleaning

Cleaning with GCRs



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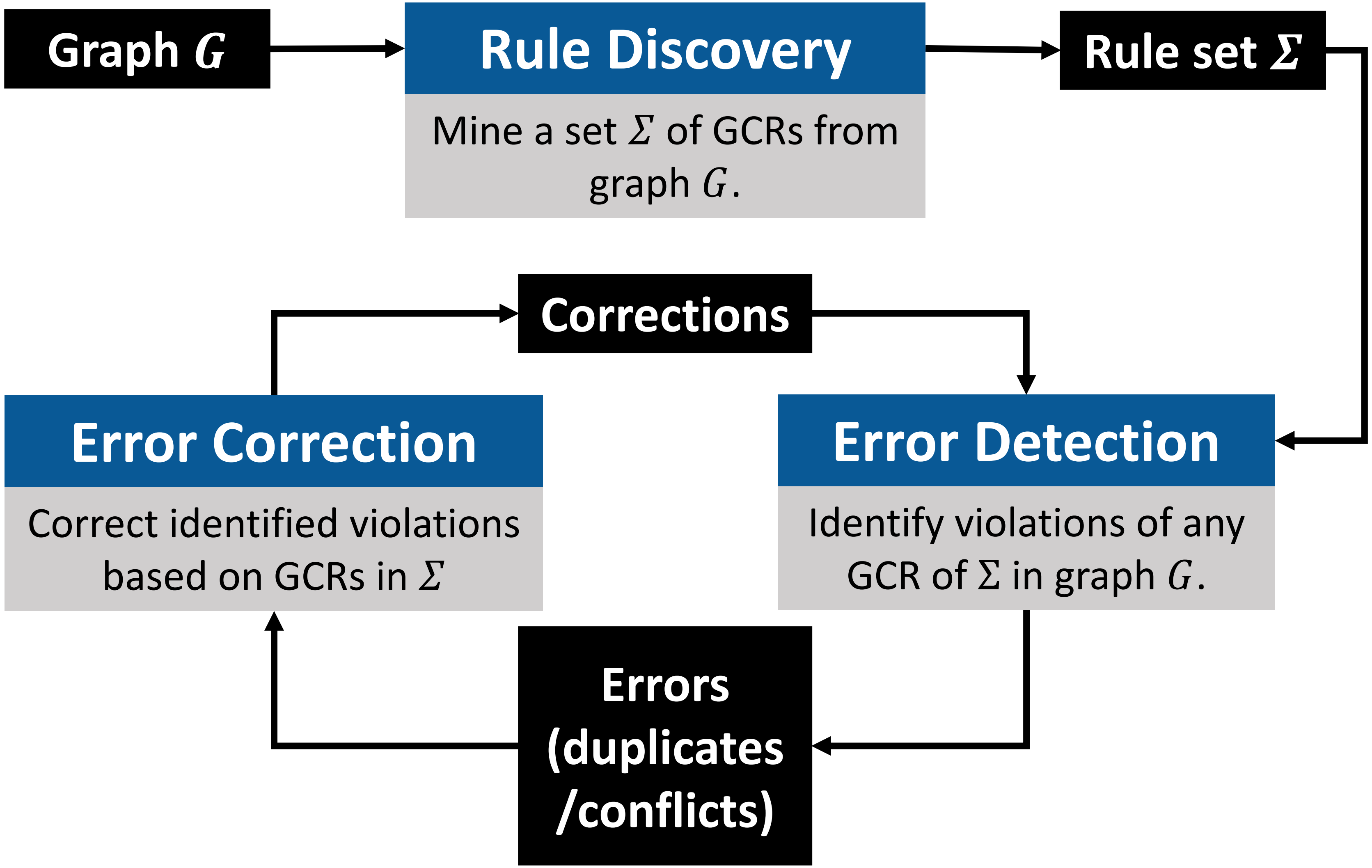

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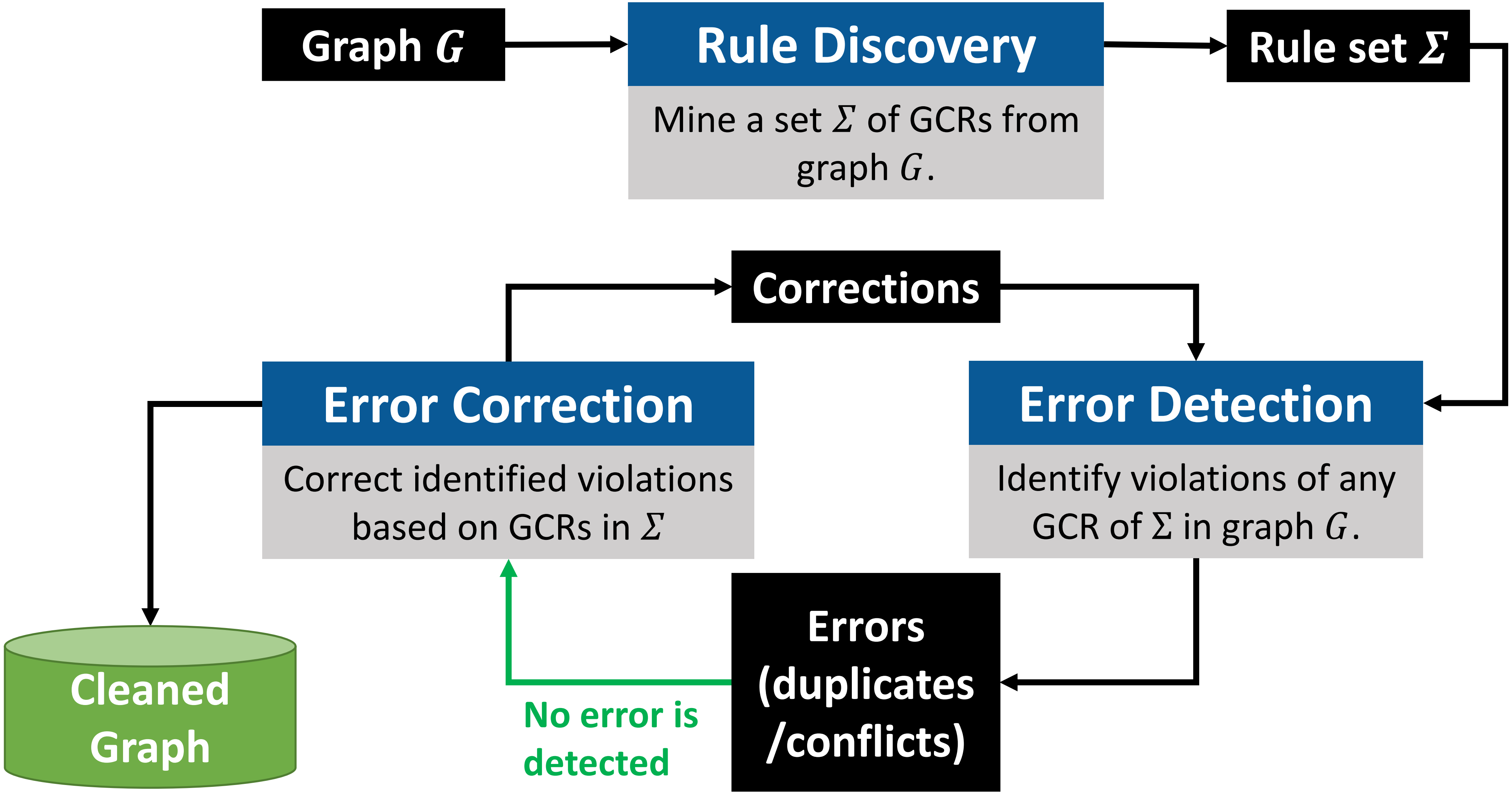


The workflow of graph cleaning

Single-machine solutions are often preferred:

- **Physical constraints on deployed hardware.**
  - A cluster on premise may not be feasible, e.g., at an edge location.
- **A cloud deployment is not viable.**
  - Prohibitive cost: network bandwidth at $0.05–0.09 per GB[1].
  - Privacy concerns.

[1] https://aws.amazon.com/pricing

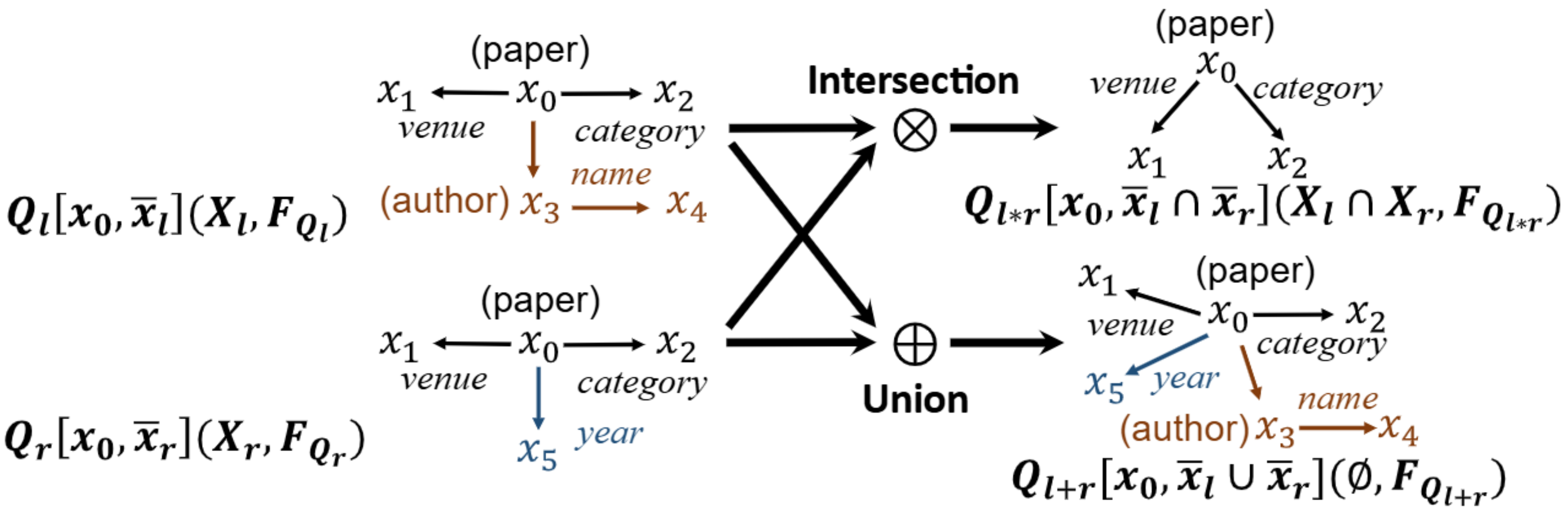
Single-machine graph cleaning is a practical need!

Single-Machine Graph Cleaning: Challenges

- **Computation heavy.**
  - > 9h processing time on a 32-node cluster.
- **Excessive intermediate data.**
  - > 150GB intermediate result, way exceeding the memory capacity of a typical machine.
- **Parallel model for maximum resource utilization.**
  - Idle caused by I/O, data transfer, and task dependencies.

No prior single-machine systems can handle the task!

Optimization 1: Bundled Processing



- ✓ **Motivation**: Repetitive computation by matching common substructures.
- ✓ **Solution**: Bundle similar patterns into a group and match them together.

Optimization 2: Data Compression

Conditional succinct matches

Matches			Conditions		
$x_0.\mathrm{id}$	$x_1.\mathrm{val}$	$x_2.\mathrm{val}$	$x_4.\mathrm{val}$	$x_0.\mathrm{title}$	$x_5.\mathrm{val}$
u_3	OSDI	CS	{J, S}	MR	null
u_4	OSDI	CS	{J, S}	GFS	null
u_1	OSDI	null	{M, P, J, S}	TF	2016
u_2	OSDI	null	{M, P, J, S}	tf	2016

$\Big\}$ Filtered out by $x_2.\mathrm{val} = \mathrm{CS}$

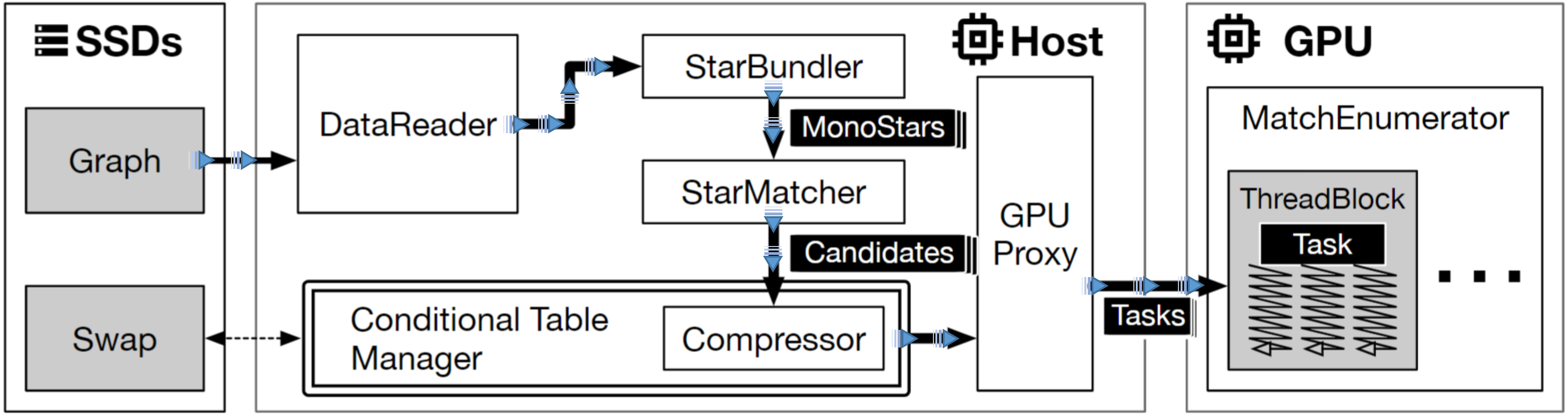
Unfolded matches

$x_0.\mathrm{id}$	...	$x_4.\mathrm{val}$	...
u_3	...	J	...
u_3	...	S	...
...	...	...	...

- ✓ **Motivation**: Intermediate data has up to $O(|V|^{|Q|})$ materialized candidates.
- ✓ **Solution**: Conditional succinct table for compression.

Reduce I/O overhead by at least 4.7×

Optimization 3: Pipelined Architecture



Stage 1
Star Matching

Stage 2
Match enumeration

Maximally overlapping I/O, CPU and GPU operations

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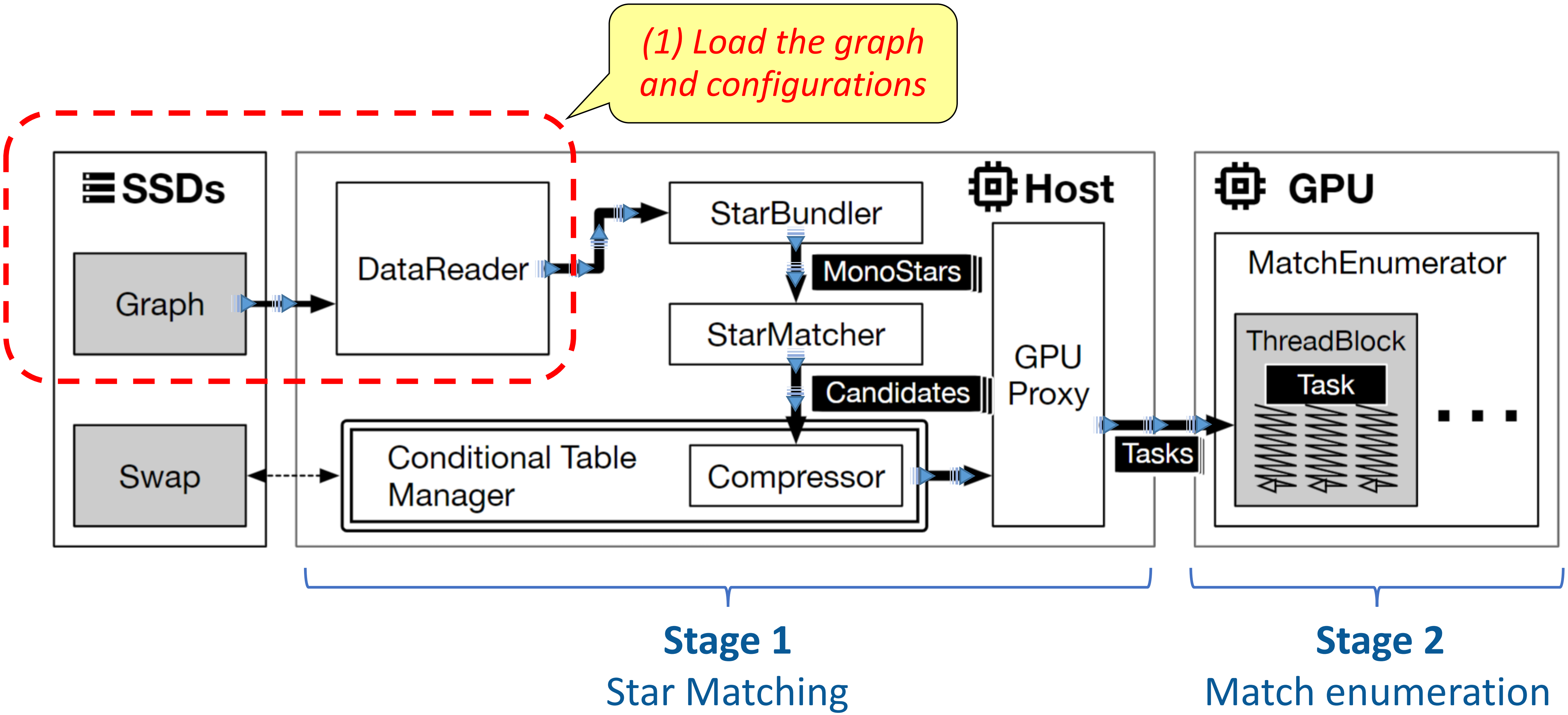

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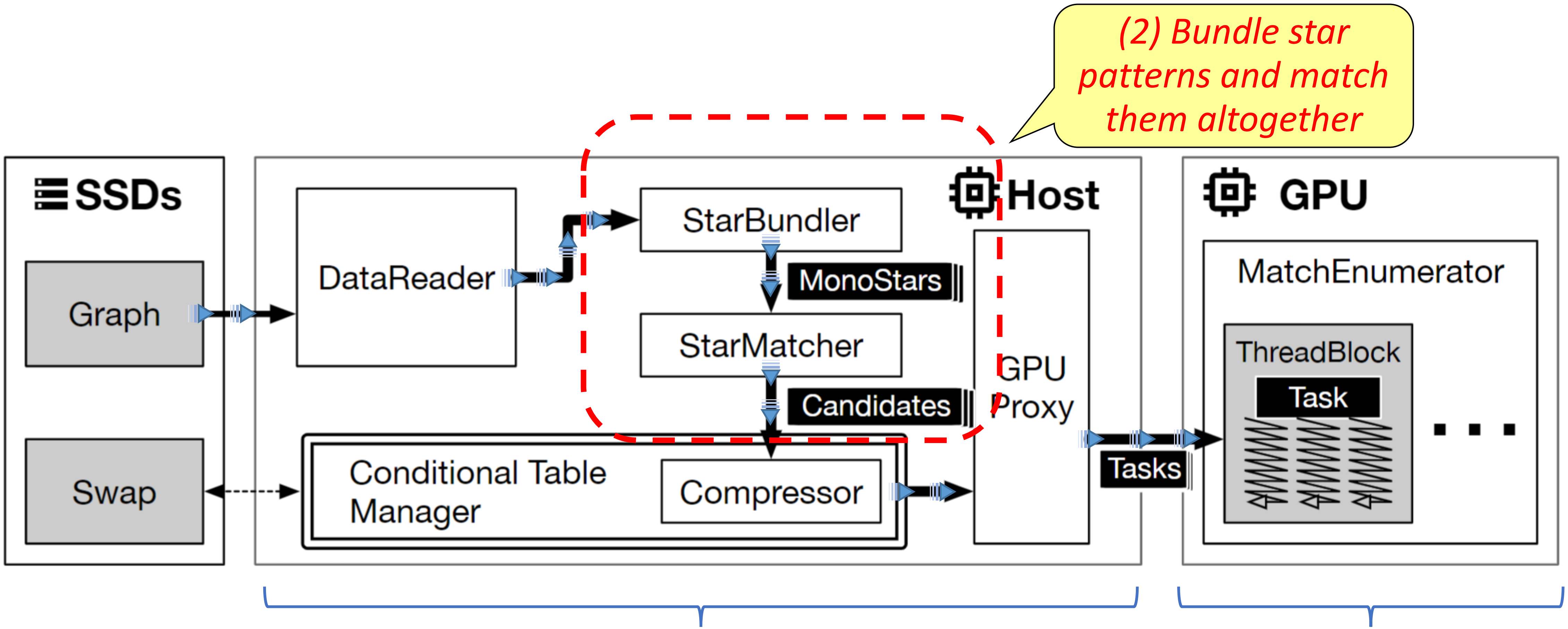

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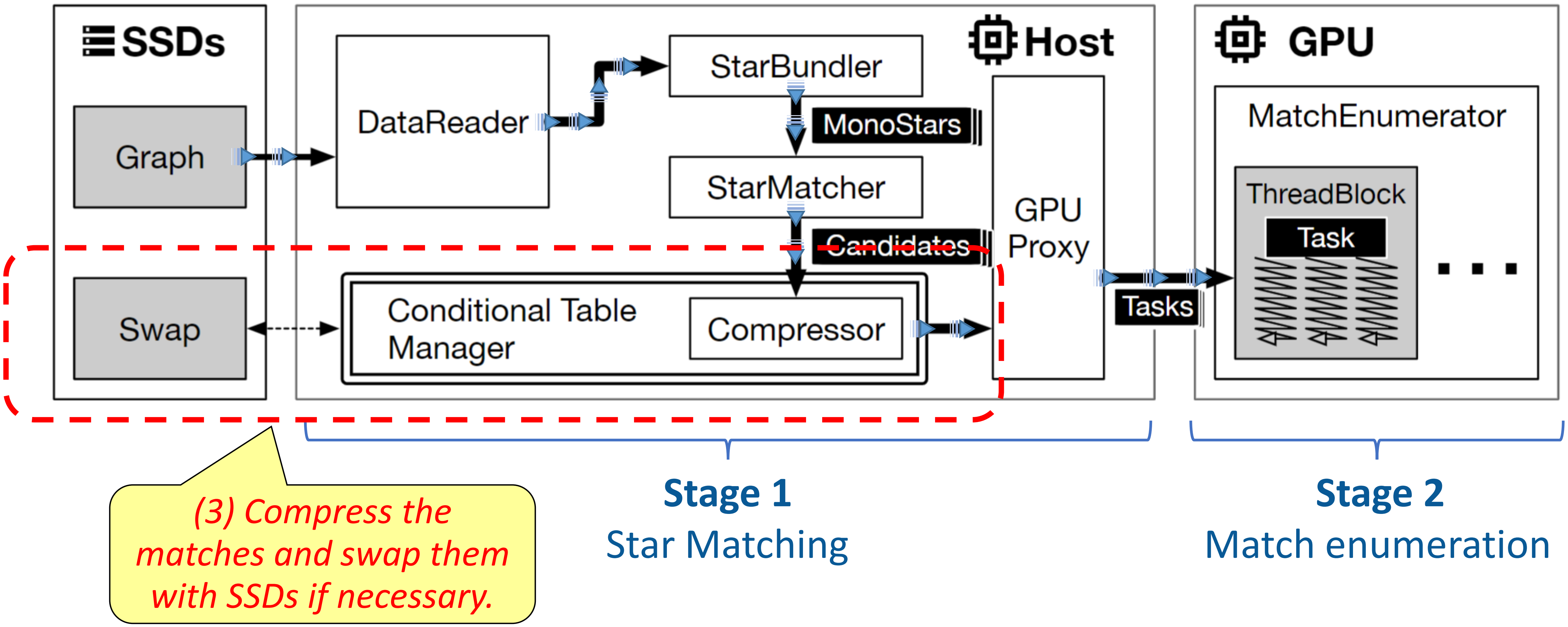

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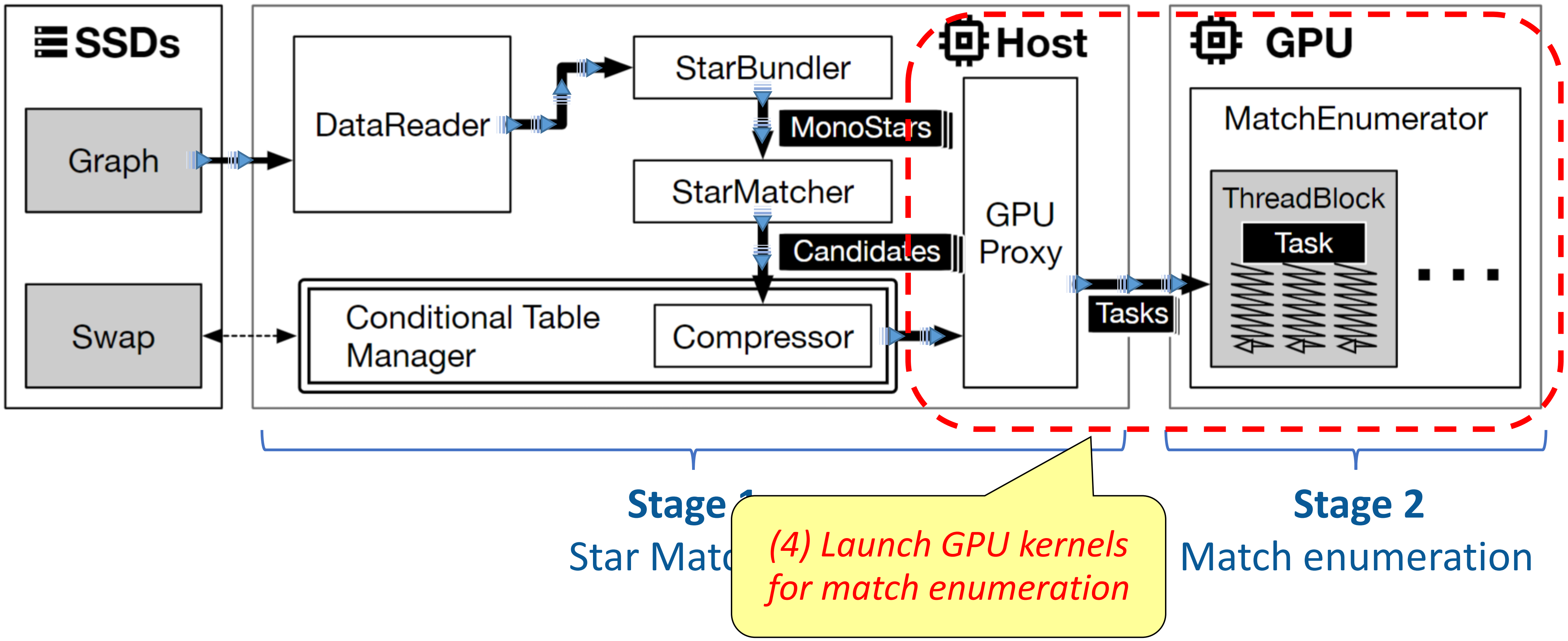

Maximally overlapping I/O, CPU and GPU operations

Guided Tour

In our demonstration, we will walk the participants through

- **Data management**: visualize the input graph and GCRs;
- **GCR discovery**: configure and launch a rule discovery task;
- **GCR application**: inspect the errors detected/corrected by each GCR.

We will use BioGRID, a real PPI graph in our demonstration.

System Evaluation: Accuracy

System	BioGRID			SemScholar		
	Time	ER-F1(%)	CR-F1(%)	Time	ER-F1(%)	CR-F1(%)
MiniClean	312.7s	97.5	97.2	4089.1s	94.6	70.6
Ditto	7.7×	91.0	N/A	4.3×	90.3	N/A
KGClean	11.9×	N/A	54.9	11.9×	N/A	29.8

- **ER tasks**: outperforms ER model ***Ditto*** by 4.3%--6.5%.
- **CR tasks**: outperforms CR model ***KGClean*** by 40.4%--42.3%.
- **Efficiency**: 11.9× faster than ML baselines.

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$\Delta = 6.5\%$ $\Delta = 4.3\%$

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Single-machine (BioGRID)		Scalability (SemScholar)		Ablation study (SemScholar)	
System	**Time (s)**	**System**	**Time (s)**	**System**	**Time (s)**
Blaze	OOM	GCRClean-32-Node	8.09×	noBundle	1.35×
MiniGraph	65.34×	MiniClean-2-GPU	0.64×	noPipelinedPar	1.26×
Hyperblocker	11.92×	MiniClean-4-GPU	0.48×	noIndPar	1.12×
MiniClean-1-GPU	259.6s	MiniClean-1-GPU	4251.08s	MiniClean-2-GPU	2993.7s

- **Single-machine**: 65.34× faster than **MiniGraph**; 11.92× faster than **Hyperblocker**.
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