gMark: Schema-driven data and workload generation for graph databases

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Joint work with G. Bagan (Lyon), A. Bonifati (Lyon), R. Ciucanu (Oxford), A. Lemay (Lille), and N. Advokaat (Eindhoven)

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We present gMark, an open-source framework for generation of synthetic graphs and workloads.

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For example

- multi-query optimization,
- mapping discovery and query rewriting in data integration systems,
- workload-driven graph database physical design,

and, in general, flexible specification and generation of diverse workloads addressing particular experimental studies.

https://github.com/graphMark/gmark

Given a graph schema, gMark

- generates synthetic instances of the schema (of desired size)
- generates query workloads with targeted structure and runtime behavior (which holds for all instances of the schema)

We adopt successful aspects of the state of the art

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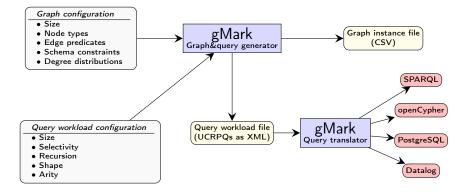
and, like the LDBC SNB Interactive, gMark supports focused stress-testing of query optimization choke-points, through fine control of query parameters such as selectivities.

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 support for flexible generation of query workloads including recursive path queries, which are fundamental for graph analytics; New features of gMark include

- support for flexible generation of query workloads including recursive path queries, which are fundamental for graph analytics; and,
- query selectivity estimation solution, in a purely instance-independent schema-driven fashion.
 - hence, more scalable, more predictable, and easier to explain/understand.

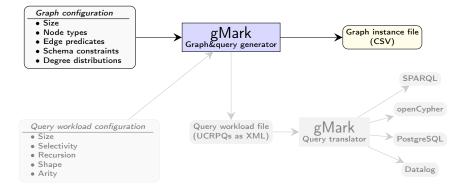
Overview of the gMark workflow



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Graph generation

gMark graph generation



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Graph configurations

The user can specify in the graph configuration (i.e., graph schema):

- Size: # of nodes
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- Edge predicates: finite set of edge labels e.g., authoredBy, referencedBy
- Schema constraints: proportion of nodes/edges of given type e.g., 20% of all nodes are authors
- **Degree distributions**: on the in- and out-degree of edge predicates (uniform, normal, zipfian)

e.g., the out-distribution of citation authoredBy author is Gaussian with parameters $\mu = 3, \sigma = 1$

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Graph configurations: Uniprot schema

Node type	Constr.	
gene	35%	
protein	31%	
author	20%	
citation	10%	
organism	1%	
Node types		

Edge predicate	Constr.
authoredBy	64%
encodedOn	6%
referencedBy	3%
occursIn	2%

Edge predicates

source type predicate target type	In-distr.	Out-distr.
protein encodedOn gene	Zipfian	Gaussian
protein occursIn organism	Zipfian	Uniform
protein referencedBy citation	Zipfian	Gaussian
citation authoredBy author	Zipfian	Gaussian

In- and out-degree distributions

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Hence, gMark follows a 'best-effort' strategy in instance generation, i.e., it attempts to achieve the exact values of the input parameters and relaxes them whenever this is not possible.

We have adapted the scenarios of several popular use cases into meaningful gMark configurations, while also adding new gMark features:

- Bib: our default bibliographical use-case
- LSN: LDBC social network benchmark
- WD: WatDiv e-commerce benchmark
- SP: SP2Bench DBLP benchmark

	100K	1M	10M	100M
Bib	0m0.057s	0m0.638s	0m8.344s	1m28.725s
LSN	0m0.225s	0m1.451s	0m23.018s	3m11.318s
WD	0m2.163s	0m25.032s	4m10.988s	113m31.078s
SP	0m0.638s	0m7.048s	1m28.831s	15m23.542s

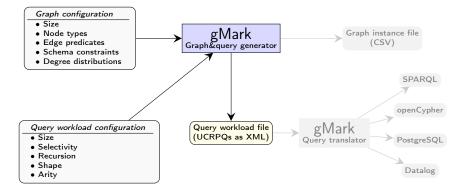
Graph generation times, with varying graph sizes (# nodes)

Generation time depends heavily on density of instances (e.g., WD has 100x number of edges than Bib)

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Query workload generation

gMark query generation



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UCRPQ: Unions of Conjunctions of Regular Path Queries

- Core constructs of the W3C's SPARQL 1.1, Oracle's PGQL, and and Neo4j's openCypher
- Well understood theoretical properties (e.g., polynomial data complexity)

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UCRPQ includes **recursive queries** (via the Kleene star *), with applications in social networks, bioinformatics, etc.

gMark generates UCRPQ \rightarrow the first schema-driven tool to support recursive queries and their generation in concrete syntaxes.

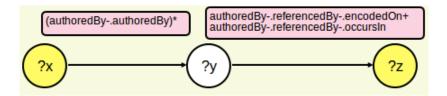
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Example of UCRPQ

for each researcher, select all of the biological entities (i.e., genes and organisms) relevant to proteins studied in papers authored by people in the researcher's coauthorship network

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 $(?x,?z) \leftarrow (?x,(\mathtt{a}^{-}\cdot\mathtt{a})^{*},?y),(?y,(\mathtt{a}^{-}\cdot\mathtt{r}^{-}\cdot\mathtt{e}+\mathtt{a}^{-}\cdot\mathtt{r}^{-}\cdot\mathtt{o}),?z)$

(a=authoredBy, r=referencedBy, e=encodedOn, o=occursIn)

Example of UCRPQ

for each researcher, select all of the biological entities (i.e., genes and organisms) relevant to proteins studied in papers authored by people in the researcher's coauthorship network

$$(?x,?z) \leftarrow (?x,(a^-\cdot a)^*,?y),(?y,(a^-\cdot r^-\cdot e + a^-\cdot r^-\cdot o),?z)$$

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#rules	1
#conjuncts	2
#disjuncts	1, 2
path lengh	2, 3, 3

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Schema-driven workload generation

The user can specify in the query workload configuration:

- Size: #queries, #conjuncts/#disjuncts/path length per query
- Selectivity: constant, linear, quadratic.
- Recursion: probability to generate Kleene star above a conjunct.

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- Selectivity: constant, linear, quadratic.
- Recursion: probability to generate Kleene star above a conjunct.
- Shape: chain, star, cycle, star-chain.
- Arity: arbitrary (including 0 i.e., Boolean).

The graph configuration is also input to the query generator.

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Approach

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Assigning selectivities required us to develop a non-trivial infrastructure for instance-independent reasoning over query behavior, based on a Selectivity Algebra.

Selectivity estimation quality of gMark

- Given a binary query Q and a graph G, we assume that $|Q(G)| = O(|nodes(G)|^{\alpha}).$
- α is the selectivity value (0-constant, 1-linear, 2-quadratic).

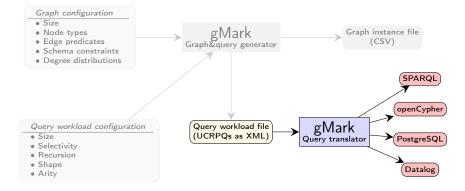
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- Given a binary query Q and a graph G, we assume that $|Q(G)|=\mathcal{O}(|\mathit{nodes}(G)|^{\alpha}).$
- α is the selectivity value (0-constant, 1-linear, 2-quadratic).
- Experiments confirmed the assumption and the estimation quality.

	Constant	Linear	Quadratic
LSN-Len	0.200 <u>+</u> 0.417	1.189 ± 0.261	2.032±0.059
LSN-Dis	0.182 <u>+</u> 0.364	1.325 <u>+</u> 0.318	2.046 <u>+</u> 0.074
LSN-Con	0.190 <u>+</u> 0.391	1.244 <u>+</u> 0.326	2.017±0.032
LSN-Rec	0.196 <u>+</u> 0.409	1.090 <u>+</u> 0.492	1.564 <u>+</u> 0.889
Bib-Len	0.003±0.010	0.921±0.122	1.405±0.337
Bib- <i>Dis</i>	0.000 <u>+</u> 0.000	0.995 <u>+</u> 0.012	1.607 ± 0.261
Bib-Con	0.023 <u>+</u> 0.029	0.986 <u>+</u> 0.112	1.409 <u>+</u> 0.296
Bib-Rec	0.100 <u>+</u> 0.316	0.982 <u>+</u> 0.073	1.493 <u>+</u> 0.335
WD-Len	0.016±0.044	1.427±0.392	2.004±0.022
WD-Dis	0.009 <u>+</u> 0.022	1.412 <u>+</u> 0.380	1.999 <u>+</u> 0.014
WD-Con	-0.010 <u>+</u> 0.026	1.540 <u>+</u> 0.495	1.750 <u>+</u> 0.708
WD-Rec	0.587 <u>+</u> 0.830	-	1.976 ± 0.012
SP	0.074 ± 0.130	1.064 ± 0.034	2.034±0.295

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gMark query translator



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Query translation

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SPARQL	openCypher
<pre>PREFIX : <http: example.org="" gmark=""></http:> SELECT DISTINCT ?x ?z WHERE { ?x (^:a/:a)* ?y . ?y ((^:a/^:r/:e) (^:a/^:r/:o)) ?z .}</pre>	<pre>MATCH (x)<-[:a]-()-[:a]->(y), (y)<-[:a]-()<-[:r]-()-[:e]->(z) RETURN DISTINCT x, z UNION MATCH (x)<-[:a]-()-[:a]->(y), (y)<-[:a]-()<-[:r]-()-[:o]->(z) RETURN DISTINCT x, z;</pre>
Datalog	SQL
g0(x,y)<- edge(x1,a,x0),edge(x1,a,x2), x=x0,y=x2. g0(x,y)<- g0(x,z),g0(z,y). g1(x,y)<- edge(x1,a,x0),edge(x2,r,x1), edge(x2,e,x3),x=x0,y=x3. g1(x,y)<- edge(x1,a,x0),edge(x2,r,x1), edge(x2,o,x3),x=x0,y=x3. query(x,z)<- g0(x,y),g1(y,z).	WITH RECURSIVE c0(src, trg) AS (SELECT edge.src, edge.src FROM edge UNION SELECT edge.trg, edge.trg FROM edge UNION SELECT s0.src, s0.trg FROM (SELECT trg as src, src as trg,

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On my laptop, gMark easily generates workloads of one thousand queries for Bib in \sim 0.3s; LSN and SP in \sim 1.5s; and for the richer WD scenario in \sim 10s.

Query translation of the thousand queries into all four supported syntaxes for each of the four scenarios required $\sim 0.1 s.$

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Example Application. We performed an extensive performance study of four state-of-the-art systems under the four use-case schemas.

Our main finding was that performance on queries containing recursive path navigation (i.e., RPQs) was typically impractical

 indicates the need for further study of the engineering of this basic class of graph queries

Wrap Up



Novel contributions of gMark

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 schema-driven graph and query-workload generation, featuring instance-independent selectivity estimation;

Recap

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- schema-driven graph and query-workload generation, featuring instance-independent selectivity estimation;
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- discovery of the performance difficulties of existing graph DBMS's on evaluating a basic class of graph queries
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Recap

Novel contributions of gMark

- schema-driven graph and query-workload generation, featuring instance-independent selectivity estimation;
- finely controlled query workload-centered approach
 - versus query-centered approaches nb. both are valid and needed!
- discovery of the performance difficulties of existing graph DBMS's on evaluating a basic class of graph queries
 - Regular Path Queries

Come see us at our VLDB 2016 demo!

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Looking ahead to gMark v2.0

To-do/wishlist.

- richer queries
 - support of constants in queries
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- align our work with LDBC activites?

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Thank you!