

Credit Distribution through Data Provenance in Relational Scientific Databases

Dennis Dosso^a, Susan B. Davidson^b, Gianmaria Silvello^a

^a*Department of Information Engineering, University of Padua, Italy*

^b*Department of Computer and Information Science, University of Pennsylvania, United States*

Abstract

In the current world of research data is a fundamental method to disseminate scientific knowledge, to determine scholarship, and to provide credit and recognition to the authors of research endeavors. However, issues like data citation, handling and counting the credit generated by such citations are still open research questions.

In this context, data credit has recently emerged as a new measure of value, defined and built on top of the data citation theory. Data credit is a real value that represents the importance of data cited by a paper, or by another research entity. As such, credit can be used to annotate data contained in curated scientific databases, and it can be considered as a measure for their importance and impact in the research world. As such, it is a new method that, together with traditional citations, helps to recognize the value of data and its creators in a world more and more dependent on data.

In this paper we explore the problem of Data Credit Distribution, the process by which credit is divided and assigned to the data in a database that are responsible for the production of data being cited by a research entity.

We adopt as use case the IUPHAR/BPS Guide to Pharmacology (GtoPdb), a curated and well-known scientific relational database. We define two new distribution strategies, functions that perform this task, based on two form of data provenance, why-provenance, and how-provenance.

Using different distribution strategies, we show how credit can highlight areas of a database that are frequently used, and how it can work as a new bibliometric measure for data and their corresponding curators. Credit in particular rewards data and authors based on their research impact, and not

merely on the number of citations. Also, we show how different distribution strategies, based on different types of data provenance, can be more sensible to the role of an input tuple in the generation of the output, and thus rewarding it differently.

Keywords: Data Citation, Data Credit

1 Introduction

Citations are an essential component of scientific research, enabling research products to be found as well as the relationships between research products to be understood. They form a basis on which to give credit to authors, papers, and venues [55, 19, 20]. Citations are used, among other things, to decide on tenure, promotion, hiring, and funding of grants for researchers [41, 21, 32, 38].

Nowadays, science and research are increasingly digital. There are numerous curated databases that are at the core of scientific research efforts [12]. It is therefore generally accepted that data must be cited and citable [39, 15], and that data citations should contribute to the scientific reputation of researchers, scientists, data curators, and creators [4, 50]. It is also accepted that data citations should be counted alongside of traditional citations, and contribute to bibliometrics indicators [7, 44].

A central problem in data citation is how to attribute credit to data creators and curators [11]. How to handle and count the credit generated by data citation, and how it contributes to traditional and new bibliometrics, are long-standing research issues Garfield [28], Borgman [9]. However, even when correctly applied, data citations and the bibliometric computed using them do not always correctly reward the creators of data used in a database. Data, in fact, is often cited at the “database level” or the “webpage level”. In the first case, the whole database is cited and therefore all credit goes to the key personnel of the database. In the second case, the database has a website with webpages that can be individually cited. The webpages use data extracted from the database, which is aggregated by topic and built to resemble a traditional research paper. Often the creators and curators of the webpage’s data are not credited or only marginally credited for their work [3].

Recently, the concepts of *data credit* and *Data Credit Distribution* (DCD) [26, 36, 54] have emerged, built on top of methodologies for data citation. Data

credit is a value that is computed based on the importance of the data being cited in a paper, and represents the impact of the data on the citing paper. The Data Credit Distribution problem consists of distributing this credit to elements in the databases in the citation graph that are responsible for the generation of the data being cited. The goal of DCD is to improve and expand the reach of data citation, rather than being an alternative to it. This means that to employ DCD techniques, we need data citations in some form.

[37] defined credit as a “quantity” that describes the importance of a research entity, such as papers or data mentioned in a citation, and proposed the idea of a *distribution* of credit from research entities, such as papers or data, to other research entities through citations. This can be done by exploiting the structure of the *citation graph*, a directed graph whose nodes are publications and edges are citations. This graph is the model at the core of systems such as Google Scholar and the Web of Science. Zeng et al. [54] and Fang [26] further explored this concept by defining frameworks for the computation and distribution of credit between papers, authors, and data used by papers in the citation graph.

In this paper, we consider data credit as a data value measure in a (curated) scientific database; credit can be assigned to data of any kind and at any level of granularity. Therefore the concept of “data” is left intentionally vague, although in this paper we focus on relational databases. Credit is a positive *real* value, acting as a proxy for the value of data based on the measure of citations, accesses, clicks, downloads, or other surrogates for data use. We call Data Credit Distribution the process, method, or algorithm used to assign credit to a given datum or dataset.

The DCD problem differs from the traditional citation setting since:

1. In a traditional setting, when a paper cites another paper, a +1 “credit” is given to the cited paper (and to its authors). It does not matter why or how paper p_1 cites paper p_2 ¹, the result is always +1 from p_1 to p_2 and thus a +1 to the citation count of the authors of p_2 . With a different credit distribution strategy, the “value” given to the cited entity can be *proportional* to the role played in the citing entity. Hence, we can weigh the importance of the cited entities and assign credit according to their role.

¹Note that there is vast research on this topic and many alternative proposals, but none of them currently work at a large scale.



Figure 1: Overview of the credit distribution pipeline.

2. Traditional citations are considered to be *atomic*. A citation from p_1 to p_2 can never be broken into pieces and assigned in part to p_2 and in part to other papers or data that contributed to p_2 . This is due to the intrinsic difficulty in grasping the role and “weight” of the other papers and data, and in automating the credit assignment process. In contrast, we consider data credit to be a *non-atomic* real value, which can be divided and distributed to multiple components of a database.
3. Credit can be *transitive*, that is, it can be propagated through one cited entity to other entities cited by it that contributed to its content.

We study the DCD problem in the context of relational databases (RDBs) since they are widely used² and are the main focus of current work in data citation methods [14, 12, 45]. RDBs are also frequently a test-bed for new methods that can be adapted to other databases, e.g., graphs or document databases. Furthermore, the “portions” of data in an RDB that can be credited can be defined at different levels of granularity, in particular: (i) the whole database, (ii) tables, and (iii) tuples.

The DCD process is summarized in Figure 1:

²The “relational database market alone has revenue upwards of \$50B” [1].

- 82 **Step 1** Scientists and experts contribute the curated information contained
83 in a scientific database. These are called the “Data Curators”.
- 84 **Step 2** Other researchers use the data in their research, and when possible,
85 cite them.
- 86 **Step 3** The citation to the data generates credit, that can be used as a
87 proxy for the impact of the data on the citing paper. This credit is
88 represented as a real value $k \in \mathbb{R}_{>0}$.
- 89 **Step 4** Given the database instance I and the query Q , it is possible to
90 compute the *data provenance* of $Q(I)$. The provenance of $Q(I)$ is a
91 form of metadata that describes the generation process undertaken by
92 Q , and the data used in I to generate the output [17]. Many different
93 notions of provenance have been proposed in the literature for data in
94 database management systems [22, 13, 30], describing different kinds
95 of relationships between data in the input and the output of a query.
96 As reported in [17], these provenances have been used in several appli-
97 cations beyond giving information on how queries work, for example,
98 annotation propagation and the view update problem. In this paper,
99 we consider three types of provenance: lineage, why-provenance, and
100 how-provenance.
- 101 **Step 5** Provenance is input to the CDC problem, whose aim is to compute
102 the *Credit Distribution Strategy* (CDS, also referred only as Distribu-
103 tion Strategy, DS). The CDS is a function that distributes k to the data
104 in the input database I , and is defined on the basis of citation policies
105 decided at the database administration level or at the domain commu-
106 nity level. In this paper, since we base CDS on data provenance, we
107 describe three CDS, each one based on a different form of provenance.
- 108 **Step 6** Once the CDS is computed, it is used to distribute the given credit
109 k to the parts of the database that are responsible for the generation
110 of $Q(I)$. Transitively, this credit is also divided and given to the corre-
111 sponding authors of those data.

112 This paper expands our recent work in [24], which addressed the problem
113 of how to reward data and data curators who are typically overlooked in
114 current citation systems. In that work, we first defined the problem of DCD

115 in relational databases, and proposed a viable Distribution Strategy (DS)
 116 based on *lineage*, which is the simplest form of *data provenance*. The lineage
 117 of a tuple t in the output $Q(I)$ is defined as the set of all and only the tuples
 118 in the database instance I that are “relevant” to the production of t , that
 119 is the tuple that are used by Q in the production of t . The lineage-based
 120 strategy equally redistributes the credit k to the tuples in the lineage set,
 121 thus each tuple receives credit $k/|L_t|$, where L_t is the lineage set of t .

122 One may argue that this DS is too simplistic, since lineage only tells
 123 the relevant tuple used to produce the output, and does not convey any
 124 information about their role or importance in the query. Therefore, one may
 125 desire to give more credit to the tuples that are more relevant or *essential*
 126 to the production of the output, i.e. those tuples that, if removed, would
 127 prevent the output tuple from appearing in the final result, or those tuples
 128 used more than once by the query.

129 Therefore, in this paper, we expand the ideas in [24] by proposing two
 130 new DSs based on other forms of data provenance: why-provenance [13]
 131 and how-provenance [30]. We compare them with the lineage-based solu-
 132 tion, and discuss why one may be preferred to another depending on the
 133 application and its goals. In particular, we show that why-provenance and
 134 how-provenance are more sensitive to the *role* of a tuple in a query, i.e. how
 135 many times the tuple is used and how it is used. The DS based on why-
 136 provenance give more reward to tuples that are essential to the production
 137 of the result set, whereas the DS based on how-provenance also takes into
 138 consideration the different ways that a tuple is used.

139 For evaluation, we use a well-known curated database, the IUPHAR/BPS³
 140 Guide to Pharmacology [31], also known as GtoPdb⁴, which contains ex-
 141 pertly curated information about diseases, drugs, cellular drug targets, and
 142 their mechanisms of action. We chose GtoPdb for two main reasons: (i) it
 143 is a widely-used and valuable curated relational database, (ii) many papers
 144 in the literature use, and cite its data (i.e., families, ligands, and receptors).
 145 Real queries used in papers can therefore be seen as data citations which, in
 146 turn, can be used to assign data credit.

147 We perform three sets of experiments. In the first one, real queries are ex-

³International Union of Basic and Clinical Pharmacology/British Pharmacology Soci-
 ety

⁴<https://www.guidetopharmacology.org/>

148 tracted from papers published in the British Journal of Pharmacology (BJP),
 149 that represent data citations to GtoPdb, and are used to distribute credit
 150 in the database using the three different provenance-based DSs. In the sec-
 151 ond and third experiment we analyse the behaviour of the different DS when
 152 complex citation queries are employed.

153 **Contributions.** Contributions of this work include:

- 154 • The definition of new distribution strategies for the problem of Data
 155 Credit Distribution, based on why-provenance and how-provenance;
- 156 • An in-depth analysis of the effects of credit distribution on real-world
 157 curated data and of the differences between the three proposed Distri-
 158 bution Strategies.

159 **Outline.** The rest of the paper is organized as follows: Section 2 presents the
 160 background and related work. Section 3 describes the use case we adopted.
 161 Section 4 briefly presents the forms of provenance used in the paper. Section
 162 5 describes the problem of DCD and the proposed DS. In Section 6 we present
 163 the experimental evaluation. Finally, Section 7 draws some conclusions and
 164 outlines future work.

165 2. Background

166 *Data in Research.* As described by Jim Gray in his last talk [33], the world of
 167 research is rapidly transitioning towards the *fourth paradigm of science*, that
 168 is, data-intensive scientific discovery, where data are important for scientific
 169 advances as well as for traditional publications [6].

170 The scientific community is promoting an *open research culture* [43],
 171 founded on methods and tools to share, discover, and access experimental
 172 data. The community has identified the FAIR principles (Findable, Acces-
 173 sible, Interoperable, and Reusable) [52], that should be enforced by every
 174 database. In particular, data should be accessible from the articles, journals,
 175 and papers that cite or use them [19]. Aspects such as the need for the *repro-*
 176 *ducibility* of experiments through the used data; the *availability* of scientific
 177 data; the *connections* between data and the scientific results are all needed
 178 aspects for the fourth paradigm, and are all relevant to the domain of *data*
 179 *citation* [34].

180 *Data Citation: Principles and Motivations.* Data Citation principles were
 181 first described in detail in [18], and later summarized and endorsed by the
 182 Joint Declaration of Data Citation Principles (JDDCP) [40]. The principles
 183 are divided into two groups [48]. The first one contains principles concerning
 184 the role of data citation in scholarly and research activities such as the (i)
 185 *importance* of data (why data citation is important and why data should be
 186 considered as first-class citizens); (ii) *credit* and *attribution* to the creators
 187 and curators of the data; (iii) *evidence*; (iv) *verifiability*; and *interoperability*,
 188 with these last three requiring data citation methods to be flexible enough to
 189 operate through different communities. The second group defines the main
 190 guidelines to establish a data citation systems, and contains principles such
 191 as the (i) *unique identification* of the data being cited; (ii) (*open*) *access* to
 192 data; (iii) guarantee of *persistence* and *availability* of citations even after the
 193 lifespan of the cited entity; the (iv) *specificity* of a citation, i.e. it must lead
 194 to the data set originally cited.

195 It is possible to outline six main motivations for data citation [48]:

- 196 • *Data attribution*: identify the individuals that should be credited for
 197 data with variable granularity.
- 198 • *Data connection*: connect papers to the data being used.
- 199 • *Data Discovery*: citations helps to find data records and subsets that
 200 would be otherwise not findable via search engines.
- 201 • *Data Sharing*: share data obtained by researchers within the whole
 202 community.
- 203 • *Data Impact*: highlight the results obtained in writing papers using
 204 specific data, the frequency and modality data were used.
- 205 • *Reproducibility*: data citation greatly impacts the reproducibility of
 206 science [5]. Many authoritative journals ask to share data and provide
 207 valid methodologies to reproduce experiments.

208 2.1. Data Citation in Relational Databases

209 In this paper, we develop our methods and experiments on relational
 210 databases. RDBs have been the main target of data citation methods since
 211 the surge of the data-centric research paradigm. The RDA “Working Group

212 on Data Citation: Making Dynamic Data Citable”⁵ [46] has been working in
213 the last years on large, dynamic, and changing datasets. The working group
214 has finished the development of its guidelines and has now moved on into an
215 adoption phase. The datasets considered by the WG are often relational.

216 In one of its most recent sessions [47], the Working Group (WG) on
217 Data Citation reported that there are various implementations of its guide-
218 lines for Data Citation on MySQL/Postgres relational databases. Some of
219 these databases are: DEXHELPP⁶ (Social Security Records); NERC (ARGO
220 Global Array); EODC (Earth Observation Data Centre) [29]; LNEC (River
221 dam monitoring); MDS (Million Song Database) [8]; CBMI⁷ (Center for
222 Biomedical Informatics); VMC (Vermont Monitoring Cooperative); CCA⁸
223 (Climate Change Center Austria); VAMDC (Virtual Atomic and Molecular
224 Data Center) [25, 56].

225 More examples of work on data citation in relational databases are [12,
226 53, 2, 23]. The website <https://fairsharing.org/> keeps a long updated
227 list of curated and scientific databases (many of which are relational or graph-
228 based) following FAIR guidelines. These databases are citable since they are
229 compliant with the most recent guidelines, and they are in the vast majority
230 of cases accessible via dynamically created Webpages. In all these databases
231 is, therefore, possible to implement DCD on top of the existing infrastructures
232 for citing data.

233 Data citation techniques are primarily applied to relational databases
234 because of their diffusion and also because the portions of data that are to
235 be cited are easily identified: the whole database, a relation, a tuple, or
236 even an attribute. Many papers [10, 12, 2] consider more complex citable
237 units, recognizing that often the *views* of a database are the ones to be cited.
238 Generally, a *view* is a query on the database. To this end, [53] suggested
239 decomposing the database in a set of views, where each view is associated
240 with its citation.

241 At present, the most common practices to cite databases include:

- 242 1. A database cited as a whole, even though only parts of the databases
243 are used in the papers or datasets. Alternatively, the so-called “data pa-

⁵<https://www.rd-alliance.org/groups/data-citation-wg.html>

⁶<http://www.dexhelpp.at/>

⁷[https://medicine.missouri.edu/centers-institutes-labs/
center-for-biomedical-informatics](https://medicine.missouri.edu/centers-institutes-labs/center-for-biomedical-informatics)

⁸<https://ccca.ac.at/startseite>

- pers” can be cited, being traditional papers that describe a database [16].
 In this case, all the credit from the citations goes to the database administrators or to the authors of the data papers.
2. Subsets of data, obtained by issuing queries to a database, are individually cited. This is the solution adopted by the *Resource Data Alliance* (RDA) working group on Data Citation [46]. In this case, the credit generated from citations can be distributed among the contributors of the portions of data being cited, and/or to the database administrators.
 3. The database is accessible via a series of Webpages that arrange the content of the database by topic or theme. Examples in the life science domain include the Reactome Pathway database [35], the GtoPdb [31], and the VAMDC [56]. Every single Webpage is unequivocally identifiable and can be individually cited.

Despite all the research efforts dedicated to the study and promotion of data citation, none of the largest citation-based systems, such as Elsevier Scopus, Web of Science, Microsoft Academia, or Google Scholar, consider scientific datasets as citable objects in academic work. Clarivate Analytics Data Citation Index (DCI) [27] is an exception, since its infrastructure tracks data usage in scientific domains and provides the technical means to connect datasets and repositories to scientific papers. However, DCI considers only citations to (previously registered and approved) databases as a whole and does not count citations to database portions such as views, tables, or tuples.

2.2. Data Credit

Data credit is related to data citation: they both aim to recognize the work of data creators and curators. Data credit can therefore also be seen as a by-product of data citation, since credit attribution is impossible without the presence of data citations.

[36] suggests the need for a *modified citation system* that includes the idea of *transient* and *fractional credit*, to be used by developers of research products as software and data. In the paper two considerations are made: (i) research objects such as data and software are currently not formally rewarded or recognized by the community; (ii) even in traditional papers, the contribution of each author to the work is hard to understand, unless explicitly specified in the paper. This is even more true for data, where different groups of people work on the same database.

In [36] credit is defined as a “quantity” that describes the importance of a research entity, such as papers, software, or data, mentioned in a citation.

281 We add that the concept of credit can be built on top of the existing infras-
 282 tructure handling traditional and data citations. [36] further explores the
 283 idea of a *distribution* of credit from research entities (i.e., papers and data)
 284 to other research entities through citations that connect them. Thanks to
 285 traditional citations and now also to data citations, this distribution is fi-
 286 nally possible, at least between papers and data. Some problems related to
 287 traditional citations can thus be solved by citations:

- 288 1. Credit rewards research entities that to date are not (formally) recog-
 289 nized (a goal shared with data citation).
- 290 2. Credit can reward authors *proportionally* to their role in generating
 291 the entity. The more an author contributes to a paper, the more credit
 292 is given to him. [55] work on something similar with their zp-index,
 293 which includes in its formulation the position (and thus the role) of a
 294 publication author to represent its impact in the work itself.
- 295 3. Credit can be *transitively* channeled through a chain of papers citing
 296 each other, thus enabling the rewarding of older papers **that are no**
 297 **more cited, since other papers summarize or report their con-**
 298 **tent. Gianmaria: I do not understand this token, what do you**
 299 **mean with: papers that are no more cited?** but are nevertheless
 300 crucial in a research area for the influence of their content.

301 [26] presents a framework to distribute the credit generated by a paper to
 302 its authors and to the papers in its reference list in a transitive way. Let us
 303 consider the *citation graph* as the graph where the nodes are papers and the
 304 links are the citations among them. In this graph, every paper is a source of
 305 credit, which is then transferred to the neighboring nodes. The quantity of
 306 credit received by each cited paper depends on its impact/role in the citing
 307 paper. So far, this theoretical framework is limited to papers, but it can be
 308 easily extended to a citation graph including both papers and data.

309 [54] proposes the first method to compute credit within a network of
 310 papers citing data. Adopting a network flow algorithm, they simulate a
 311 random walker to estimate a score for each dataset, leveraging real-world
 312 usage data to compute the credit. This is the first step towards an automatic
 313 credit computation procedure. This proposal is, however, limited to assigning
 314 credit to whole datasets, and it does not deal with the granularity of data.
 315 It does not work to assign credit to a single research entity within a dataset.
 316 Differently from [54], we do not treat the credit computation process, but we
 317 focus on the distribution process.

318 2.3. Data Provenance

319 To distribute credit, we base our methods on *data provenance*. Data
 320 provenance is information that describes the origin and the process of cre-
 321 ation of data. It can also be seen as metadata pertaining to the derivation
 322 history of the data. It is particularly useful to help users to understand
 323 where data are coming from, and the process they went through. Data ci-
 324 tation and data provenance are closely linked [3] since both are forms of
 325 annotations on data retrieved through queries. Data provenance has been
 326 widely studied in different areas of data management. In this paper, we fo-
 327 cus on provenance for database management systems (DBMS). For further
 328 details on data provenance, please refer to surveys like [17] and [49].

329 [17] presents four main types of data citation for DBMS: *lineage* [22],
 330 *why-provenance* [13], *how-provenance* [30] and *where-provenance* [13].

331 Let us start with the first three provenances. Given a database instance
 332 I , a query Q , and the result $Q(D)$, consider one tuple t of the output. Its
 333 provenance is information about its generation through the tuples of the
 334 input that are used by Q . Different types of provenance convey different
 335 levels of information. Since these three provenances are computed for each
 336 tuple of the output, they are also referred to as *tuple-based*.

337 Lineage is somehow the simplest among the forms of provenance. It has
 338 been defined in different ways [17], but it can be thought of as the set of all
 339 the tuples that are used in some way by the query to produce the output
 340 tuple, the ones that are somehow *relevant* to its generation.

341 The definition of why-provenance is based on the notion of *witness set*.
 342 A witness is a set of relevant tuples that guarantees the existence of t in
 343 $Q(D)$. The lineage is therefore an example of a witness. The why-provenance
 344 of a tuple t is a peculiar set of witnesses – described in [13] – that are
 345 computed from the query, called *witness basis*. A witness basis may be
 346 composed of more than one witness. Therefore, the why-provenance contains
 347 more information than the lineage, since it describes *alternative* ways in
 348 which the same output may be generated.

349 The how-provenance takes the form of a polynomial, called *provenance*
 350 *polynomial*, where the variables are taken from the set of identifiers of the
 351 tuples (provided that each tuple in I has an identifier) and the coefficients are
 352 taken from \mathbb{N} . This provenance also contains information on *how* the input
 353 tuples are used. For example, when two tuples are combined by a join, they
 354 are also combined in the polynomial by the \cdot operator. When two or more

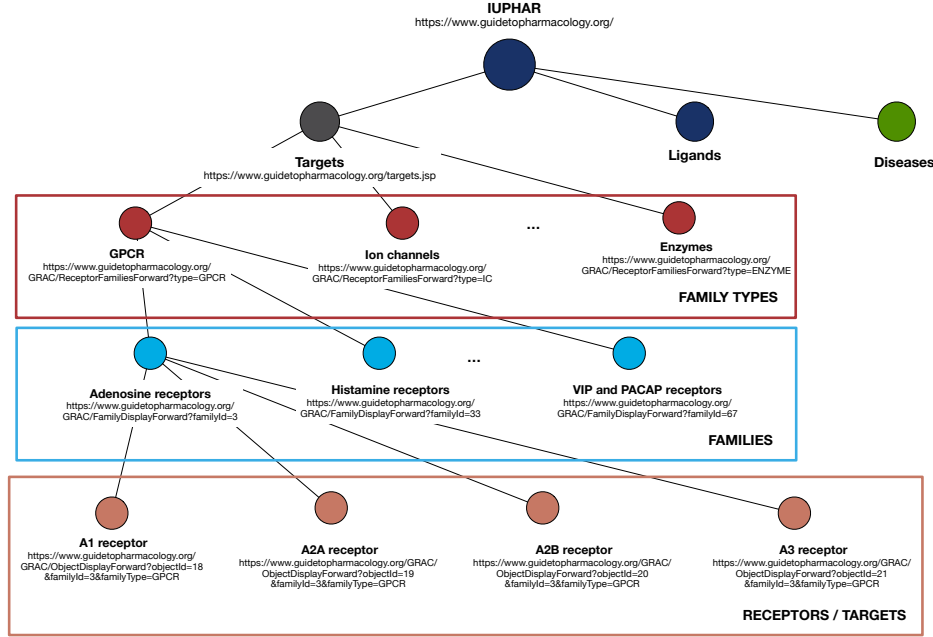


Figure 2: Partial map of the GtoPdb hierarchical structure grouping the targets into families and family types.

355 tuples become equivalent due to a union or a projection, the corresponding
 356 monomials are combined by the $+$ operator.

357 It has been shown in [17] that the how-provenance is the more general
 358 and informative of the three, containing the other two.

359 Where-provenance, differently from the other three, is *attribute-based*, so
 360 we do not take it into account in this work since we consider the tuple as the
 361 finest citable unit.

362 3. Use Case: GtoPdb

363 As use case we refer to the IUPHAR/BPS Guide to Pharmacology [31]
 364 or GtoPdb⁹. GtoPdb is a well-known and well structured scientific relational
 365 database that contains expertly curated information about diseases, drugs
 366 in clinical use, their cellular targets, and the mechanisms of action on the
 367 human body. It is curated and maintained by the GtoPdb Committee, and

⁹<https://www.guidetopharmacology.org/>

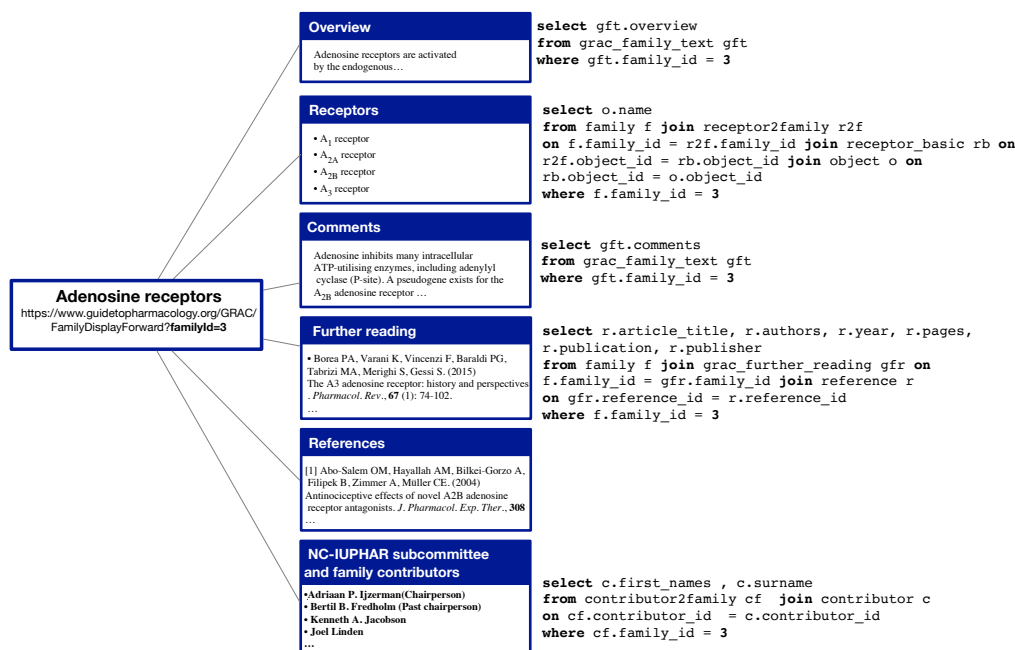


Figure 3: Basic web-page structure of “Adenosine receptors” family (ID 3), with queries used to retrieve the information contained in every section, except references.

by 96 subcommittees, comprising 512 scientists collaborating with in-house curators who draw the information contained in the database from high-quality pharmacological and medicinal chemistry literature. Roughly 1000 researchers from all over the world have contributed to the database, and the curators wanted to give recognition to these contributors. This led to some early work on data citation [10].

GtoPdb is relational, but its logical structure is hierarchical as shown in Figure 2. The information contained in the database is also organized into webpages focused on specific diseases, targets or ligands, and families for easier access by users. As depicted in Figure 2, the database can be thought of as a tree where the root is the database; the first level consists of all targets, ligands, and diseases; and the lower levels consists of specific targets, ligands and diseases. In this paper, we focus on targets; thus at the third level in the figure we show examples of family types, at the fourth level we show specific families of targets (a finer level of granularity), and finally, at the last level, the single targets (also known as receptors).

GtoPdb provides access to the webpages corresponding to all these nodes

385 through URLs. The webpages corresponding to target families all present a
386 similar structure, as shown in Figure 3 for the “Adenosine receptors” family.
387 Each page has an *Overview*, a brief text describing the content of the page;
388 a list of *Receptors* comprising the family; a section of *comments* about the
389 family; the *References*, a list of the papers consulted by the curators of the
390 page, similar to a reference list of a paper; the *further reading* list, reporting
391 papers that an interested reader may want to consult to obtain more insight
392 on the family; and a final section called *How to cite this family page*, con-
393 taining text snippets useful to cite the specific page or the whole database.
394 Figure 3 shows the SQL code that retrieves the information used to build the
395 corresponding sections (apart from the References section). Therefore, each
396 family page can be considered a full-fledged traditional publication, consist-
397 ing of title, authors, abstract (the overview), content, and references.

398 In practice, many papers in the literature only reference GtoPdb (the
399 root) without including a reference to the specific page being cited. That is,
400 they only cite a paper describing GtoPdb as a whole (e.g., [31]) and refer
401 to targets, ligands, diseases, etc. only by name. Thus, citations to specific
402 families are *de-facto* “hidden” to citation systems such as Google Scholar,
403 and useless for the computation of bibliometrics.

404 In certain “lucky” cases, as with papers available in PDF and published
405 in the British Journal of Clinical Pharmacology ¹⁰ (BJCP), when a family,
406 ligand, receptor name, etc. are used, they have a hyperlink pointing to the
407 corresponding webpage in GtoPdb. Therefore, the citations to the families
408 can be detected and counted using the URLs reported in the papers. How-
409 ever, these citations to GtoPdb webpages are not counted as such by citation
410 systems, so they are not converted into credit for curators and collaborators.

411 For our running example, consider Table 1. This simplified version of
412 GtoPdb illustrates three tables: **family**, **contributor** and **contributor2family**.
413 The first table, **family**, has tuples representing families with three attributes:
414 the id of the family, its name, and type. Table **contributor** consists of peo-
415 ple who have helped generate the data of the database. The third table,
416 **contributor2family**, serves as a link between the families and the people
417 who contributed to them. For instance, “John Smith” (c_1) contributed to
418 “Dopamine Receptors” (f_1) as well as to the “YANK Family” (f_4). We use
419 this example throughout the rest of the paper. In particular, we are using

¹⁰<https://bpspubs.onlinelibrary.wiley.com/journal/13652125>

family			contributor2family		
id	name	type	id	family_id	contributor_id
f_1	Dopamine Receptors	gpcr	$c2f_1$	f_1	c_1
f_2	Bile Acid Receptor	gpcr	$c2f_2$	f_1	c_2
f_3	FAK Family	enzyme	$c2f_3$	f_2	c_3
f_4	YANK Family	enzyme	$c2f_4$	f_4	c_1

contributor		
id	Name	Country
c_1	John Smith	UK
c_2	Jim Doe	UK
c_3	Hans Zimmerman	Germany
c_4	Roberta Rossi	Italy

Table 1: Example of a database consisting of three tables. **family** includes some receptor families in the database; **contributor** contains the name and country of contributors; **contributor2family** connects contributors to the families they contributed to.

the *id* attribute of the tables as *provenance token* of its corresponding tuples, that is, as a symbol that serves to identify a tuple when talking about provenance.

4. Data Provenances

In this section, we present the three types of provenance used in this paper: lineage, why-provenance, and how-provenance.

4.1. Lineage

Lineage was first introduced by Cui et al. [22]. Given a database instance I and query Q , lineage associates with each tuple $o \in Q(I)$ the set of tuples in the input that helped “produce” it [17]. As an example, consider the following SQL query **Q1**, applied to the database described in Table 1, that asks for the names of families curated by researchers based in the United Kingdom (UK):

```

Q1: SELECT DISTINCT f.name
FROM family AS f JOIN contributor2family AS c2f
ON f.id = c2f.family_id
JOIN contributor AS c ON c2f.contributor_id = c.id
WHERE c.country = 'UK'
```


id	name	lineage
o_1	Dopamine Receptors	$\{f_1, c2f_1, c_1, c2f_2, c_2\}$
o_2	YANK Family	$\{f_4, c2f_4, c_1\}$

Table 2: Result of an SQL query applied to the database instance in Table 1, which asks for the names of families curated by a researcher based in the UK. Attribute `id` is not part of the output and was added to succinctly identify each tuple as provenance token. Each tuple is also annotated with its lineage.

Table 2 shows the query result, which consists of two tuples. We add an extra attribute `id` so that we can easily refer to each result tuple. The lineage for tuple o_1 is the set $\{f_1, c2f_1, c_1, c2f_2, c_2\}$, since the tuple f_1 was joined with $c2f_1$ and then with c_1 , and was also joined with $c2f_2$ and c_2 . No other tuple is used in the database to produce o_1 . For tuple o_2 the lineage is $\{f_4, c2f_4, c_1\}$. Lineage is defined for each tuple of the output, and can differ between tuples.

4.2. Why-Provenance

Why-Provenance was first defined in terms of a deterministic semistructured data model and query language [13]. While why-provenance can be defined in many ways, we refer to [17], where it is expressed in terms of the relational model using the relational algebra.

In particular, while lineage aims to find all and only the tuples in the input relevant to the production of an output tuple, why-provenance aims to find sub-instances of the input that “witness” a part of the output. Given a tuple t in the query’s output, a *witness* is any sub-instance of the database that produces t . In particular, the whole database and the lineage of t are both witnesses of t . Since the definition of witness allows for the presence of “irrelevant” tuples, the set of all witnesses is finite (since the database instance I is finite), but it is potentially exponentially large [17].

Buneman et al. [13] defined the why-provenance of an output tuple t in the result $Q(I)$ as a special *subset* of the set of witnesses called the *witness basis*. The witnesses of the basis depend on Q ; thus, each basis’s size is bounded by the size of Q . The witnesses of the basis exclude tuples that are irrelevant to t being produced by Q , and thus the basis tends to be very small compared to the set of all possible witnesses [17]. The witnesses are also *minimal*, in the sense that if one tuple is removed from one of these witnesses, it cannot produce the output.

id	name	why-provenance
o_1	Dopamine Receptors	$\{\{f_1, c2f_1, c_1\}, \{f_1, c2f_2, c_2\}\}$
o_2	YANK Family	$\{\{f_4, c2f_4, c_1\}\}$

Table 3: Result of a SQL query applied on the database of Table 1 with the why-provenance of the corresponding results.

466 In a sense, each witness in the witness basis captures one possible way
 467 in which the query can generate the output. To better understand this,
 468 consider the example in Table 3, where each tuple in the result of query **Q1**
 469 is annotated with its why-provenance.

470 The why-provenance of output tuple o_2 has only one witness, which coin-
 471 cides with its lineage. This happens because there is only one way this output
 472 tuple can be produced, i.e., for tuple f_4 to be joined with $c2f_4$ and c_1 . On
 473 the other hand, o_1 has a witness basis with of two witnesses, since there are
 474 two possible ways in which the query can generate o_1 . One possibility is that
 475 f_1 is joined with $c2f_1$ and c_1 (the first witness), and the second possibility
 476 is that f_1 is joined with $c2f_2$ and c_2 (the second witness). This means that
 477 to generate o_1 , it is sufficient that only one of the two witnesses is present in
 478 the input database.

479 4.3. How-Provenance

480 While why-provenance describes the source tuples that witness an output
 481 tuple in the result of the query, it leaves out information about how the source
 482 tuples are used. How-provenance was therefore defined in [30] to capture this
 483 information using a *semiring* algebraic structure, and is a form of provenance
 484 that takes the form of a *polynomial*.

485 The key idea in Green et al. [30] is to use the two operators $+$ and \cdot to
 486 represent two basic transformations that source tuples undergo as a result
 487 of applying a relational query to a database [17]. Two tuples may either be
 488 joined together, as an effect of a join (represented with the \cdot operator) or
 489 merged via union or projection (represented with the $+$ operator).

490 Table 4 shows a simple example in which the two output tuples of our
 491 running example are annotated with their respective how-provenances. Tuple
 492 o_2 was produced through the join among the input tuples $f_4, c2f_4$, and c_1 .
 493 The three provenance tokens are, therefore “multiplied” together. The case of
 494 o_1 is slightly more complex. This tuple, as already discussed, can be obtained
 495 through two different joins. The two monomials composing the polynomial

id	name	how-provenance
o_1	Dopamine Receptors	$f_1 \cdot c2f_1 \cdot c_1 + f_1 \cdot c2f_2 \cdot c_2$
o_2	YANK Family	$f_4 \cdot c2f_4 \cdot c_1$

Table 4: Result of the example SQL query Q1 with the corresponding how-provenances of the output tuples annotated.

represent these two alternatives. They correspond, in a way, to the witnesses of the why-provenance of o_1 . The $+$ operator represents the fact that the two monomials describe alternative derivations. The output tuple is the result of a merge of two distinct tuples after the projection on the attribute **name**. This merge is due to the fact that the result of a relational algebra expression is always a *set* of tuples, which corresponds to the presence of the **DISTINCT** operator in an SQL query. This simple example gives the basic idea behind how-provenance and how it allows us to track the operations that produced an output tuple.

Provenance polynomials may also have monomials whose exponents and/or coefficients are greater than one, for example, $3f_1 \cdot c2f_1 \cdot c_1 + f_1 \cdot c2f_2^3 \cdot c_2^3$. This is a polynomial of a tuple produced by a query where the result of the join between the tuples f_1 , $c2f_1$, and c_1 is produced three times and then merged (e.g. as the result of a projection), and the tuples $c2f_2$ and c_2 are used three times in the operation described by the second monomial (e.g., with nested queries). *** Why would the join tuple be produced 3 times? Perhaps as a result of a union? Projection doesn't make sense ***

5. Credit Distribution and Distribution Strategies

We now give formal definitions of data credit and Data Credit Distribution (DCD), and present three different Distribution Strategies (DSs) based on the forms of provenance discussed earlier: Lineage-based DS, Why-Provenance-based DS, and How-Provenance-based DS. We also show how these strategies distribute credit in the IUPHAR example discussed earlier.

5.1. Data Credit and Data Credit Distribution

Given a database instance I , a *recipient of credit* is a unit of information within I . In the case of relational databases, recipients may be (i) the whole database; (ii) a table; (iii) a tuple; or (iv) an attribute.

523 *Data credit* is a value $k \in \mathbb{R}_{>0}$. Every recipient in a database is annotated
 524 with a quantity of credit as a proxy for its importance. In this paper, we
 525 focus on *tuples* as recipients of credit.

526 Given a *distribution strategy* (DS), *Data Credit Distribution* (DCD) takes
 527 a database instance I , quantity of credit k , and query Q over I , and splits k
 528 among the recipients of credit in I .

529 In the following, we use the notation in Cheney et al. [17]: Given an
 530 instance I , a *tuple location* (R, t) is a tuple t in relation R . With reference to
 531 the running example, $(\text{family}, \langle f_1, \text{Dopamine Receptors}, \text{gpcr} \rangle)$ is the
 532 tuple location of the first tuple in the **family** relation. The set of all tuple
 533 locations in I is called *TupleLoc*. We use this to formally define DCD at the
 534 *tuple level*.

535 **Definition 5.1. Tuple Level Data Credit Distribution (DCD) [24]**
 536 *Given a query Q over I and $k \in \mathbb{R}_{>0}$, DCD is defined by the function $f_{I,Q} :$
 537 $\text{TupleLoc} \times \mathbb{R}_{>0} \rightarrow \mathbb{R}_{\geq 0}$ such that $f_{I,Q}(t, k) = h$ where $0 \leq h \leq k$ and
 538 $\sum_{t \in \text{TupleLoc}} f_{I,Q}(t, k) = k$. The function $f_{I,Q}$ is the distribution strategy (DS).*

539 As we can see, the DS is a function that annotates each tuple in the
 540 database with a real value, which is a fraction of the given quantity k . The
 541 only constraint is that the sum of the credit annotations on tuples must be
 542 k , i.e. that no credit is generated or destroyed during the distribution. Given
 543 I and Q , many different DSs may be defined as long as they sum up to k .

544 In what follows, we use information provided by data provenance to de-
 545 fine distribution functions. For simplicity, we assume that the credit k is
 546 distributed equally across the set of output tuples (i.e. the result of a query),
 547 and discuss how the credit of one output tuple o , k_o , is distributed across the
 548 instance I .

549 5.2. A Lineage-based Distribution Strategy

550 In the lineage-based distribution strategy, each tuple in the output of
 551 a query distributes credit equally to each input tuple that appears in its
 552 lineage. More formally:

Definition 5.2. Lineage-based Distribution Strategy [24]

*Let I be a database instance, Q a query over I , $o \in Q(I)$ an output tuple and
 k_o the credit associated to o . Let L be the lineage of o and t be a tuple in I ,*

then t receives credit equal to:

$$f_{I,Q}(t, k_o) = \begin{cases} 0 & \text{if } t \notin L \\ \frac{k_o}{|L|} & \text{if } t \in L \end{cases}$$

553 Note that lineage-based DS distributes credit only to input tuples that
 554 have a role in creating o by the query Q , and that each receives an equal
 555 share of credit via o . Thus, the more tuples in a lineage set, the less credit
 556 each tuple receives.

557 As an example, consider the output tuples of Table 2, and assume that
 558 each output tuple has credit $k_o = 1$. The lineage of the first tuple, o_1 , is
 559 the set $\{f_1, c2f_1, c_1, c2f_2, c_2\}$. Therefore, each tuple in this set receives credit
 560 $1/5$. The other tuples of the database receive zero credit. The lineage of the
 561 second output tuple is $\{f_4, c2f_4, c_1\}$, therefore each of these tuples receives
 562 credit $1/3$.

563 At the end of the process, tuples f_1 , $c2f_2$ and c_2 each receive credit $1/5$,
 564 tuples f_4 and $c2f_4$ receive $1/3$, while tuple c_1 receives $8/15$. Note that if a
 565 tuple appears in more than one lineage set, then it will accumulate credit
 566 from the distribution associated with each one of these sets, implying that
 567 it has a more significant role in the context Q , as is the case with c_1 in this
 568 example.

569 Not all of the tuples in the lineage of an output tuple are necessary to be
 570 present at the same time for the output tuple to appear in the query results.
 571 For example, if the database only had the set of tuples $\{f_1, c2f_1, c_1\}$ or the set
 572 $\{f_1, c2f_2, c_2\}$, the existence of o_1 would still be guaranteed. In other words,
 573 while f_1 is always needed for o_1 to appear in the output, only one of the sets
 574 of tuples $\{c2f_1, c_1\}$ and $\{c2f_2, c_2\}$ is required. One could therefore argue that
 575 it would be more fair for f_1 to receive more credit than the other four tuples,
 576 given its role in producing o_1 .

577 This highlights one limitation of the lineage-based DS: while able to find
 578 all and only the relevant tuples of the output, it does not distinguish the
 579 *importance* of tuples in the query computations. We therefore present two
 580 other, more sophisticated, forms of distribution strategies based on why- and
 581 how-provenance.

582 5.3. A Why-Provenance-Based Distribution Strategy

583 The distribution strategy based on why-provenance first equally distributes
 584 the credit k_o among the witnesses of the witness basis for o , and then equally

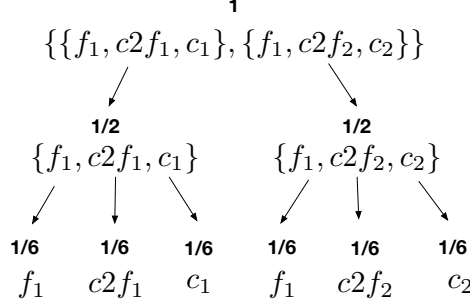


Figure 4: Distribution of credit using why-provenance-based DS for tuple o_1 .

divides the credit of a witness among the tuples in the witness. Since a tuple may appear in more than one witness, it will receive more than one portion of credit from the same distribution. More formally:

Definition 5.3. *Why-Provenance-based Distribution Strategy*

Let I be a database instance, Q a query over I , $o \in Q(I)$ an output tuple and k_o the total credit associated to o . Let $\mathcal{W} = \text{Why}(Q, I, o)$ be the witness basis of o according to Q and I , and $W \in \mathcal{W}$ be a witness.

Then tuple t in I receives credit equal to:

$$f_{I,Q}(t, k_o) = \frac{k_o}{|\mathcal{W}|} \sum_{W \in \gamma(\mathcal{W}, t)} \frac{1}{|W|}$$

where γ is a function which returns all witnesses W in which t appears:

$$\gamma(\mathcal{W}, t) = \{W \in \mathcal{W} : t \in W\}$$

Figure 4 shows the distribution of credit with why-provenance-based DS for tuple o_1 . The credit is first equally divided between the two witnesses, so that both receive credit $1/2$. The credit is then further divided among the tuples in each witness. Since each witness has three tuples, each tuple in a witness receives $1/6$ of credit. At the end of the distribution, f_1 receives a total credit of $1/3$, and the other tuples receive $1/6$ each. This distribution better reflects the role of f_1 in the generation of o_1 since, as discussed earlier, it is the only mandatory tuple for o_1 to appear in the output; only one of the two other pairs of tuples are necessary for o_1 to appear in the result.

This example illustrates that why-provenance can better reward input tuples depending on their role. Tuples that appear in more than one witness are rewarded more than others.

$$\begin{aligned}
\mathcal{H} &= \underbrace{3f_1 \cdot c2f_1 \cdot c_1}_{M_1} + \underbrace{f_1 \cdot c2f_2^3 \cdot c_2^3}_{M_2} \\
c(\mathcal{H}) &= 4 & c(M_2) &= 7 \\
mc(M_1) &= 3 & mc(M_2) &= 1 \\
e(c_2, M_2) &= 3 & \gamma(c_1, \mathcal{H}) &= \{M_1\} \\
\gamma(f_1, \mathcal{H}) &= \{M_1, M_2\}
\end{aligned}$$

Figure 5: Illustration of notation used to define the how-provenance based DS in Definition 5.4.

5.4. A How-Provenance Based Distribution Strategy

How-provenance conveys more information than why-provenance since it not only captures what tuples are relevant to the output and in which combination, but also how they are used. The “how” is captured through the provenance polynomials.

The how-provenance-based DS therefore first distributes the credit to the monomials of the polynomial accordingly to the weight represented by their coefficients, then to the tuples of each monomial accordingly to the weights represented by their exponents.

To define the DS more formally, we introduce some notation and illustrate it using the provenance polynomial \mathcal{H} shown in Figure 5.

We call c the function that, given a polynomial, returns the sum of the coefficients of the polynomial; thus $c(\mathcal{H}) = 3 + 1 = 4$. We use the same name for the function that, given a monomial, returns the sum of its exponents; thus $c(M_2) = 1 + 3 + 3 = 7$. mc is the function that takes as input a monomial and returns its coefficient. e is a function that takes as input a tuple and a monomial, and returns the exponent of the tuple in the monomial, if present; thus $e(c_2, M_2) = 3$. γ takes as input a tuple and the whole polynomial, and returns a set containing the monomials containing that tuple, if present in the polynomial; thus $\gamma(f_1, \mathcal{H}) = \{M_1, M_2\}$.

Definition 5.4. How-Provenance-Based Distribution Strategy

Let I be a database instance, Q a query over I , $o \in Q(I)$ an output tuple, \mathcal{H} be the provenance polynomial for o , and k_o the credit given to o . The credit given to tuple t in I is:

$$f_{I,Q}(t, k_o) = \frac{k_o}{c(\mathcal{H})} \sum_{M \in \gamma(t, \mathcal{H})} mc(M) \frac{e(t, M)}{c(M)}$$

id	name
oxs_1	Dopamine Receptors

lineage	why-provenance	how-provenance
$\{f_1, c2f_1, c_1, c2f_2, c_2\}$	$\{\{f_1, c2f_1, c_1\}, \{f_1, c2f_2, c_2\}\}$	$f_1^2 c2f_1 c_1 + f_1^2 c2f_2 c_2$

Table 5: Result of query Q2 applied on the database of Table 1 and its different provenances. The reported numbers are the credit distributed through the process.

628 Going back to the example of Table 4, consider o_1 with provenance poly-
629 nomial $f_1 c2f_1 c_1 + f_1 c2f_2 c_2$. The how-provenance-based DS firstly divides
630 the credit between the two monomials. Since the coefficients of each mono-
631 mial are 1, the credit is split in half. If they were, for example, 1 and 2
632 respectively, 1/3 of the credit would go to the first monomial, and 2/3 to
633 the second. Since in our example each variable has exponent 1, the credit
634 is further divided equally among the three variables. Thus, at the end of
635 the computation, f_1 receives 1/3, and the other tuples receive 1/6. If, for
636 example, the first monomial was $f_1^2 c2f_1 c_1$, then the portion of credit of this
637 monomial would be divided in this way: 1/2 to f_1 and 1/4 to each of the
638 other two tuples.

639 In this specific example, the how-provenance-based DS has the same out-
640 come as the one based on why-provenance. We therefore consider another
641 query over GtoPdb, Q2, that asks for the families of type **gpcr** that have as
642 contributor a researcher located in the UK:

```

643        Q2: SELECT DISTINCT F.name
644        FROM family as F JOIN
645        (SELECT DISTINCT f.name AS name
646        FROM family AS f JOIN contributor2family AS c2f ON f.id = c2f.family_id
647        JOIN contributor AS c ON c2f.contributor_id = c.id
648        WHERE c.country = "UK") AS R ON F.name = R.name
649        WHERE F.type = "gpcr"

```

650 The result of Q2 is shown in Table 5, and consists of one tuple, anno-
651 tated with each of the three provenances. As can be seen, lineage and why-
652 provenance are identical to those of the tuple o_1 in the previous example.
653 The how-provenance, however, is different since tuple f_1 is used twice: first
654 in the join of the inner query, and second in the join of the outer query. This
655 information is lost in the first two forms of provenances since they are sets,
656 but it is captured in how-provenance through the use of the operator ‘.’.

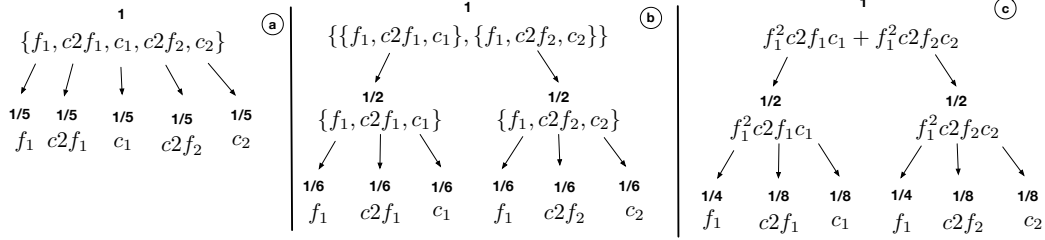


Figure 6: Comparison of different distributions strategies for tuple o_1 produced by query Q2.

Figure 6 shows the differences between the three DS for the tuple o_1 of Table 5. Subfigure 5.a uses lineage, sub-figure 5.b uses why-provenance, and sub-figure 5.c uses how-provenance. The DS based on the provenance polynomial gives credit $1/2$ to f_1 , and $1/8$ to the other tuples. This is reasonable since Q2 relies on f_1 even more than Q1 does. The distribution based on how-provenance can reward f_1 more, showing that how-provenance is even more sensitive to the tuples' role in a query than why-provenance. This is a direct consequence of the fact that, as proven in [30], how-provenance is more general than why-provenance and lineage, in the sense that it contains more information.

6. Experimental Evaluation: comparing provenances

6.1. Real-world queries

We evaluate the proposed distribution strategies on GtoPdb, and in particular we focus on target families, all of those are described in pages of the GtoPdb website. There are eight family types: *GPCR*, *Ion channels*, *NHRs*, *Kinases*, *Catalytic receptors*, *Transporters*, *Enzymes* and *Other protein targets*.

When a paper uses data from GtoPdb, it can cite the full database, the webpage of interest, or a subset of data extracted with a query. We consider as sources of citations the papers published in the British Journal of Pharmacology (BJP)¹¹, since each time they cite a webpage from GtoPdb, they report the URL of that page. From that URL it is possible to reverse-engineer the queries that are used to obtain the data contained in the pages.

¹¹<https://bpspubs.onlinelibrary.wiley.com>



Figure 7: Comparison of three DS on the same table `family` using the distribution given by the queries retrieved from papers.

680 In particular, we considered all the 889 papers in BJCP citing [31] as of
 681 October 2020. [31] is a data journal that describes the structure and evolution
 682 of GtoPdb. ERach two years the GtoPdb consortium releases such a journal
 683 to describe the evolution of the databases. At the time of writing, this paper
 684 received more than 1200 citations.

685 The queries that we inferred are the ones building the information that
 686 constitutes a target family webpage are depicted in Figure 3 (with the excep-
 687 tion of the section References). In the figure, we can see how the structure of
 688 one family, “Adenosine receptors”, is mapped into several queries to obtain
 689 the information to build the corresponding webpage. In GtoPdb, all target
 690 family pages share a similar structure (the only differences is that certain
 691 sections, such as “contributors” or “further readings”, may be absent). The
 692 same queries can therefore be used to build all the target family pages by

693 simply changing the family id used in the query (which, in the example of
694 Figure 3, is 3). All these queries are SPJ. A total of more than 12K different
695 queries were built in this way¹². We assumed that each tuple in the output
696 of each of these queries carries credit 1.

697 Figure 7 shows the heat-maps obtained by the distribution of credit per-
698 formed by the three different DS on the GtoPdb table `family`. `family` is
699 a table describing the characteristics and basic information of the receptor
700 families and, as can be seen in Figure 3, it is often used in join with other
701 tables in the queries that build a webpage.

702 It is immediately evident that the result of the distribution is the same
703 with the three strategies. The same effect is also obtained in the other tables
704 of the database used by the queries shown in Figure 3.

705 Why is that? It is the case that the conditions in which we produced
706 this experiment are quite peculiar. The queries that we used share similar
707 characteristics. They are all SPJ queries, each of them utilizes each table
708 only once in the join condition (there are no self-joins), and all the joins
709 are made using key attributes. In this particular condition, each tuple of
710 the output presents: (i) a how-provenance that is a single monomial with
711 coefficient 1 and exponent 1 in each variable; (ii) a why-provenance that is
712 composed by only one witness; (iii) a lineage that coincides with the only
713 witness in the witness basis. It is easy to see how, given these queries, the
714 three distributions act in the same way. The credit is always uniformly
715 distributed among the tuples appearing in each provenance.

716 To better clarify what is happening, let us consider one of the types of
717 queries used to build the output webpage, as shown in Figure 3:

```
718 Q3: SELECT c.first_names, c.surname
719 FROM contributor2family AS cf JOIN contributor AS c ON
720 cf.contributor_id = c.contributor_id
721 WHERE f.family_id = 3
```

722 Q3 returns a series of 10 tuples from the version of GtoPdb we considered.
723 The first tuple produced by this query, <Bertil B., Fredholm>, that has
724 $c_{939} \cdot c_{2f_{496}}$ as provenance polynomial. c_{939} represents the provenance token of
725 a tuple in `contributor`, the same for $c_{2f_{496}}$ in table `contributor2family`.

¹²For reproducibility purposes, the code we used for our experiments and all the pro-
duced queries can be found at the following link: https://bitbucket.org/dennis_dosso/credit_distribution_project.

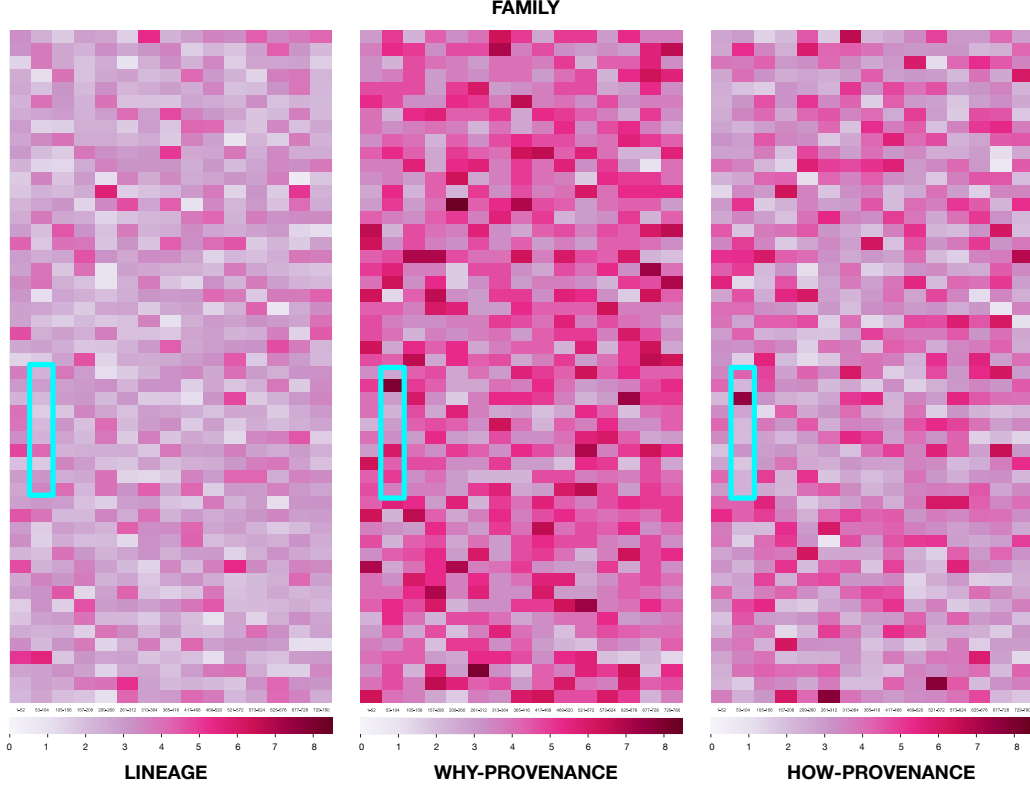


Figure 8: Comparison of three DS on the same table `family` after the distribution computed using 10K synthetic and randomly generated provenance polynomials. The tuples in the blue rectangles are used as example in the discussion connected to Figure 9.

It is easy to see that the why-provenance of this tuple is $\{\{c_{939}, cf_{496}\}\}$ and its lineage is $\{c_{939}, c2f_{496}\}$. Therefore, the credit assigned to these tuples is $1/2$ using all three DS. This actually happens for each tuple of the output of each query of GtoPdb, thus making the distributions equivalent with respect to their output.

This is not always the case with general queries and other databases. As we showed in the examples in the previous section, when two or more tuples are merged by the effect of a projection or union, we see sensible differences between the three distribution strategies.

6.2. Synthetic queries

To show how the three DS can actually behave differently, let us consider another case shown in Figure 8.

738 The figure reports a distribution of credit performed on the table **family**
739 through the generation of 10K *synthetic* polynomials. We randomly gen-
740 erated provenance polynomials that might be the how-provenance of ran-
741 domly generated synthetic queries, using the three GtoPdb tables **family**,
742 **contributor2family**, and **contributor**. An example of such synthetic poly-
743 nomial is:

$$3f_1^3c_2f_1^2c_1^2 + 2f_1c_2f_2^3c_2^3 + 4f_5c_2f_{17}^4c_{18}^3$$

744
745 As can be seen, we made sure to also include coefficients and exponents
746 that differ from 1. Its corresponding why-provenance is:

$$\{\{f_1, c_2f_1, c_1\}, \{f_1, c_2f_2, cf_2\}, \{f_5, c_2f_{17}, c_{18}\}\}$$

747
748 its lineage is:

$$\{f_1, f_5, c_2f_1, c_1, c_2f_1, c_2f_2, c_2f_{17}, c_1, c_2, c_{18}\}$$

749
750 These types of polynomials are not impossible to obtain in real life, since
751 they can be obtained by nested queries with join and union operations that
752 use multiple times the same tuples (thus the presence of exponents bigger
753 than 1) and the same combination of operations more than once (thus the
754 presence of coefficients for monomials bigger than 1). We randomly generated
755 a set of 10K such polynomials.

756 Using how-provenance, this is the distribution obtained from the example
757 polynomial we are considering:

$$f_1 = \frac{59}{315}, f_5 = \frac{1}{18}, c_2f_1 = \frac{2}{21}, c_2f_2 = \frac{2}{15}, c_2f_{17} = \frac{2}{9}, c_1 = \frac{2}{21}, c_2 = \frac{2}{15}, c_{17} = \frac{1}{6}$$

758
759 Using why-provenance, this is the output:

$$f_1 = \frac{2}{9}, f_5 = \frac{1}{9}, c_2f_1 = \frac{1}{9}, c_2f_2 = \frac{1}{9}, c_2f_{17} = \frac{1}{9}, c_1 = \frac{1}{9}, c_2 = \frac{1}{9}, c_{17} = \frac{1}{9}$$

760
761 Finally, with lineage, this is the distribution:

$$f_1 = \frac{1}{8}, f_5 = \frac{1}{8}, c_2f_1 = \frac{1}{8}, c_2f_2 = \frac{1}{8}, c_2f_{17} = \frac{1}{8}, c_1 = \frac{1}{8}, c_2 = \frac{1}{8}, c_{17} = \frac{1}{8}$$

762
763 To highlight how the distributions behave differently with these polynomi-
764 als, consider tuple f_5 . f_5 receives the highest quantity of credit when we use

765 the lineage-based distribution. Why-provenance and how-provenance reduce
766 its quantity of credit since more information is available for the computation
767 and the algorithms weigh less and less its role.

768 Generally speaking, the more complex the distribution, the more polar-
769 ized the credit is toward the tuples that are used more frequently or with a
770 higher impact in the production of the output tuple.

771 Going back to Figure 8, it is thus possible to observe empirically how the
772 three provenances behaved differently. We put the maximum value for the
773 heat-maps around 8.33, since that is the highest value reached by a tuple
774 in all three distributions. We note that lineage is the provenance that gives
775 less credit to the tuples of the **family** table. This is due to the fact that the
776 DS equally distributes the credit to all the tuples appearing in the lineage.
777 Since other two tables are used by these queries, the credit is also given to
778 the tuples of those tables.

779 Moving to the heat-map reporting the distribution performed by the DS
780 based on why-provenance, we see that this time more credit is given overall
781 to the tuples of the table. Actually, this DS is the one that distributes more
782 credit to **family** among the three strategies. This is due to the fact that the
783 DS based on why-provenance also takes into account the different ways in
784 which a tuple is used, e.g. in different joins. If the same tuple is present in
785 more than one witness, it is more probable that it will attract more credit,
786 “stealing” it from the other tuples in the witness basis. In this case, **family**
787 was able to attract more credit, taking it from the other two tables, due to
788 the role of its tuples in the queries that were executed.

789 Considering now the heat-map produced by the DS based on how-provenance,
790 we see how, although it presents more credit in its tuples than the one present
791 in the lineage heat-map, it does not reach the levels of the why-provenance
792 heat-map. This is due to the fact that this DS is even more sophisticated,
793 weighting even more than the previous DS the role of tuples in the production
794 of the output. The result is a distribution that still rewards the tuples of this
795 table more than lineage, but not in the same measure as the DS based on
796 why-provenance, since the other tuples in the other tables are able to attract
797 more credit due to their roles in the queries.

798 To show how the DS based on different provenances may actually differ
799 in their behavior also through the course of time, let us consider Figure 9.

800 In this figure we report four groups of heat-maps. Each group presents
801 three maps obtained by selecting the same ten tuples from the GtoPdb
802 **family** table after an incremental distribution of credit (the tuples of ranks



Figure 9: Comparison of the distribution of credit performed by the three DSs on a subset of 10 tuples taken from table `family` simulating the passing of time. The number on top of each group of heat-maps represent the number of queries computed.

803 ranging from 79 to 89). These are the same tuples highlighted in the blue
804 boxes in Figure 8. In particular, the four groups represents “snapshots”
805 taken during an incremental accumulation of credit on the database, at dif-
806 ferent moments chosen when a certain number of executed queries is reached
807 (specifically, 1K, 2K, 5K and 10K). Figure 8 represents the end of the process.

808 In this way we are simulating the passing of time on a database where
809 credit distribution is performed. Each group of heat-maps can be thought
810 as a snapshot of that set of tuples at a certain moment, after a certain
811 amount of queries are executed. The queries utilized are the same of the
812 experiment of the previous section. The range of credit in each map goes
813 from 0 (no credit) to 6 (maximum quantity of credit reached on a tuple at

814 the “snapshot” reached at 10K queries).

815 Focusing on the 1K and 2K groups, we see that the three DS do not
816 behave very differently. The tuples highlighted by the three are almost the
817 same. There are still small differences, in particular in tuple 5.

818 The first interesting differences appear at 5K queries. In par-
819 ticular, we note how tuple 7 is rewarded poorly by the DS based on lineage,
820 while it is rewarded more by why-provenance-based DS and most of all by the
821 DS based on how-provenance. This is due to the fact that tuple 7 appears in
822 a relative low number of lineages, but its role is critical to these queries, thus
823 the other DS reward it more. On the other hand, a tuple as 5 is rewarded by
824 the DS based on lineage and why-provenance, and less by how-provenance.
825 This means that, although tuple 5 appears in many queries and it is used in
826 different combinations, its exponents in the provenance polynomials where it
827 appears must be low, therefore giving it low credit with how-provenance. It
828 is also interesting to note how certain tuples, like 1, that up until 2K queries
829 presented the highest values of credit, are now surpassed by other tuples like
830 2. This shows how credit is able, during the passage of time, to keep track
831 of the “hotspots” in a database. The presence of new queries and new credit
832 distribute can change the hotspots in a table, showing how the interests of
833 the research community may change during time.

834 Finally, the highest differences are shown in the 10K group. In this case,
835 we see a situation similar to the one already seen with the case of 5K queries.
836 Certain tuples, like 8 or 10, receive more credit with why-provenance and
837 how-provenance, rather than with lineage. This is still due to the important
838 role of the tuple in the queries where it appears.

839 From this progression we see how, given the peculiar synthetic provenance
840 polynomials that we presented, it is actually possible to see the differences
841 between the three distribution. These differences become more and more
842 evident with the passing of time, i.e. the more credit is distributed to the
843 tuples.

844 Therefore, although all the three DS considered here are effective in dis-
845 tributing credit, they actually behave differently. The DS based on lineage
846 is sufficient when a user only wants to highlight the tuples of the database
847 that are used by a query (and not only visualized in the output). However,
848 it distributes the credit equally to the tuples of the lineage, therefore losing
849 information on the role of the tuples in the production of the output.

850 For this, a user may want (depending on the nature of the queries) to
851 use DS based on why-provenance and how-provenance. The two are more

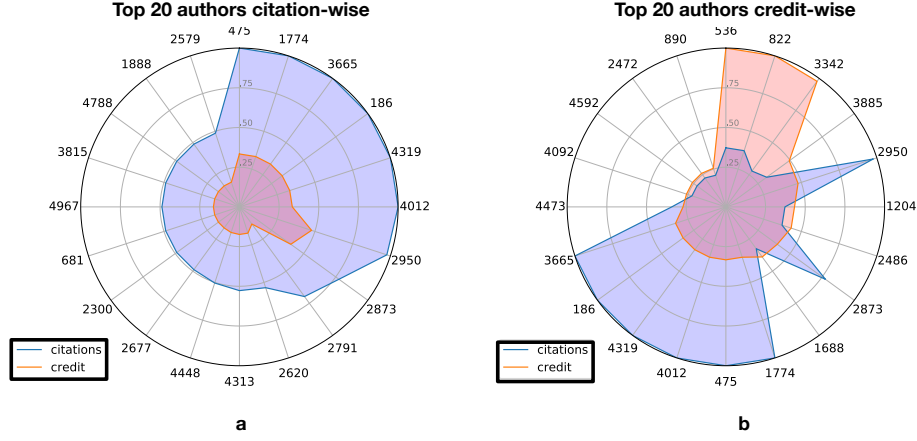


Figure 10: Radars presenting the top 20 authors citation-wise and credit wise, together with their (normalized between 0 and 1) values of citations and credit.

sensitive than the DS based on lineage (and the DS based on how-provenance is more sensible than the one based on why-provenance). Therefore, using these DS, it is possible to change the distribution of credit to the tuple, rewarding more the tuples that have a more important role in the generation of the output. These two DS can therefore be preferred when the aim of the user is to find “hotspots” in the database based on the role of the tuples.

In particular, the DS based on why-provenance rewards more the tuples that are used in different ways by queries (i.e. are members of more witnesses). The DS based on how-provenance also takes into consideration how many times a tuple is used, adding even more sensibility to the distribution. One may choose one or the other depending what are the aspects he wants to highlight in the data.

6.3. Credit vs Citations

For our last set of experiments, we confront traditional citations and credit, to see if they differ in their behaviour in the case of rewarding the curators of data. Consider first Figure 10, where we report two radar plots. The first plot presents the top 20 author (we identify the authors with their ID instead of their name), ordered based on the normalized value of citations distributed by the queries taken from the papers published in BJP as described in Section 6.1, together with their normalized value of credit. An author transitively receives credit from the data of which he or she is the cu-

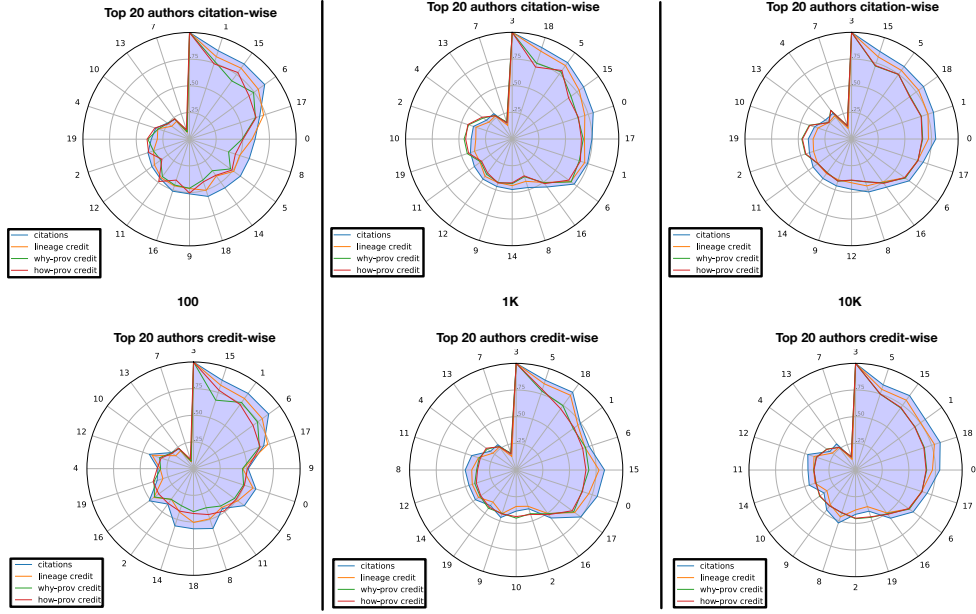


Figure 11: Radars presenting 20 authors ordered citation-wise and credit-wise, together with their (normalized between 0 and 1) values of citations and credit, through the execution of different numbers of polynomials (100, 1K, and 10K). The radar plots ordered by credit consider the credit assigned by the DS based on how-provenance.

873 rator. That is, the credit assigned to data is then split equally to the authors
874 of those tuples. As we show in Section 6.1, there is no difference for these
875 queries in the distribution of credit between the three DS, thus these values
876 are equal for the three distributions. The second plot is similar to the first
877 one, but the authors are ordered based on the received credit.

878 As we see, the quantity of credit does not follow the quantity of citations,
879 i.e. it is not true that an author that presents the highest number of citations
880 also has the highest value of credit. As shown in Figure 10.b, the authors with
881 the highest value of credit do not also have the highest number of citations.
882 This means that there are citations that are much more “valuable” for an
883 author in terms of credit. This is due to the fact that the quantity of credit
884 assigned by these citations is very high, i.e. the impact of those cited data
885 is high.

886 This shows how credit is able to reward authors that are cited less than
887 others but, nonetheless, have a high impact on the research community.

888 Consider now Figure 11. In this case, we produced 100, 1K, and 10K syn-

889 thetic polynomials and we distributed credit and assigned citations through
890 them. Since these polynomials correspond to queries whose authors are not
891 easily identifiable, we created 20 “synthetic” authors, and we randomly as-
892 signed one author to each tuple in the database. The authors receive “blocks”
893 of consecutive tuples, with each block of the size varying between 10 and 40.
894 Every time a tuple was used in a provenance polynomial, we assigned one
895 citation to the author corresponding to the tuple. The same author also
896 receives the three different credits assigned to the tuple at the end of the
897 distribution process using the three DS.

898 The three radar plots in the upper row presents 20 authors are sorted
899 based on the normalized number of received citations, together with the
900 corresponding normalized quantities of credits assigned using the 3 different
901 strategies. The ones in the bottom row present the authors ordered based on
902 the quantity of credit assigned by the DS based on how-provenance. In this
903 way we can see the behavior of the different DS in rewarding the authors with
904 the highest levels of citations. Given the synthetic nature of these queries,
905 the correlation between the number of citations and the quantity of credit
906 assigned to the authors appears to be a much stronger with respect to the
907 case with the real-world queries.

908 Nonetheless, it is possible to note that credit still behaves differently,. In
909 particular we still see that certain authors that are not in the top 10 positions
910 citation-wise are still rewarded with high quantities of credit, showing their
911 importance with respect to their impact. Interestingly, scaling up to 1K
912 and 10K polynomials, it appears that the distribution performed via why-
913 provenance and how-provenance become equivalent for the authors. We can
914 note that, although not exactly equal, the values of credit assigned to the
915 authors by those DS become quite similar with these higher quantities of
916 polynomials.

917 6.4. Execution times

918 In Table 5 we report the time required to compute the distribution us-
919 ing the DS based on the three provenances as described above. As we see,
920 the execution time grows linearly with the number of polynomials that are
921 submitted to the system. With high values of polynomials (1M), the time
922 required by the DS based on lineage and why-provenance is lower than the
923 time required by the DS based on how-provenance, due to the bigger number
924 of operations the last DS requires during the computations of the portions
925 of credit to assign to the different tuples. We note that, since we created

# of polynomials	lineage	why-prov.	how-prov.
100	226.6 ms	192.0 ms	185.5 ms
200	431.2 ms	392.2 ms	403.2 ms
500	1.013 s	934.2 ms	881.8 ms
1K	2.041 s	1.934 s	1.744 s
2K	3.773 s	3.491 s	3.510 s
5K	8.992 s	8.653 s	8.889 s
10K	17.10 s	16.84 s	16.84 s
20K	34.59 s	35.30 s	39.70 s
100K	3.289 min	3.442 min	3.652 min
1M	35.91 min	34.87 min	37.91 min

Table 6: The times required to perform the three DS for different number of synthetic polynomials.

these polynomials on-the-fly, these values do not include the time required to compute the provenances. Therefore, limited to the time required to distribute credit, the three DS are equivalent in terms of performances. The first differences can be seen only with high number of polynomials, when lineage and why-provenance may be preferred if there are no requirements to assign credit with the strategy implemented by the how-provenance-based DS.

All the experiments were carried on a MacBook Pro 13-inch, 2019 with 2.4 GHz processor Intel Core i5 quad-core, 8 GB of memory at 2133 MHz with code written in Java and the support of a PostgreSQL database.

7. Conclusions

This paper expanded on our previous work on data credit and data credit distribution in [24] by defining two new distribution strategies, based on why- and how-provenance. The first distribution is based on the concept of witness, and it can give more credit to tuples that appear in more than one witness. In other words, tuples that are more important to the query and are used in different ways are also rewarded more by the strategy. The second DS, based on how-provenance, considers the frequency in which a tuple or a combination of tuples is used in the query through the information contained in the provenance polynomial. In this case, the distribution is even more sensitive than the first one to the role and importance of tuples.

947 To show the differences between the three DS (also considering the one
 948 based on lineage, defined in our previous work), we performed different ex-
 949 periments on GtoPdb, a curated scientific relational database, with the use
 950 of both real and synthetic queries. In the first set of experiments, we used
 951 SPJ queries extracted by data citations present in papers published in the
 952 British Journal of Pharmacology. Employing these queries, we were able to
 953 distribute the credit to the tuples in different tables of the database, high-
 954 lighting the tuples used more than others. We showed that with these queries,
 955 the three strategies produce the same distribution. These are SPJ queries
 956 that do not present self-joins, and therefore the formulas at the base of the
 957 DS have the same output.

958 In the second set of experiments, we synthetically produced more complex
 959 provenance polynomials, corresponding to more complex synthetic queries,
 960 that present exponents and coefficients different than 1. In this way, we
 961 showed that, even though all three DS can highlight all the tuples used by
 962 the queries in the database, the three have different behaviors. While the DS
 963 based on lineage rewards all the tuples used by a query in equal measure, the
 964 strategy based on why-provenance tends to reward the tuples more critical
 965 to the query. In particular, why-provenance can consider the different ways
 966 in which one tuple is used in a query. How-provenance is even more sensitive
 967 to the tuples' role: it can also consider the frequency by which a tuple or a
 968 set of tuples is used in the case of more complex queries. Depending on the
 969 goal of a user, one provenance may be preferred to another.

970 We also showed how the differences between the DS become more and
 971 more evident with the passing of time, i.e. when more and more polynomials
 972 are processed by the system.

973 In the third set of experiments we compared the citations to the authors
 974 to the credit brought to them. We showed how, both in the real-world and
 975 synthetic scenarios the credit rewards more the authors that have a higher
 976 impact, i.e. the authors connected to the data that produce the highest
 977 quantities of credit, and not necessarily the data with the highest citation
 978 count. In this sense, credit appears to be an useful new measure to discover
 979 data and their corresponding curators that have a high impact in the research
 980 world, even when they are cited few times or do not appear at all in the data
 981 that are cited (i.e. the case of data used to build the output of a query but
 982 that is not visualized in the output itself).

983 In future work, we plan to explore the different potential applications of
 984 credit on relational databases. One example is the so-called *data pricing*.

985 Data pricing consists of giving a price to a query submitted by a user who
 986 wants to buy the produced information. Currently, a commonly used strategy
 987 to face data pricing is based on query rewriting. A database stores a set of
 988 views correlated with their price. When a new query arrives, the system tries
 989 to rewrite it using the stored views and obtain a query price. This process
 990 is computationally expensive. We plan to distribute credit through carefully
 991 planned and representative queries and use it as information to define a new,
 992 faster, and potentially more flexible pricing function.

993 Another application is *data reduction* [42], concerned with reducing the
 994 vast mole of data that is produced in the evolving world of research and
 995 information technology. Data reduction deals with different aspects of dealing
 996 with huge amounts of data, such as finding reduced and relevant data streams
 997 from the multiple gigabytes of data produced by big data systems every
 998 second or dealing with the curse of dimensionality which requires unbounded
 999 computational resources to uncover actionable knowledge patterns [51].

1000 Data credit can also help to find “hotspots” and “coldspots”. A hotspot
 1001 is data in a database (a tuple or a single attribute, for example) that presents
 1002 a high quantity of credit and is therefore valuable for the set of queries that
 1003 distributed that credit. On the other hand, a coldspot is data that present
 1004 low quantities of credit and can be considered useless or less relevant and can
 1005 therefore be removed or moved in another cheaper and less efficient memory
 1006 location.

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