Credit Distribution through Data Provenance in Relational Scientific Databases

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ABSTRACT

In the current world of research data is a fundamental tool 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, recently data credit has emerged as a new measure of value, built on top of the data citation theory. Data is a real value that represents the importance of data cited by a paper, or another research entity, in the context defined by that entity. As such, credit can be used to annotate data contained in curated scientific databases, and be considered as a measure for their importance. 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 explored 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. In particular, we define two new distribution strategies, functions that perform this task, based on two form of data provenance, namely why-provenance, and how-provenance.

As use case and for evaluation purposes, we adopt the IUPHAR/BPS Guide to Pharmacology (GtoPdb), a curated relational database. We use these two strategies, together with a third one, based on lineage, previously defined in another our paper, to 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 corresponding curators. Credit in particular rewards data and authors based on their research impact, and not merely on the number of citations.

Our experiments also highlight the fact that the why-provenance-based strategy is more sensible than lineage to the role of an input tuple in the generation of an output, rewarding more tuples that have a more fundamental role. Even more so with the how-provenance-based strategy.

1 INTRODUCTION

Citations are an essential component of 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 (Zou and Peterson, 2016; Cousijn et al., 2019; Cronin, 1984). Citations are used, among other things, to decide on tenure, promotion, hiring, and funding of grants for researchers (Meho and Yang, 2007; Cronin, 2001; Hartley, 2017; Kosten, 2016).

Nowadays, science and research are increasingly digital. There are numerous curated databases that are at the core of scientific research efforts (Buneman et al., 2016). It is therefore generally accepted that data must be cited and citable (Lawrence et al., 2011; Callaghan et al., 2012), and that data citations should contribute to the scientific reputation of researchers, scientists, data curators, and creators (Altman et al., 2015; Spengler, 2012). It is also accepted that data citations should be counted alongside of traditional citations, and contribute to bibliometrics indicators (Belter, 2014; Peters et al., 2016).

A central problem in data citation is how to attribute credit to data creators and curators (Buneman et al., 2020). 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, 1999; Borgman, 2016). 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 (Alawini et al., 2018).

Recently, the concepts of *data credit* and *Data Credit Distribution* (DCD) (Fang, 2018; Katz, 2014; Zeng et al., 2020) 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, data citations (at any level of granularity) must be available.

Katz et al. (2020) 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 base of systems such as Google Scholar and Web of Science. Zeng et al. (2020) and Fang (2018) further explored this concept by defining frameworks for the automatic 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, as proposed to some extent in a traditional setting by the zp-index (Zou and Peterson, 2016) for the role of authors in a paper.

2. Traditional citations are considered to be *atomic*. One 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 used [2] and are the main focus of current work in data citation methods (Buneman and Silvello, 2010; Buneman et al., 2016; Pröll and Rauber, 2013). 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.

We summarize the DCD process in Figure 1:

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

[2] The "relational database market alone has revenue upwards of $50B" (Abadi et al., 2020).

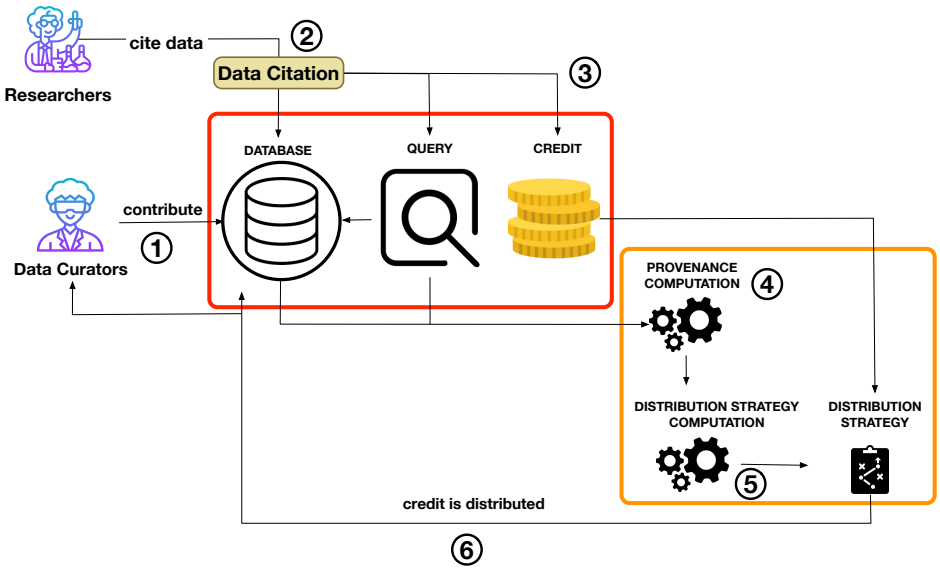

Figure 1. Overview of the credit distribution pipeline.

Step 1 Scientists and experts contribute to the information contained in a scientific database. These are called the "Data Curators". **SUSAN: Are they "contributing to" or "contributing"?**

Step 2 Other researchers use the data in their research, and when possible, cite the data.. **SUSAN: The rest of this Step is confusing. Rewrote. What dos it matter how researcheers access the data? and the sentence was not complete.**

Step 3 The citation to the data generates credit, that can be used as a proxy for the impact of the data in the citing paper. This credit is represented as a real value $k \in \mathbb{R}_{>0}$.

Step 4 Given the database instance I and the query Q, it is possible to compute the *data provenance* of $Q(I)$. The provenance of $Q(I)$ is a form of metadata that describes the generation process undertaken by Q, and the data used in I to generate the output (Cheney et al., 2009). Many different notions of provenance have been proposed in the literature for data in database management systems (Cui et al., 2000; Buneman et al., 2001; Green et al., 2007; Dosso et al., 2020), describing different kinds of relationships between data in the input and the output of a query. As reported in (Cheney et al., 2009), these provenances, beyond the intrinsic information on how queries work, have been used in several applications, as the study of annotation propagation and view update. In this paper, we consider three types of provenance: lineage, why-provenance, and how-provenance.

Step 5 The provenance is the input of the CDC problem, whose aim is the computation of the *Credit Distribution Strategy* (CDS, also referred only as Distribution Strategy, DS). The CDS is a function that distributes k to the data in the input database I. CDS functions are to be defined on the basis of citation policies decided at the database administration level or, even better, at the domain community level. Certainly, we are in a one-solution-does-not-fit-all scenario, but CDS can be defined with great variability and flexibility, thus allowing for ample customization. In this paper, we describe CDS based on data provenance, and they are therefore closely related to the kind of provenance computed in step 4. In this work, we describe three CDS, each based on one of the three considered provenances.

Step 6 Once the CDS is computed, it is then used to distribute the given credit k to the parts of the database that are responsible for the generation of $Q(I)$. Transitively, this credit is also divided and given to the corresponding authors of those data.

In this paper, we expand the work already discussed in our paper (Dosso and Silvello, 2020), where we first asked how to correctly reward data and data curators that are usually left without credit from the current citation systems. In that paper we first defined the problem of DCD in relational databases

(Definition 5.1) and we proposed the possibility to solve the problem by using *lineage*, a form of *data provenance* (Definition 5.2), to define a distribution strategy. The lineage of a tuple t in the output $Q(I)$ is defined as the set of all and only the tuples in the database instance I that are "relevant" to the production of t, that is the tuple that are used by Q in the production of t. The lineage-based strategy equally redistributes the credit k to the tuples in the lineage set, thus each tuple receives credit $k/|L_t|$, where L_t is the lineage set of t.

One may argue that this may not be the perfect solution to the problem, since lineage only tells the relevant tuple used to produce the output. It does not convey any information about their role or importance in the query. Therefore, one may instead desire to give more credit to the tuples that are more relevant or essential to the production of the output, i.e. those tuples that, if removed, would prevent the output tuple to appear in the final result, or those tuples that are used in more than one operation by the query.

Therefore, in this paper, we expand the research done in (Dosso and Silvello, 2020) by proposing new Distribution Strategies, based on other forms of data provenance. Namely, why-provenance (Buneman et al., 2001) and how-provenance Green et al. (2007). We compare them also with the lineage-based one to highlight their differences and how one may be preferred instead of another. In particular, we show that why-provenance and how-provenance are more sensitive to the role of a tuple in a query (depending on how many times the tuple is used or how it is used). The DS based on why-provenance rewards more the tuples that are essential to the production of a tuple. The DS based on how-provenance also takes into consideration in how many different ways a tuple is used, presenting an even higher level of sensibility.

For our experiments, we use a well-known curated database, the IUPHAR/BPS[3] Guide to Pharmacology (Harding et al., 2018), also known as GtoPdb[4], which contains expertly curated information about diseases, drugs, cellular drug targets, and their mechanisms of action. We chose GtoPdb for two main reasons: (i) it is a widely-used and valuable curated relational database, (ii) many papers in the literature use, and cite its data (i.e., families, ligands, and receptors). Real queries used in papers can therefore be seen as data citations which, in turn, can be used to assign data credit.

We perform three sets of experiments. In the first one, real queries are extracted from papers published in the British Journal of Pharmacology (BJP), that represent data citations to GtoPdb, and are used to distribute credit in the database using three different DS, based on the three forms of provenance considered. We show how, given the peculiar nature of the queries, the three distributions do not present particular differences in this context and why this is the reason. In the second and third sets of experiments we show how, using more complex queries, it is possible to see differences, brought forth by the different distributions deriving from the provenance used, and how the more complex the provenance used, the more sensitive to the role of the tuples in the production of t the distributions become.

Our paper *contributes* to the following:

- Defining new form of Distribution Strategies for the problem of Data Credit Distribution, based on why-provenance and how-provenance;
- In-depth analysis of the effects of credit distribution over real-world curated data and of the differences between the three Distribution Strategies based on the forms of provenance deployed.

Outline The rest of the paper is organized as follows: Section 2 presents the related works; Section 3 describes the use case we adopted; section 4 briefly presents the provenances used in the paper; Section 5 describes the problem of DCD and the new DS developed in this paper; in Section 6 we present the evaluation of our approach. Finally, Section 7 presents our conclusions and potential future work.

2 BACKGROUND

Data in Research As described by Jim Gray in his last talk (Hey et al., 2009), the world of research is rapidly transitioning towards the *fourth paradigm of science*, that is, data-intensive scientific discovery, where data are important for scientific advances as well as for traditional publications (Bechhofer et al., 2013). The scientific community is promoting an *open research culture* (Nosek et al., 2015), founded on methods and tools to share, discover, and access experimental data. The community has identified the FAIR principles (Wilkinson et al., 2016) (Findable, Accessible, Interoperable, and Reusable), that should

[3] International Union of Basic and Clinical Pharmacology/British Pharmacology Society

[4] `https://www.guidetopharmacology.org/`

be enforced by every database. In particular, data should be accessible from the articles, journals, and papers that cite or use them (Cousijn et al., 2019). Aspects such as the need for the *reproducibility* of experiments through the used data; the *availability* of scientific data; the *connections* between data and the scientific results are all needed aspects for the fourth paradigm, and are all relevant to the domain of *data citation* (Honor et al., 2016).

Data Citation: Principles and Motivations Data Citation principles were first described in detail in (CODATA-ICSTI Task Group on Data Citation Standards and Practices, 2013), and later summarized and endorsed by the Joint Declaration of Data Citation Principles (JDDCP) (Martone, 2014). The principles are divided into two groups (Silvello, 2018). The first one contains principles concerning the role of data citation in scholarly and research activities such as the (i) *importance* of data (why data citation is important and why data should be considered as first-class citizens); (ii) *credit* and *attribution* to the creators and curators of the data; (iii)*evidence*; (iv) *verifiability*; and *interoperability*, with these last three requiring data citation methods to be flexible enough to operate through different communities. The second group defines the main guidelines to establish a data citation systems, and contains principles such as the (i) *unique identification* of the data being cited; (ii) *(open) access* to data; (iii) guarantee of *persistence* and *availability* of citations even after the lifespan of the cited entity; the (iv) *specificity* of a citation, i.e. it must lead to the data set originally cited.

It is possible to outline six main motivations for data citation (Silvello, 2018):

- *Data attribution*: identify the individuals that should be credited for data with variable granularity.
- *Data connection*: connect papers to the data being used.
- *Data Discovery*: citations to data records or subsets act as entry points to data otherwise not findable via search engines.
- *Data Sharing*: share data obtained by researchers within the whole community.
- *Data Impact*: highlight the results obtained in writing papers using specific data, the frequency and modality data were used.
- *Reproducibility*: data citation greatly impacts the reproducibility of science (Baggerly, 2010). Many authoritative journals ask to share data and provide valid methodologies to reproduce experiments.

2.1 Data Citation in Relational Databases

In this paper, we develop our methods and experiments on relational databases. RDBs have been the main target of data citation methods since the surge of the data-centric research paradigm. The RDA "Working Group on Data Citation: Making Dynamic Data Citable"[5] (Rauber et al., 2016) has been working in the last years on large, dynamic, and changing datasets. The working group has finished the development of its guidelines and has now moved on into an adoption phase. The datasets considered by the WG are often relational.

In one of its most recent sessions (Rauber et al., 2015), the Working Group (WG) on Data Citation reported that there are various implementations of its guidelines for Data Citation on MySQL/Postgres relational databases. Some of these databases are: DEXHELPP[6] (Social Security Records); NERC (ARGO Global Array); EODC (Earth Observation Data Centre) (Gößwein et al., 2019); LNEC (River dam monitoring); MDS (Million Song Database) (Bertin-Mahieux et al., 2011); CBMI[7] (Center for Biomedical Informatics); VMC (Vermont Monitoring Cooperative); CCA[8] (Climate Change Center Austria); VAMDC (Virtual Atomic and Molecular Data Center) (Dubernet et al., 2016; Zwölf et al., 2016).

More examples of work on data citation in relational databases are (Buneman et al., 2016; Wu et al., 2018; Alawini et al., 2017; Davidson et al., 2017; Buneman and Silvello, 2010). The website `https://fairsharing.org/` keeps a long updated list of curated and scientific databases (many of which are relational or graph-based) following FAIR guidelines. These databases are citable since they are compliant with the most recent guidelines, and they are in the vast majority of cases accessible via

[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`
[8] `https://ccca.ac.at/startseite`

dynamically created Webpages. In all these databases is, therefore, possible to implement DCD on top of the existing infrastructures for Data Citation.

Data citation techniques are primarily applied to relational databases because of their diffusion and also because the portions of data that are to be cited are easily identified: the whole database, a relation, a tuple, or an attribute. Many papers (Buneman, 2006; Buneman et al., 2016; Alawini et al., 2017) consider more complex citable units, recognizing that often the *views* of a database are the ones to be cited. Generally, a *view* is a query on the database. To this end, (Wu et al., 2018) suggested decomposing the database in a set of views, where each view is associated with its citation.

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

1. A database cited as a whole, even though only parts of the databases are used in the papers or datasets. Alternatively, the so-called "data papers" can be cited, being traditional papers that describe a database (Candela et al., 2015).
   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 (Rauber et al., 2016).
   In this case, the credit from citations can be distributed amongst those contributing to the portions of data returned by the cited queries 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 (Joshi-Tope et al., 2005), the GtoPdb (Harding et al., 2018), and the VAMDC (Zwölf et al., 2016). 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) (Force et al., 2016) 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 since they both refer to recognizing the work of data creators and curators. In a sense, data credit can be seen as a by-product of data citation since credit attribution is not possible without the citations to data.

Kats in (Katz, 2014) 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 (Katz, 2014) credit is defined as a "quantity" that describes the importance of a research entity, such as papers, software, or data, mentioned in a citation. We add that the concept of credit can be built on top of the existing infrastructure handling traditional and data citations. (Katz, 2014) further explores the idea of a *distribution* of credit from research entities (i.e., papers and data) to other research entities through citations that connect them. Thanks to traditional citations and now also to data citations, this distribution is finally possible, at least between papers and data. Some problems related to traditional citations can thus be solved by citations, as highlighted in (Katz, 2014):

1. Credit rewards research entities that to date are not (formally) recognized (a goal shared with data citation).

2. Credit can reward authors in a *proportionate* way, taking into consideration their role in generating the entity. The more an author contributed to a paper, the more credit is given to him.

3. Credit can be *transitively* transmitted through a chain of papers citing each other. This allows them to reward papers that are no more cited but that are nevertheless important in a research area for the influence of their content. This is something that only credit can do but is possible because of the existence of a network of citations among the entities.

(Fang, 2018) presents a framework to distribute the credit generated by a paper to its authors and to the papers in its reference list in a transitive way. Let us consider the *citation graph* as the graph where the nodes are papers and the links are the citations among them. In this graph, every paper is a source of credit, which is then transferred to the neighboring nodes. The quantity of credit received by each cited paper depends on its impact/role in the citing paper. So far, this theoretical framework is limited to papers, but it can be easily extended to a citation graph that comprises papers and data.

(Zeng et al., 2020) proposes the first method designed to compute credit within a network of papers citing data. Adopting a network flow algorithm, they simulate a random walker to estimate a score for each dataset, leveraging real-world usage data to compute the credit. This is the first step towards an automatic credit computation procedure. However, it is limited to assigning credit to the whole datasets, without considering the granularity of data. Therefore, this is not a way to assign credit to a single research entity within a dataset. Differently from (Zeng et al., 2020), we do not treat the credit computation process, but we focus on the distribution process.

2.3 Data Provenance

To distribute credit, we base our methods on a form of metadata, called *data provenance*, which describes the origin and life of data.

In the past, data was stored in curated databases or in other trusted sources of information kept under centralized control (Cheney et al., 2009). With the advent of the Internet, this assumption is no longer valid (Lynch, 2001). Data are today created, shared, copied, cited, reported, moved around, and combined indiscriminately. On the other hand, data management is growing in complexity (Simmhan et al., 2005) also thanks to new algorithms, applications, and more abundant storage capacity. In such an environment, it becomes more and more difficult to keep track of the origins, the reliability, and the process of elaboration of data used in research. One way to face such challenges is the deployment of data provenance.

Data provenance is information attached to data that describes its origin and the process which created it. It can also be seen as metadata pertaining to the derivation history of the data. It is becoming more and more important in these years since with the advent of the internet and the evolution of the fourth paradigm of science it is necessary to keep track of the life cycle of data to guarantee its quality and reliability (Simmhan et al., 2005; Cheney et al., 2009). It is particularly useful to help users to understand where data are coming from, and the process they went through. Data warehouses and curated databases are examples where provenance information is essential since in both environments enormous and often manual effort is usually expended in the construction of the resulting database (Cheney et al., 2009). Data citation and data provenance are closely linked (Alawini et al., 2018) since both are forms of annotations on data retrieved through queries.

Data provenance has been widely studied in different areas of data management. In this paper, we focus on provenance in the database management systems environment. For further details on data provenance, please refer to surveys like (Cheney et al., 2009) and (Simmhan et al., 2005).

In (Cheney et al., 2009) four main types of data citation for database management systems are discusses: *lineage* (Cui et al., 2000), *why-provenance* (Buneman et al., 2001), *how-provenance* (Green et al., 2007) and *where-provenance* (Buneman et al., 2001).

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

Lineage is somehow the simplest among the forms of provenance. It has been defined in different ways (Cheney et al., 2009), but it can be thought of as the set of all the tuples that are used in some way by the query to produce the output tuple, the ones that are somehow *relevant* to its generation.

The definition of why-provenance is based on the notion of *witness set*. A witness is a set of relevant tuples that guarantees the existence of t in $Q(D)$. The lineage is therefore an example of a witness. The

why-provenance of a tuple t is a peculiar set of witnesses – described in (Buneman et al., 2001) – that are computed from the query, called *witness basis*. A witness basis may be composed of more than one witness. Therefore, the why-provenance contains more information than the lineage, since it describes *alternative* ways in which the same output may be generated.

The how-provenance takes the form of a polynomial, called *provenance polynomial*, where the variables are taken from the set of identifiers of the tuples (provided that each tuple in I has an identifier) and the coefficients are taken from $\mathbb{N}$. As suggested by the name, this provenance also conveys information on how the input tuples are used in Q. For example, when two tuples are combined by a join, they are also combined in the polynomial by the $\cdot$ operator. When two or more tuples become equivalent due to a union or a projection, the corresponding monomials are combined by the $+$ operator.

It has been shown in (Cheney et al., 2009) that the how-provenance is the more general and informative of the three, containing the other two.

The where-provenance, differently from the other three, is *attribute-based*. Given a tuple t and an attribute A of $Q(I)$, the where-provenance of the value $t \bullet A$ is the set of cells in I from where $t \bullet A$ has been copied. In this sense, the where-provenance describes from *where* an attribute is coming with respect to the starting database from which it was computed.

In this paper, we base our methods to distribute credit on these four provenances. Moreover, we define three new kinds of provenances that are the attribute-based counter-parts of lineage, why-provenance, and how-provenance. We also show how these new provenances are more informative about their original counter-parts.

3 USE CASE: GTOPDB

As use case we refer to the IUPHAR/BPS Guide to Pharmacology (Harding et al., 2018), also known as GtoPdb[9]. GtoPdb is a well-known and well structured scientific relational database that contains expertly curated information about diseases, drugs in clinical use, their cellular targets, and the mechanisms of action on the human body. The data are drawn from high-quality pharmacological and medicinal chemistry literature. Curated and maintained by the GtoPdb Committee and by its 96 subcommittees, it comprises a total of 512 scientists collaborating with in-house curators. Approximately 1000 researchers from many parts of the world have contributed to the database and the curators desire to give recognition to the contributors that led to some early work on data citation (Buneman, 2006).

GtoPdb is relational in nature, however its logical structure is hierarchical, as shown in Figure 2, and the information contained in the database is also organized into webpages focused on specific diseases, targets or ligands and families (i.e. groups) of them, for an easier access by the users. As depicted in Figure 2, the database can be thought as a tree where the root is the database itself in its entirety, the first level is composed by the Targets, Ligands and Diseases considered in their entirety. In this paper we focus on target and target families, thus in the figure, at the third level, we show some of the family types, that is groups of targets. At the third level we show families of targets, a finer level of granularity, and finally, at the last level, the single targets, also known as receptors.

The GtoPdb provides access to the webpages corresponding to all these nodes through URLs, as shown in the figure. The webpages corresponding to target families all present a similar structure, as shown in Figure 3 for the "Adenosine receptors" family. Each page has an *Overview*, a brief text describing the content of the page; a list of *Receptors* composing the family; a section of *comments* about the family; the *References*, a list of the papers consulted by the curators of the page, not different from a reference list at the end of a research paper; the *further reading* list, reporting papers that an interested reader may want to consult to obtain more insight on the family; and a final section called *How to cite this family page*, containing text snippets useful to cite the specific page or the whole database. In Figure 3 we show the SQL code that retrieves the information that is used to build the corresponding sections (apart from the References section). Each family page can therefore be considered as a full-fledged traditional publication, comprising title, authors, abstract (the overview), content, and references.

What happens is that many papers in the literature use the GtoPdb's information without including a reference to the specific page being cited. Instead, they only cite one data paper describing GtoPdb (e.g. the more recent (Harding et al., 2018)) and refer to targets, ligands, diseases, etc. only by their name.

[9] `https://www.guidetopharmacology.org/`

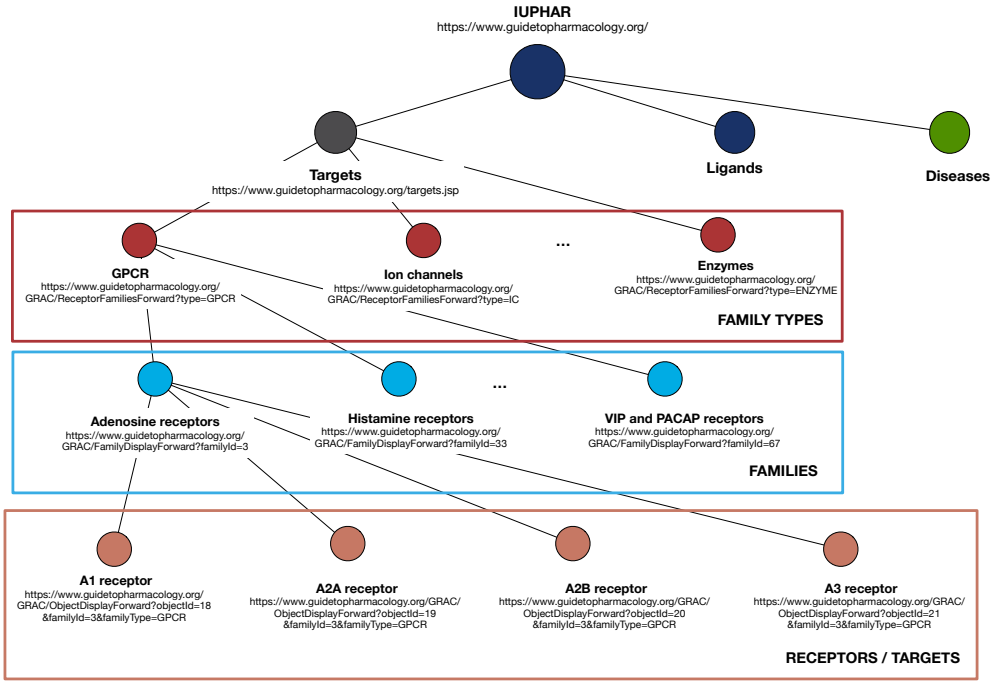

Figure 2. Partial map of the GtoPdb hierarchical structure grouping the targets into families and family types.

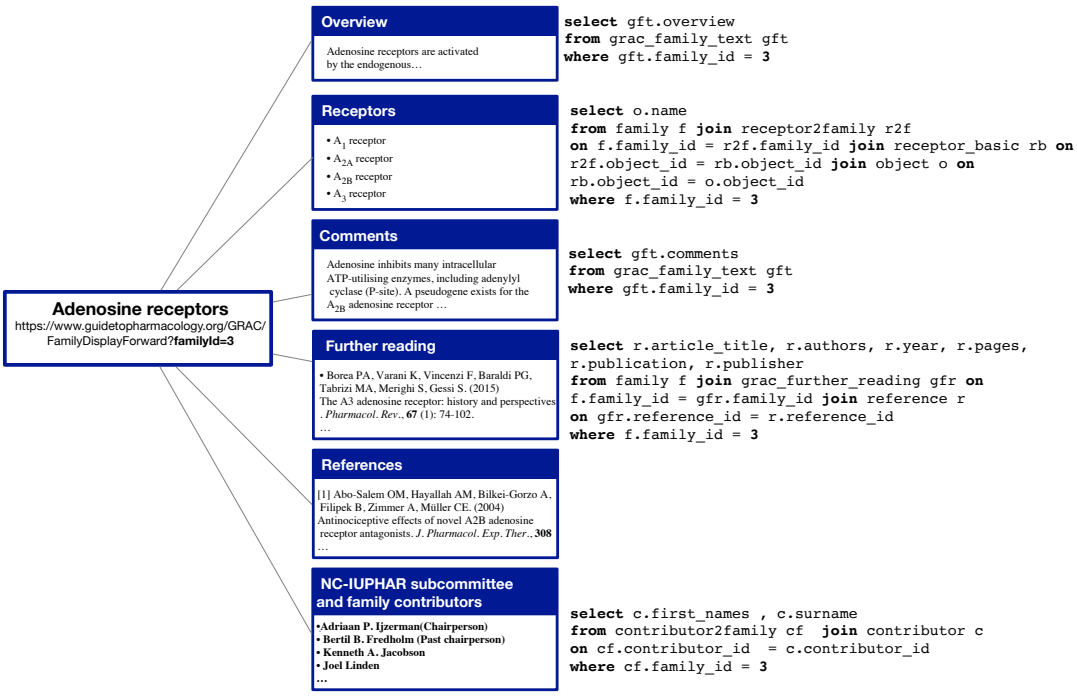

Figure 3. Basic web-page structure of "Adenosine receptors" family (ID 3), with queries used to retrieve the information contained in every section, except references.

family

id	name	type
f_1	Dopamine Receptors	gpcr
f_2	Bile Acid Receptor	gpcr
f_3	FAK Family	enzyme
f_4	YANK Family	enzyme

contributor2family

id	family_id	contributor_id
$c2f_1$	f_1	c_1
$c2f_2$	f_1	c_2
$c2f_3$	f_2	c_3
$c2f_4$	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 composed by three tables. `family` includes some receptor families in the database; `contributor`, with the name and country of contributors of the database; `contributor2family`, connecting the contributors to the families they contributed to.

Thus, the citations to the specific families turn out to be *de-facto* "hidden" to the citation systems such as Google Scholar, and useless for the computation of bibliometrics.

In certain "lucky" circumstances, as in the case of papers published as PDF in the British Journal of Clinical Pharmacology [10] (BJCP), when a family, a ligand, a receptor name etc. are used, they also have a hyperlink pointing to the corresponding webpage in GtoPdb. Therefore, in these cases, the citations to the families can be spotted and counted by using the URLs reported in the papers. All these citations to GtoPdb webpages in any case are not counted as such by the citation systems, so they are not converted into credit for curators and collaborators.

For our running example, consider Table 1. This simplified version of GtoPdb illustrates three relations: `family`, `contributor` and `contributor2family`.

The tuples of the first table represent four families, composed by three attributes: the id of the family, its name and type. `contributor` contains the people who have helped to generate the data of the database. Finally, table `contributor2family` serves as a link between the families and the people who contributed to them. For instance, "John Smith" ($\mathtt{c}_1$) contributed to "Dopamine Receptors" ($\mathtt{f}_1$) as well as to the "YANK Family" ($\mathtt{f}_4$). We use this example throughout the rest of the paper.

4 DATA PROVENANCES

4.1 Lineage

Lineage was first introduced by Cui et al. in (Cui et al., 2000), and it associates each tuple $o \in Q(I)$ in the output of a query to a set of tuples in the input. In general, the lineage of one tuple o is a collection of tuples that helped to "produce" it (Cheney et al., 2009). To give an idea of what can happen with the lineage of tuples, 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'
```

Table 2 reports the query result, composed of two tuples. The attribute id is added by us to easily identify them.

Using the ids of the single tuples to identify them, for tuple o_1 the lineage 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, but also with $c2f_2$ and c_2. No other tuple is used in the database to produce o_1. For tuple o_2, instead, the lineage is $\{f_4, c2f_4, c_1\}$. Therefore, as we see, the lineage is defined for each tuple of the output, and it can be different for tuples in the same output.

[10] `https://bpspubs.onlinelibrary.wiley.com/journal/13652125`

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 a SQL query applied on the database of Table 1, asking the names of the families curated by a researcher based in the UK. The id attribute is added to help identify the two tuples. Every tuple is annotated with its lineage, we use the id of the tuples to identify them.

4.2 Why-Provenance

Why-Provenance was first defined in (Buneman et al., 2001) in terms of a deterministic semistructured data model and query language. While why-provenance can be defined in many ways, in this paper we refer to the definition given by (Cheney et al., 2009), expressed in terms of relational model and relational algebra query language for SPJRU queries.

In particular, while lineage aims to find all and only the tuples in the input that are 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 output of the query, 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 the witnesses is finite (if the database instance I is finite), but it is potentially exponentially large Cheney et al. (2009).

(Buneman et al., 2001) defined the why-provenance of an output tuple t in the result $Q(I)$ as a *particular subset* of the set of witnesses, that is, a particular selection of witnesses. This subset is called *witness basis*. The witnesses of the witness basis depend on the syntax of Q, thus the size of each witness basis is bounded by the size of Q. In particular, the witnesses of the witness basis exclude tuples that are irrelevant to t being produced by Q. Thus, the basis tends to be very small when compared to the set of all possible witnesses (Cheney et al., 2009). Also, the witnesses are minimal, in the sense that if one tuple is removed from one of these witnesses, then it is no more able to produce the output. This is not true for the lineage. For example, it is sufficient to consider the lineage of o_1 in the example above, where the tuples $c2f_2$ and c_2 may be eliminated without affecting 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-provenances of the corresponding results.

In a sense, each witness in the witness basis captures one possible "way" in which the output can be generated by the query. To better understand this property, consider the example in Table 3, where we reported the result of query `Q1` with the tuples annotated with their why-provenance.

Output tuple o_2 presents a why-provenance that is composed of only one witness, that coincides with its lineage. This is because there is only one way in which this output tuple can be produced, i.e. for tuple f_4 to be joined with $c2f_4$ and c_1. On the other hand, o_1 presents a witness basis made of two witnesses. These two sets fundamentally represent the two possible ways in which the query can generate o_1. One possibility is that f_1 is joined with $c2f_1$ and c_1, and is represented by the first witness. The second possibility is that f_1 is joined with $c2f_2$ and c_2. This means that to generate o_1 it is sufficient that only one of the two witnesses is present in the input database.

4.3 How-Provenance

While why-provenance describes the source tuples that witness the existence of an output tuple in the result of the query, it leaves out some information. How-provenance was firstly defined in (Green et al., 2007), based on the introduction of a *semiring* algebraic structure, and it is a form of provenance that takes the form of a *polynomial*.

The idea behind the framework proposed in (Green et al., 2007) is to use the two operators $+$ and $\cdot$ to represent two basic transformations that source tuples undergo as a result of applying a relational query to a source database (Cheney et al., 2009). Two tuples may either be joined together, as an effect of a

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.

join (represented through the $\cdot$ operator) or merged via union or projection (represented through the $+$ operator).

To give a simple example of how how-provenance works, refer to Table 4, where the two output tuples of our running example are annotated with their respective how-provenances. Tuple o_2 was produced through the join among the input tuples $f_4, c2f_4$, and c_1. The three provenance tokens are therefore represented "multiplied" together. The case of o_1 is slightly more complex. This tuple, as already discussed, can be obtained through two different joins. The two monomials composing the polynomial 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 alternatives and it is due to the fact that the output tuple is the result of a merge of two distinct tuples after the projection on the attribute `name`. This merge is, in turn, due to the presence of the `DISTINCT` operator in the SQL query. This simple example gives a first basic idea behind how-provenance and how it allows us to track the operations that produced an output tuple.

5 CREDIT DISTRIBUTION AND DISTRIBUTION STRATEGIES

5.1 Data Credit and Data Credit Distribution

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

As already defined in (Dosso and Silvello, 2020), *data credit* is a value $k \in \mathbb{R}_{>0}$ used to represent the value of a recipient in a database. Every recipient in a database is annotated with a given quantity of credit, a proxy for its importance in a certain context. In this paper, we focus on tuples as recipients of credit.

Data Credit Distributions (DCD) considers a database instance I, a certain quantity of credit k (here, without loss of generality, considered as given), and a query Q producing a result set $Q(I)$. DCD consists in defining a function, here called *distribution strategy* (DS), to split credit into portions to be assigned to the tuples in I.

In the following we used some of the notation in (Cheney et al., 2009): a *tuple location* is defined as a tuple in one relation of I, tagged with its name. It is indicated with (R,t), where R is the relation in the database, and t is the tuple in R. With reference to the running example, `(family,` $\langle f_1$`, Dopamine Receptors, gpcr`$\rangle$`)` is the tuple location of the first tuple in the `family` relation. The set of all the tuple locations in I is called *TupleLoc*. The following is the definition of DCD at *tuple level*. We refer to the level of tuple because the credit is annotated to tuples.

Definition 5.1 ***Data Credit Distribution at tuple level*** *(DCD) (Dosso and Silvello, 2020)*
Given a database instance I, a query Q over I and the value $k \in \mathbb{R}_{>0}$, DCD is defined as the computation of the function $f_{I,Q} : TupleLoc \times \mathbb{R}_{>0} \to \mathbb{R}_{\geq 0}$ such that $f_{I,Q}(t,k) = h$ where $0 \leq h \leq k$ and $\sum_{t \in TupleLoc} f_{I,Q}(t,k) = k$.

As we see, the DS is a function that annotates each tuple in the database with a real value, which is a fraction of the given quantity k. The only constraint is that the sum of the credit fractions annotation the tuples must be k (i.e. no credit is generated nor destroyed during the distribution). Given I and Q, many different DS may be defined as long as they sum up to k. We use the information provided by data provenance to define sensible functions that take into account the issued query.

5.2 A Lineage-based Distribution Strategy

With the information provided by the lineage, we defined the following DS:

Definition 5.2 *Lineage-based Distribution Strategy (Dosso and Silvello, 2020)*
Let I be a database instance, Q a query over I, $o \in Q(I)$ an output tuple and k the credit associated to o. Let L be the lineage of o and t be a generic tuple in I. t receives a credit equal to:

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

The DS is defined for one tuple of the output. Therefore, to perform credit distribution for a whole set of output tuples, it is necessary to first divide the credit to each tuple in the output, and then compute the distribution for each one of them. In this paper, we assume that each output tuple carries credit equal to 1. This lineage-based DS distributes credit only among tuples that have a role, whichever it is, in the creation of o by the query Q. Each of them receives an equal share of the credit. The more the tuples in a lineage set, the less the quantity of credit each of them receives.

As an example, consider the output tuples of Table 2. Each output tuple has credit $k = 1$. The lineage of the first tuple is the set $\{f_1, c2f_1, c_1, c2f_2, c_2\}$. Therefore, each tuple in this set receives credit $1/5$. The other tuples of the database receive credit 0. The lineage of the second output tuple is $\{f_4, c2f_4, c_1\}$, therefore each of these tuples receives credit $1/3$ in this case.

At the end of the process of distribution over the whole output, tuples $f_1, c2f_2, c_2$ all have credit $1/5$, tuples f_4 and $c2f_4$ have credit $1/3$, while tuple c_1 has credit $8/15$. If one tuple appears in more than one lineage set, it will accumulate the credit from the distribution associated with each one of these sets, implying its bigger relevance in the context of the considered query, as is the case with c_1 in this example.

Not all of the tuples of the lineage of o_1 are necessary at the same time for the generation of the tuple. If the database only had the set of tuples $\{f_1, c2f_1, c_1\}$ or the set $\{f_1, c2f_2, c_2\}$, its existence would still be guaranteed. In other words, only one among the couples of tuples $\langle c2f_1, c_1\rangle$ and $\langle c2f_2, c_2\rangle$ is really necessary, while f_1 is absolutely mandatory. One could argue that it would be fairer for f_1 to receive more credit than the other four tuples, given its role in the production of o_1.

This highlights one limitation of the DS based on lineage: while able to find all and only the relevant tuples of the output, it is unable to distinguish the *importance* of tuples in the query computations. This information could be incorporated in the definition of a DS in order to distribute credit based on the actual role that tuples play in the computation.

For this reason, we present in this paper more sophisticated forms of Distribution Strategies, based on the other two provenances discussed above.

5.3 A Why-Provenance-Based Distribution Strategy

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 the total credit associated to o. Let t be a generic tuple in I. Let us call $\mathscr{W} = Why(Q,I,o)$ the witness basis of o according to Q and I, where $W \in \mathscr{W}$ is a generic witness. Let us call $\gamma(\mathscr{W},t) : (\mathscr{W},t) \mapsto \mathscr{P}(\mathscr{P}(TupleLoc))$ the function which returns the set of all the witnesses $W \in \mathscr{W}$ such that $t \in W$. The tuple t receives a credit equal to:

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

This strategy first equally distributes the credit among the witnesses of the witness basis then, successively, it further equally divides the credit among the tuples in a witness. Since one tuple may appear in more than one witness, it will receive more than one portion of credit from the same distribution.

Figure 4 represents the distribution of credit with this DS with the why-provenance of tuple o_1. The credit is first divided among the two witnesses, that both receive credit $1/2$. The credit is then further divided among the tuples in each witness. Each tuple in each witness receives $1/6$ of credit. At the end of the distribution, f_1 receives a cumulative total credit of $1/3$, the other tuples receive $1/6$ each. This distribution better reflects the role of f_1 in the generation of o_1 since, as we discussed, it is the only mandatory tuple for the production of the output, while we need only one of the two other couples of tuples to get the result.

From this example, it is immediately evident how why-provenance can better reward the tuples depending on their role. Tuples that appear in more than one witness are rewarded more than others. This means that tuples that are more important to the generation of the output, since they are used more by the query, are rewarded more than tuples that are "interchangeable" with others.

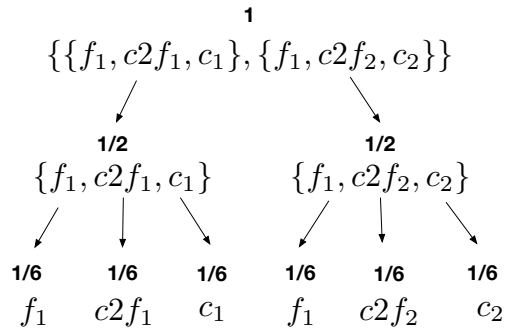

Figure 4. Exemplification of the distribution of credit through the why-provenance based DS for tuple o_1.

5.4 A How-Provenance Based Distribution Strategy

The how-provenance conveys more information than the why-provenance since it does not only capture what tuples are relevant to the output and in which combination, but also how they are used. To define the Distribution Strategy based on the how-provenance, we first need some other preliminary definitions.

Consider the provenance polynomial $\mathscr{H} = H(Q, I, o)$ of a tuple o. We define:

1. $c(\mathscr{H}) = n$ the function $c : \mathbb{N}[TupleLoc] \mapsto \mathbb{N}$ that, given a polynomial, returns the sum of its coefficients;
2. $c(M)$ the function $c : \mathscr{M} \mapsto \mathbb{N}$ that, given a monomial M, returns the sum of its exponents (with $\mathscr{M} \subset \mathbb{N}[TupleLoc]$ such that $\mathscr{M}$ is made only by the monomials M in $\mathbb{N}[TupleLoc]$);
3. $e(t, M)$ the function $e : TupleLoc \times \mathscr{M} \mapsto \mathbb{N}$ that, given in input a tagged tuple and a monomial, returns the exponent of that tuple inside the monomial;
4. $mc(M)$ the function $mc : \mathscr{M} \mapsto \mathbb{N}$ that, given in input one monomial, returns its coefficient;
5. $\gamma(t, \mathscr{H})$ the function $\gamma : TupleLoc \times \mathbb{N}[TupleLoc] \mapsto \mathscr{M}$ that, given a tuple t and a provenance polyomial $\mathscr{H}$, returns the (possibly empty) set of monomials M in $\mathscr{H}$ such that t appears in M.

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 and k the total credit associated to o. Let also t be a generic tuple in I. The credit given to t is:

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

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

Going back to the example of Table 4, consider o_1, that has provenance polynomial $f_1 c2 f_1 c_1 + f_1 c2 f_2 c_2$. The DS firstly divides the credit between the two monomials. Since the coefficients are both 1, the credit is split in half. If they were, for example, 1 and 2 respectively, $1/3$ of the credit would go to the first monomial, $2/3$ to the second. Since in our example each variable has exponent 1, the credit is further divided equally among the three variables. Thus, at the end of the computation, f_1 receives $1/3$, the other tuples receive $1/6$. If, for example, the first monomial was $f_1^2 c2 f_1 c_1$, then the portion of credit of this monomial would be divided in this way: $1/2$ to f_1 and $1/4$ to each of the other two tuples.

One may observe that, in this example, the how-provenance-based distribution has the same outcome of the strategy based on why-provenance. Consequently, one may ask if there is a significant difference between the two strategies. As an example consider this new query `Q2`, that asks for the families of type gpcr that have as contributor a researcher localized in the UK from GtoPdb:

id	name
oxs_1	Dopamine Receptors

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

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.

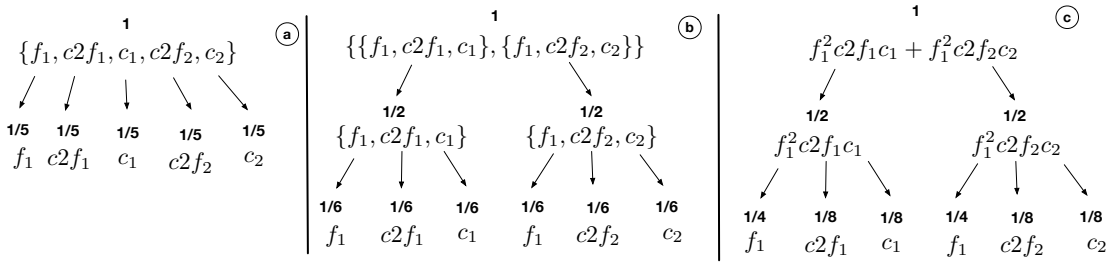

Figure 5. Comparison of different distributions strategies from the credit of tuple o_1 produced by query `Q2`.

```
Q2: SELECT DISTINCT F.name
FROM family as F JOIN
(SELECT DISTINCT f.name AS 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') AS R ON F.name = R.name
WHERE F.type = 'gpcr'
```

Table 5 presents the result, composed of one tuple, annotated with the three provenances. As can be seen, lineage and why-provenance are identical to the ones of the tuple o_1 in the previous example. The how-provenance is different since tuple t_1 is used twice: firstly in the join of the inner query, secondly in the join of the outer query. This information is lost in the first two provenances since they are sets, but it is maintained in the how-provenance through the use of the operator '$\cdot$'.

Figure 5 shows the differences between the three DS for the tuple o_1 of Table 5. In subfigure 5.a we used lineage, in sub-figure 5.b we used why-provenance, and in sub-figure 5.c we used how-provenance. The DS based on the provenance polynomial gives credit $1/2$ to f_1, and $1/8$ to the other tuples, as can be seen. This is reasonable since `Q2` utilizes f_1 even more than `Q1`. The distribution based on how-provenance can reward f_1 more, proving that how-provenance is even more sensitive to the role of the tuples in a query than why-provenance, while in this case, the why-provenance is not sensible to this difference. This is somehow a direct consequence of the fact that, as demonstrated in (Green et al., 2007), how-provenance is more general than why-provenance and lineage, in the sense that it contains more information.

6 EXPERIMENTAL EVALUATION: COMPARING PROVENANCES

In this paper, we perform our experiments on GtoPdband in particular we focus on target families, all of those are described in webpages. GtoPdb in particular identifies 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 family webpage of interest, or a subset of data extracted with a query. In this work we consider a full-fledged data citation context in which papers cite the specific *data* subset of interest and not the webpage or the full database acting as data proxies. Therefore, when a paper cites family data, it is actually citing a set of queries needed to retrieve all the information provided by the family webpage, i.e. one query for each section composing a page, as depicted in Figure 3. The figure maps the structure of one family, "Adenosine receptors", and the queries to obtain the information to build the corresponding page, apart from the list of references. In

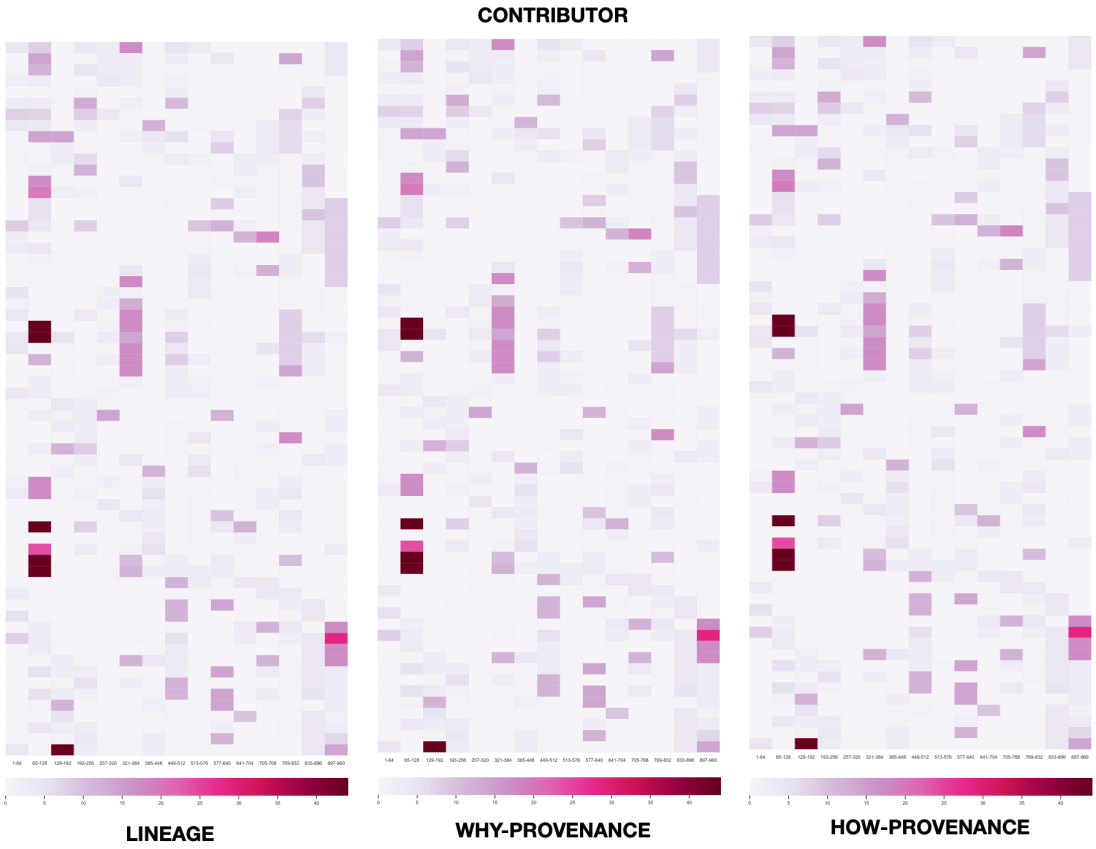

Figure 6. Comparison of three DS on the same table `contributor` using the distribution given by the queries retrieved from papers.

GtoPdb, all family pages share a similar structure (the only differences may be the presence/absence and length of the receptors lists, further readings, and contributors sections). The same queries are therefore used to build all other pages by simply changing the family id (which, in our example, is 3). All these queries are SPJ.

As already stated, many papers that draw information from the GtoPdb website[11] cite papers published every two years by the GtoPdb Committee on Receptor Nomenclature and Drug Classification (NC-IUPHAR). To obtain a set of citations capable of representing what actually happens, we consider a paper subset citing the 2018 GtoPdb (Harding et al., 2018) data paper. At the time of writing, this paper received more than 1200 citations.

As explained in Section 3, in the papers published in the British Journal of Clinical Pharmacology, that cite GtoPdb, the name of families are hyperlinks that point to the corresponding webpages. We considered all the 460 papers in BJCP citing (Harding et al., 2018) as of February 2020. URL references to family pages were automatically extracted to guide in building the queries to produce corresponding webpages. A total of $5,945$ different queries were built in this way. [12]

Figure 6 shows the heat-maps obtained by three different DS on the table `contributor`. It is immediately evident that the result of the distribution is the same with the three strategies. The same result is also obtained in the other tables of the database used by the considered queries. Why is that? It is the case that the conditions in which we produced this experiment are quite peculiar. The queries that we used all share similar characteristics. They are all SPJ queries, each of them utilizes each table only once in the join condition (there are no self-joins) and all the joins are made using key attributes. In this particular condition, each tuple of the output presents: (i) a how-provenance that is a single monomial

[11] `https://www.guidetopharmacology.org`

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

with coefficient 1 and exponent 1 in each variable; (ii) a why-provenance that is composed by only one witness; (iii) a lineage that coincides with the only witness in the witness basis. It is easy to see how, given these queries, the three distributions act in the same way. The credit is always uniformly distributed among the tuples appearing in each provenance.

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

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

`Q3` returns a series of 10 tuples from the version of GtoPdb we considered. The first tuple produced by this query, `<Bertil B., Fredholm>`, has $c_{939} \cdot c2f_{496}$ as provenance polynomial. c_{939} represents the provenance token of a tuple in `contributor`, the same for $c2f_{496}$ in table `contributor2family`. 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.

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, alternatives appear. These are represented as multiple witnesses and multiple monomials.

To give an example of how the CDS can differ from one another in their behavior, let us consider a different query:

```
Q4: SELECT f.name AS name
FROM family AS F JOIN
(SELECT DISTINCT f.family_id, f.name
FROM "family" AS f JOIN contributor2family AS cf ON
f.family_id = cf.family_id
JOIN contributor c ON
cf.contributor_id = c.contributor_id
WHERE c.country = 'UK') AS R
ON F.name = R.name
```

Here the innermost query retrieves all the names and ids of the families written by an author from the UK producing a relation called *R*. This relation is then joined with the table `family` on the attribute `name`.

One output tuple of this query is `<Histamine receptors>`, that has the following provenance polynomial:

$$f_{625}(f_{625}c2f_{656}c_{184} + f_{625}c2f_{113}c_{180} + f_{625}c2f_{283}c_{198} + \\ + f_{625}c2f_{550}c_{865} + f_{625}c2f_{573}c_{101} + f_{625}c2f_{95}c_{109})$$

As already discussed, the different monomials represent possible *alternatives* of combinations of tuples that produce the considered output tuple. Tuple f_{625} is used each time with different joins, thus it appears in each monomial. The last join, performed in the outmost query, is responsible for the final multiplication of f_{625} with the rest of the polynomial between parenthesis.

From this polynomial we compute the why-provenance as a set of six different witnesses:

$$\{\{f_{625}, c2f_{656}, c_{184}\}, \\ \{f_{625}, c2f_{113}, c_{180}\} \\ \{f_{625}, c2f_{283}, c_{198}\}, \\ \{f_{625}, c2f_{550}, c_{865}\}, \\ \{f_{625}, c2f_{573}, c_{101}\}, \\ \{f_{625}, c2f_{95}, c_{109}\}\}$$

And corresponding lineage:

$$\{f_{625}, c2f_{656}, c_{184}, c2f_{113}, c_{180}, c2f_{283}, c_{198}, c2f_{550}, c_{865}, c2f_{573}, c_{101}, c2f_{95}, c_{109}\}$$

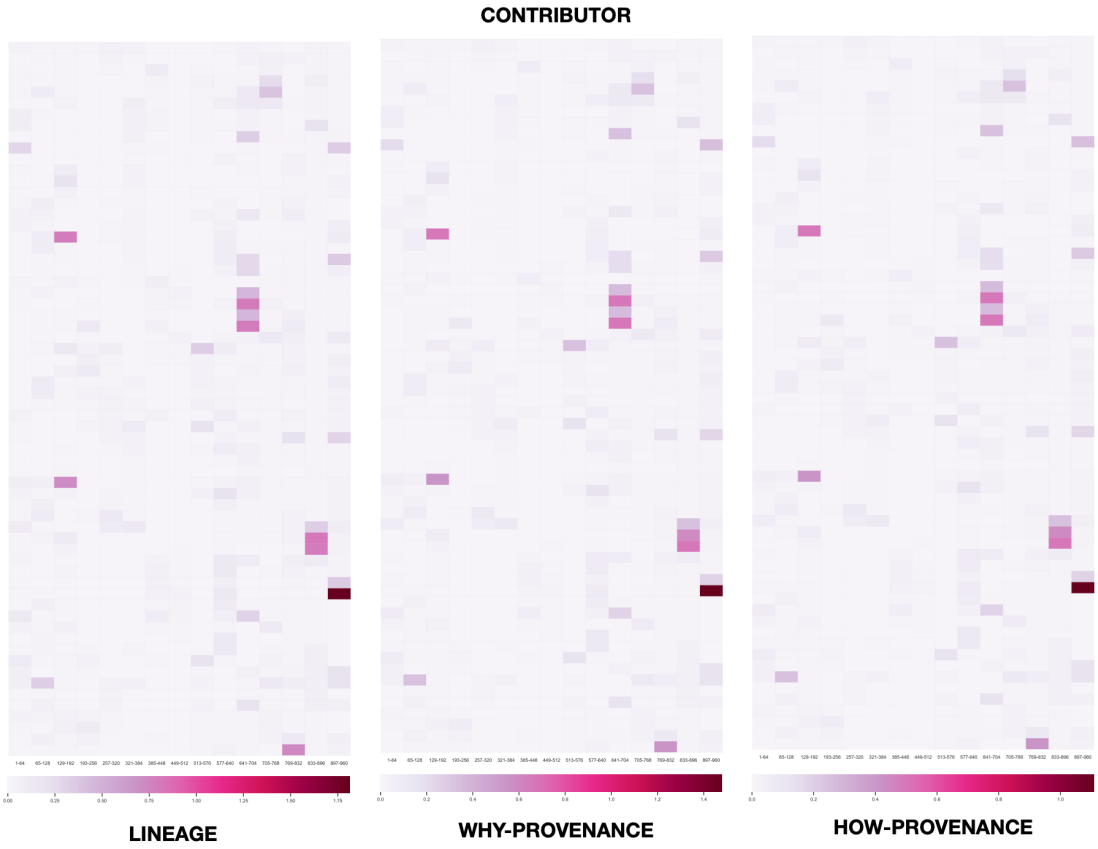

Figure 7. Comparison of three DS on the same table `family` after the distribution of the credit connected to query `Q4`.

This was only one tuple among the 86 obtained from this query. If we assign credit 1 to all these tuples and distribute it with the different strategies, we obtain the result shown in Figure 7 for the table `contributor`. At first sight, it may appear that the three distributions produce the same result. This is only partially true: the heat maps appear equal, but the absolute values assigned to each tuple are different. This is more evident if we look at the legend of each heat-map, where the maximum quantity of credit is different for each distribution. The one performed through lineage is around 1.8, the why-provenance's one is around 1.4, and the one based on how-provenance is around 1.1.

To understand what is happening with this query in this specific table, consider the output tuple `<Histamine receptors>` and its provenances, as discussed above. Let us focus on its lineage. There are a total of six authors for this family and 13 tuples in total in the lineage. Thus, using the lineage-based DS, each tuple belonging to the `contributor` table (i.e. $c_{184}, c_{180}, c_{198}, c_{865}, c_{101}, c_{109}$) receives credit equal to $1/13$. Tuple f_{625} too receives a portion of credit equal to $1/13$.

Let us consider now why-provenance. Tuple f_{625} appears six times in six different witnesses composed of 3 elements each. From each witness it receives a portion of credit equal to $1/18$, thus its total credit is $1/3$. On the other hand, all the authors appear only once in each witness, thus each of them receives credit $1/18$. In this case, why-provenance is recognizing more credit to tuple f_{625}, since it appears in each witness. The consequence is that this distribution is equally *subtracting* credit from the other tuples in the witnesses and giving it to f_{625}. In Figure 7 we are only looking at table `contributor`. This same effect is reproduced for each tuple of the output of query `Q4`, thus the *absolute* credit values on the tuples vary depending on the deployed strategy. What happens is that the tuples in table `contributor` receive less credit than the one received using lineage, but in the same proportions. The heat map appears thus equal to the one obtained with lineage. This same effect is also present with the how-provenance-based CDS. In this case, tuple f_{625} is rewarded even more, since it appears with an exponent 2 in each monomial, thus attracting even more credit.

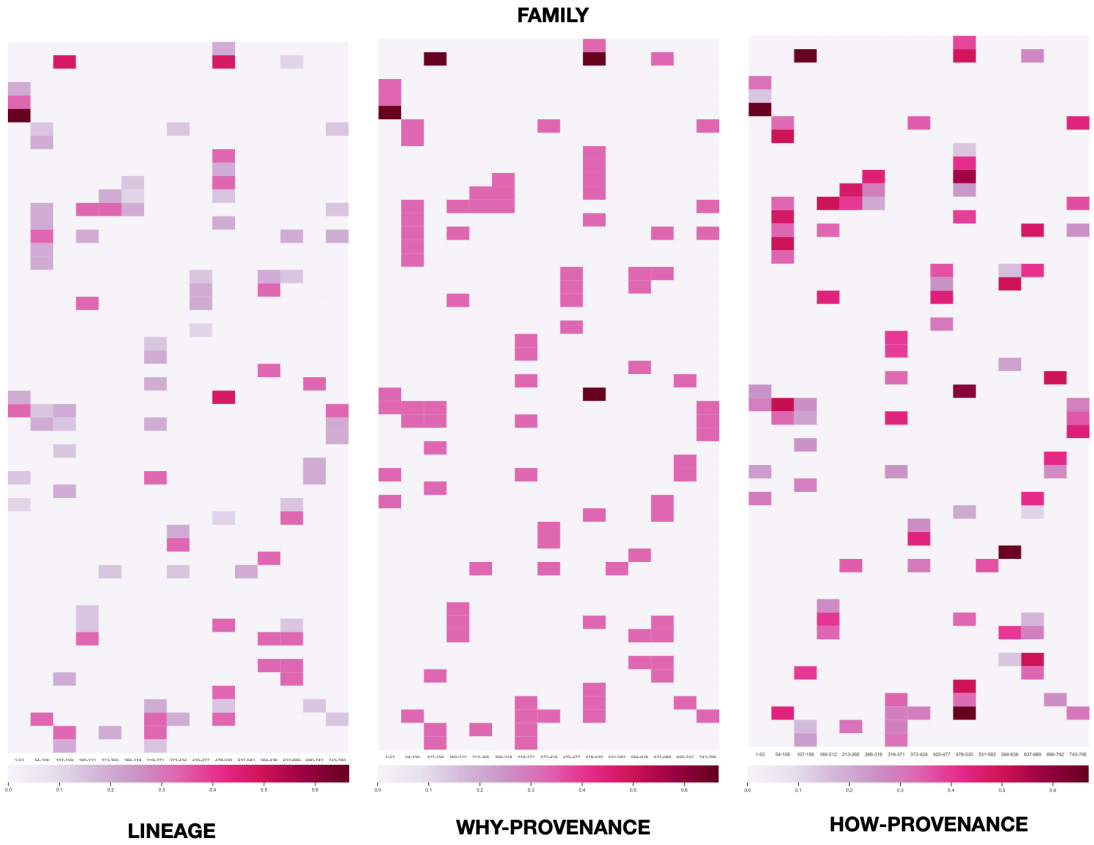

Figure 8. Comparison of three DS on the same table `family` after the distribution computed on provenances randomly generated.

This is also why when we look at the legend for each part of Figure 7, the maximum value reached with the lineage-based DS is higher than the one reached with the why-provenance-based DS, which in turn is higher than the one obtained with the how-provenance. This is because the different strategies reward less and less the tuples of table `contributor` and more the ones in table `family`.

This clearly shows the ability of the different strategies to adapt to situations. All three of them can highlight the relevant tuples in the table. However, they differ in the way they reward the tuples. Depending on the task, one provenance can be preferred to the other. If the only interest is to highlight the relevant tuples, lineage is sufficient. If the interest is also to reward more the tuples that are more fundamental to the output, one can also choose why- or how-provenance, knowing that how-provenance rewards even more than why-provenance the relevant tuples that are indispensable for the output.

One may ask now if it is possible to obtain results whose heat maps are visibly different. Consider for this Figure 8. The figure reports a distribution of credit performed on `family` through the generation of *synthetic* polynomials. In this last case, we did not produce full-fledged queries. Rather, we randomly generated provenance polynomials that might be the how-provenance of randomly generated synthetic queries. An example of such synthetic polynomial is:

$$3f_1^3c2f_1^2c_1^2 + 2f_1c2f_2^3c_2^3 + 4f_5c2f_{17}^4c_{18}^3$$

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

$$\{\{f_1, c2f_1, c_1\}, \{f_1, c2f_2, cf_2\}, \{f_5, c2f_{17}, c_{18}\}\}$$

its lineage is:

$$\{f_1, f_5, c2f_1, c_1, c2f_1, c2f_2, c2f_{17}, c_1, c_2, c_{18}\}$$

These types of polynomials are not impossible to obtain. They can be obtained by writing nested queries with join and union operations that use multiple times the same tuples (thus the presence of exponents bigger than 1) and that use the same combination of operations more than once (thus the presence of coefficients for monomials bigger than 1). We randomly generated a set of 100 such polynomials.

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

$$f_1 = \frac{59}{315}, f_5 = \frac{1}{18}, c2f_1 = \frac{2}{21}, c2f_2 = \frac{2}{15}, c2f_{17} = \frac{2}{9}, c_1 = \frac{2}{21}, c_2 = \frac{2}{15}, c_{17} = \frac{1}{6}$$

Using why-provenance, this is the output:

$$f_1 = \frac{2}{9}, f_5 = \frac{1}{9}, c2f_1 = \frac{1}{9}, c2f_2 = \frac{1}{9}, c2f_{17} = \frac{1}{9}, c_1 = \frac{1}{9}, c_2 = \frac{1}{9}, c_{17} = \frac{1}{9}$$

Finally, with lineage, this is the distribution:

$$f_1 = \frac{1}{8}, f_5 = \frac{1}{8}, c2f_1 = \frac{1}{8}, c2f_2 = \frac{1}{8}, c2f_{17} = \frac{1}{8}, c_1 = \frac{1}{8}, c_2 = \frac{1}{8}, c_{17} = \frac{1}{8}$$

To highlight how the distributions behave differently with these polynomials, consider tuple f_5. f_5 receives the highest quantity of credit when we use the lineage-based distribution. Why-provenance and how-provenance reduce its quantity of credit since more information is available for the computation and the algorithms weigh less and less its role.

Generally speaking, the more complex the distribution, the more polarized the credit is toward the tuples that are used more frequently or with a higher impact in the production of the output tuple. Looking at the heat-maps of Figure 8, it appears that lineage tends to distribute credit more "equally" among the tuples, with only one or two tuples receiving higher quantities of credit, primarily because they are used in many different queries.

Why-provenance produces more tuples that are rewarded with high values of credit. Moreover, it appears that the other tuples that are not on the top of the spectrum are rewarded even more evenly compared to the DS based on lineage. That is, why-provenance, in this case, rewarded many tuples with roughly the same quantity of credit, and few tuples (but more compared to the DS based on lineage) with higher quantities of credit. This is due to the fact that why-provenance not only rewards the presence of a tuple in the computation but also the ways in which it is used.

How-provenance, finally, produces the distribution more sensible to the way a tuple is used in a query. Compared to the previous two DS, it also takes into consideration how many times a tuple is used, and weighs this factor in the distribution. It is interesting to see how certain tuples that received the lowest values of credit with lineage are now rewarded with higher values, showing that their fundamental role in certain queries outshines the fact that other tuples were used more frequently in the set of queries.

For our last set of experiments, consider Figure 9. We still use the 100 polynomials described above, and the credit distributed through them. Since these polynomials correspond to queries whose corresponding authors are not easily identifiable, we considered 20 "synthetic" authors and we randomly assigned one author to each tuple in the database. The authors receive "blocks" of consecutive tuples, with each block of the size varying between 10 and 40. Every time a tuple was used in a provenance polynomial, we assigned one citation to the author corresponding to the tuple. The same author also receives the three different credits assigned to the tuple at the end of the distribution process using the three DS.

Figure 9 presents the radar plot where the 20 authors are sorted based on the normalized number of received citations, together with the corresponding normalized quantities of credits. Credit presents a different behavior from the one of citations, and each form of credit, i.e. the credit obtained from the different DS, behaves differently from the others. It appears, for example, that authors T, C, and R that are low in the number of citations, are still rewarded more than other more cited authors in terms of credit. This is because, even if the tuples of these authors received fewer citations, they still received more credit than other more cited tuples. This shows how credit can be an effective new method to use together with traditional citations to reward curators, highlighting aspects that are lost using the traditional bibliometrics.

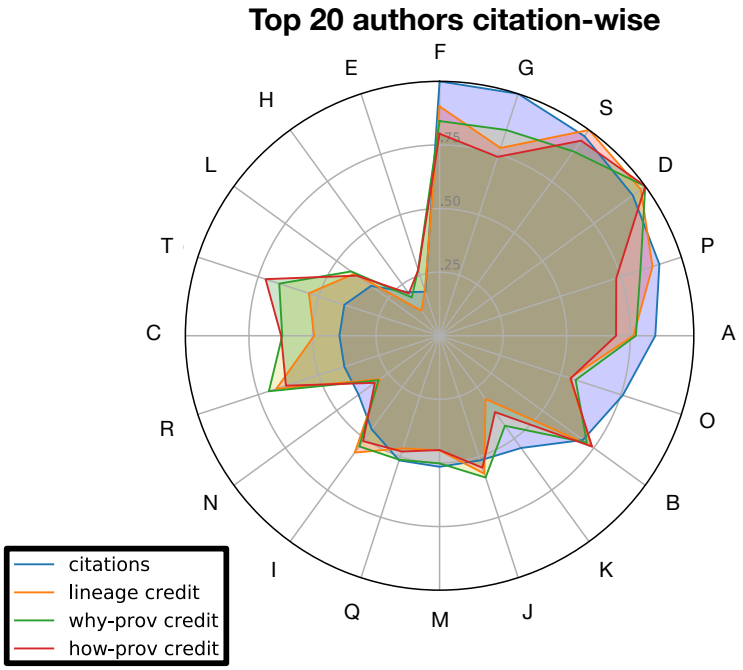

Figure 9. Top 20 authors by number of citations and their credit given through the three different DS.

The three DS are all effective ways to distribute credit and there is not one distribution that is preferable to the other all the time. It all depends on the needs of the users. Lineage is to be preferred when users only want to see the tuples used in queries and to reward more the tuples that are used in many queries. It only rewards based on the *presence* of the tuples. Why-provenance is more versatile when users also want to take into consideration how many ways a tuple is used, thus, in a way, its *versatility* inside the queries that used it. Finally, how-provenance also counts how many times a tuple is used, its *frequency* in the computation of a query.

7 CONCLUSIONS

In this paper, we expanded on our previous work on data credit and data credit distribution by defining two new distribution strategies, based on the 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 by a query, are also rewarded more by the distribution. The second distribution, based on how-provenance, is also able to consider the frequency in which a tuple or a combination of tuples are used in the query through the information contained in the provenance polynomial, and in this sense, it is even more sensitive than the first one.

To show the differences between the three DS (also considering the one based on lineage, defined in our previous work), we performed different experiments on GtoPdb, a curated scientific relational database. In the first set of experiments, we used SPJ queries extracted by data citations present in papers published in the British Journal of Pharmacology. Through the use of these queries, we were able to distribute the credit to the tuples in different tables of the database, highlighting the tuples that are used more than others. We showed that with these queries the three strategies produce the same distribution. This is because, with the specific type of queries that do not present self-joins, the formulas at the base of the strategies produce the same output. The tuples are, in this specific case, used in the same way by the tuples, thus the DSs do not register any particular difference in the role of the tuples.

In the second and third sets of experiments, we considered more complex queries, i.e. nested queries whose provenance polynomials presents coefficients and exponents bigger than 1. In this way, we discovered that, even though all three DS can highlight all the tuples used by the queries in the database, the three have different behaviors. While the DS based on lineage rewards all the tuples used by a query in

equal measure, the strategy based on why-provenance tends to reward more the tuples more important to the query. In particular, why-provenance can take into consideration the different ways in which one tuple is used in a query. How-provenance is even more sensitive to the role of the tuples: it can also consider the frequency by which a tuple or a set of tuples is used in the case of more complex queries. Depending on the goal of a user, one provenance may be preferred over another.

In the fourth set of experiments, we showed how, when compared with traditional citations, the credit distributed with the three strategies works as a new tool highlighting different aspects of the role of an author in the research context identified by queries. Authors that have a limited number of citations can still have a high quantity of credit due to the importance of the data to which they contributed in the context of the queries.

In our future work, we plan to explore the different potential applications of credit on relational databases. One example is the so-called *data pricing*. Data pricing consists of giving a price to a query submitted by a user who wants to buy the produced information. Currently, the most used strategy to face data pricing is based on query rewriting. A database stores a set of views, correlated with their price. When a new query arrives, the system tries to rewrite it using the stored views and obtain a price for the query. This process is computationally expensive. We plan to distribute credit through the use of carefully planned and representative queries and use it as information to define a new faster, flexible, and fair pricing function.

Another application is *data reduction* Milo (2019), concerned with reducing the huge mole of data that is produced in the evolving world of research and information technology. Data reduction deals with different aspects of dealing with huge amounts of data, such as finding reduced and relevant data streams from the multiple gigabytes of data produced by big data systems every second or dealing with the curse of dimensionality which requires unbounded computational resources to uncover actionable knowledge patters (Ur Rehman et al., 2016).

Data credit can also help in this regard by helping to find "hotspots" and "coldspots". A hotspot is data in a database (a tuple or a single attribute, for example), that presents a high quantity of credit and is therefore valuable for the set of queries that distributed that credit. On the other hand, a coldspot is data that present low quantities of credit and therefore can be considered as useless or less relevant, and can therefore be removed or moved in another cheaper and less efficient memory location.

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