GENSYNTH: Synthesizing Datalog Programs without Language Bias

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Abstract

Existing techniques for learning logic programs from data typically rely on language bias mechanisms to restrict the hypothesis space. These methods are therefore limited by the user's ability to tune them such that the hypothesis space is simultaneously large enough to include the target program but small enough to admit a tractable search. We propose a technique to learn Datalog programs from input-output examples without requiring the user to specify any language bias. It employs an evolutionary search strategy that mutates candidate programs and evaluates their fitness on the examples using an off-the-shelf Datalog interpreter. We have implemented our approach in a tool called GENSYNTH and evaluate it on diverse tasks from knowledge discovery, program analysis, and relational queries. Our experiments show that GENSYNTH can learn correct programs from few examples, including for tasks that require recursion and invented predicates, and is robust to noise.

1 Introduction

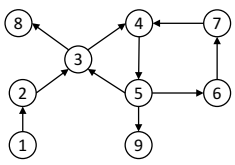
The problem of learning logic programs from input-output data has been widely studied in artificial intelligence, formal methods, and machine learning. Such programs offer a variety of benefits by virtue of being explainable, interpretable, generalizable, verifiable, and composable.

Datalog (Abiteboul, Hull, and Vianu 1994), a logic programming language, is commonly targeted due to its rich expressivity, declarative rule-based semantics, and efficient implementations. In this setting, the input-output data are specified in the form of tuples over finite relations; the goal is to synthesize a Datalog program that, when executed on the given input tuples, produces the given output tuples.

Figure 1 shows an example task in which the input data is a binary relation edge encoding edges in a directed graph, and the output data is a binary relation scc representing pairs of nodes in the input graph that belong to the same strongly connected component (SCC). A correct and concise solution is the following recursive program:

```
path(x,y) :- edge(x,y).
path(x,y) :- edge(x,z), path(z,y).
scc(x,y) :- path(x,y), path(y,x).
```

The first rule defines the base case for the predicate path, stating that any edge from x to y implies a path from x to y. The second rule defines the inductive step for path: an edge from x to z and a path from z to y implies a path from x to y. Finally, the third rule states that a path from x to y and a path from y to x implies that x and y are in the same scc.



(a)

Input tuples (EDB)
edge (3, 4)
edge (4, 5)
edge (5, 3)
···

(b)

Output tuples (IDB)	
scc (3, 3)	scc (4, 3)
scc (3, 4)	scc (4, 5)
scc (3, 5)	···
scc (4, 4)	

(c)

Figure 1: Example of a directed graph (a) and its representation as a set of tuples (b). An edge from x to y is represented as tuple edge(x, y). The goal is to realize relation scc(x, y), indicating that x and y belong to the same SCC in graph (a).

Note that this solution is non-trivial, as it is a recursive program requiring complex joins and an *invented predicate* path. An invented predicate is a hidden intermediate concept often necessary for synthesis but not specified in the schema or input-output example.

Existing approaches to this problem are broadly classified into Inductive Logic Programming (ILP), e.g. Metagol (Muggleton 1991); Answer Set Programming (ASP), e.g. ILASP3 (Law 2018); program synthesis, e.g. ProSynth (Raghothaman et al. 2020); and neural learning, e.g. NTP (Rocktäschel and Riedel 2017). Despite using notably different search techniques, however, all of these approaches rely on various language bias mechanisms or restrictions on expressiveness to limit the hypothesis space. We draw comparisons between various contemporary tools in Table 1.

Approaches with significant language bias mechanisms, such as metarules (Metagol), candidate rules (ProSynth), or templates (NTP) run quickly only under a carefully crafted small set of these entities, hereafter called templates. This belies the considerable user burden of authoring the templates which then fundamentally biases the tool toward a specific subset of programs that the author has in mind. Since the runtime of these template-based tools become impractical far before they can consider a large sample space, these approaches are critically limited by the user's ability to strike a balance when providing templates: too many and the tool times out, too few and it fails to synthesize a solution.

[*]Both authors contributed equally to the paper.

	Metagol	ProSynth	NTP	ILASP3	Popper	GenSynth
Hypotheses	Definite	Datalog	Datalog	ASP	Definite	Datalog
Language bias	Metarules	Candidate rules	Templates	Modes	None	None
Predicate invention	✓	○	○	○	✗	✓
Recursion	✓	✓	✓	✓	✓	✓
Noise handling	✗	✗	✓	✓	✓	✓

Table 1: Comparison of state-of-the-art tools. Metagol and Popper can also synthesize Datalog programs since Datalog programs are definite. GenSynth and Metagol support automatic predicate invention, whereas ProSynth, NTP, and ILASP3 only support prescriptive predicate invention, in which the schema of all invented predicates are specified.

For example, consider the metarules that Metagol needs to synthesize scc:

```
metarule([P,Q],[P,A,B],[[Q,A,B]]).
metarule([P,Q,P],[P,A,B],[[Q,A,C],[P,C,B]]).
metarule([P,Q,Q],[P,A,B],[[Q,A,B],[Q,B,A]]).
```

There are hundreds of possible metarules of this length, and without substantial background information about the problem or knowledge of a potential solution, it would be extremely difficult to craft a small set of templates that contains these three rules. In practice, even the ordering of the metarules significantly impacts Metagol's performance; oftentimes an unlucky ordering will result in Metagol timing out. When using rule enumeration techniques, tuning the hyperparameters of an enumerator for a specific benchmark to guide the search space is still time consuming and difficult. ProSynth times out on the SCC task when the enumerator is not provided with benchmark-specific hyperparameters obtained either through knowledge of the solution or through tedious trial and error. Finally, template-based neural approaches, such as NTP, fare no better. NTP requires the user to specify not only templates, but how often a template rule should be instantiated and suffers from the same bias and runtime issues as the other approaches.

ILASP3 does not require metarules, but still has language bias in the form of modes, which restrict how often predicates may appear in a clause. Furthermore, ILASP3 is biased due to its support of prescriptive invented predicates; it can only synthesize invented predicates if their schema has been specified in advance. Given that it is not always obvious if an invented predicate is even needed, this is a non-trivial task (Cropper, Dumancic, and Muggleton 2020). Under the hood, ILASP3 first generates candidate rules before running the search algorithm, so it is burdened by the same issues that afflict Metagol, ProSynth, or NTP. In practice, ILASP3 takes about 4 times longer on SCC than GENSYNTH, even after we, within ILASP, explicitly specify the arity and typing of the path invented predicate and enable the `anti-reflexive` and `positive` settings.

Popper has no language bias but it cannot handle predicate invention. Thus its search space is limited not by its language bias but by its severe restrictions on expressiveness. Popper is not publicly available for comparison but would not be able to synthesize at least 12 of the 42 noise-free benchmarks in our evaluation which need invented predicates.

Our Approach. We introduce GENSYNTH[1], a template-free end-to-end Datalog synthesis tool. By end-to-end, we mean that only an input-output example and input-output schema are provided; in our case, there are no templates, meta-rules, meta-programs, or modes to specify. Furthermore, GENSYNTH automatically synthesizes invented predicates and is therefore free from the bias introduced by approaches that use prescriptive invented predicates. Despite such an unconstrained search space, GENSYNTH is able to generate small and interpretable solutions to Datalog problems, including non-trivial ones like scc.

We frame the synthesis task as a search problem through the space of Datalog programs—a very complex surface with a sparse fitness function and riddled with local minima. We depict the algorithm by following one program throughout the run using the SCC example in Figure 2. The algorithm consists of an *accretion phase*, where accretions mutate a program until it has the desired fitness, and a *reduction phase*, where reductions mutate the program decreasing its size but maintaining its fitness. The accretion phase is inspired, in part, by how humans write programs: they start with a simple piece of code and make small changes each time they desire a new feature or encounter a bug.

Our first insight is to combine the search with the rule generation, which occurs implicitly as a result of the mutations. This allows us to prune most of the search space dynamically as the algorithm progresses rather than pruning the search space manually up front, as in template-based approaches. For example, the set of programs explored at generation $A4$ is very highly constrained; all offspring of this program are similar to the parent. This is a good way to constrain the search space, since we have learned by $A4$ that this space of programs is likely to have a high fitness. This constrained search space then makes it much more likely that we reach the program with fitness 1.0 found at generation $A5$.

Another insight is to use mutations to traverse a very complex and coarse surface in an effective way. Differentiable approaches such as Difflog (Si et al. 2019) or neural approaches using SGD struggle as they become trapped in local minima. Using mutations, which only slightly modify the program, makes it likely that a parent and offspring have similar fitness scores, but mutations strung together allow for leaps over local minima.

We also aim to maximize throughput; bottom-up tools like ProSynth that run thousands of candidate rules simultaneously suffer from poor scalability as they overwhelm the Datalog interpreter. GENSYNTH, on the other hand, runs mostly very small programs. It further maximizes throughput by considering only the space of valid programs and taking advantage of its parallelism.

[1]Available at https://jonomendelson.github.io/gensynth/

Gen.	Program	F1	Mutation
$A0$	c_1: scc(x, y) :- edge(x, y).	0.3429	**Recurse** on c_1 to create c_1', c_2 and c_3. **Swap** on c_1' to create c_1''.
$A1$	c_1'': scc(x, y) :- inv(y, x). c_2: inv(x, y) :- edge(x, y). c_3: inv(x, y) :- inv(z, y), edge(x, z).	0.6667	**Append Literal** to c_1'' to create c_1'''. **Append Clause** to create c_4.
$A2$	c_1''': scc(x, y) :- inv(y, x), inv(x, y). c_2: inv(x, y) :- edge(x, y). c_3: inv(x, y) :- inv(z, y), edge(x, z). c_4: scc(x, y) :- edge(x, y).	0.9259	**Extend** on c_1''' to create c_1''''. **Append Literal** on c_4 to create c_4'.
$A4$	c_1'''': scc(x, y) :- inv(y, z), inv(x, y), inv(z, x). c_2: inv(x, y) :- edge(x, y). c_3: inv(x, y) :- inv(z, y), edge(x, z). c_4': scc(x, y) :- edge(y, x), scc(x, x).	0.9804	$c_4' \rightarrow^* c_4''$ as explained in box below. **Append Clause** to create c_5.
$A5$	c_1'''': scc(x, y) :- inv(y, z), inv(x, y), inv(z, x). c_2: inv(x, y) :- edge(x, y). c_3: inv(x, y) :- inv(z, y), edge(x, z). c_4'': scc(x, y) :- edge(x, z), scc(y, x), inv(z, x). c_5: inv(x, y) :- edge(x, y).	1.0	c_4': scc(x, y) :- edge(y, x), scc(x, x). **[Swap]** scc(x, y) :- edge(x, y), scc(x, x). **[Extend]** scc(x, y) :- edge(x, z), scc(x, x), inv(z, y). **[Swap]** c_4'': scc(x, y) :- edge(x, z), scc(y, x), inv(z, x).

Gen.	Program	F1	Mutation
$R0$	c_1: scc(x, y) :- inv(y, z), inv(x, y), inv(z, x). c_2: inv(x, y) :- edge(x, y). c_3: inv(x, y) :- inv(z, y), edge(x, z). c_4: scc(x, y) :- edge(x, z), scc(y, x), inv(z, x). c_5: inv(x, y) :- edge(x, y).	1.0	**Remove Repeating Clauses** to remove c_2.
$R2$	c_1: scc(x, y) :- inv(y, z), inv(x, y), inv(z, x). c_3: inv(x, y) :- inv(z, y), edge(x, z). c_4: scc(x, y) :- edge(x, z), scc(y, x), inv(z, x). c_5: inv(x, y) :- edge(x, y).	1.0	**Minimize Clauses** to remove c_4.
$R4$	c_1: scc(x, y) :- inv(y, z), inv(x, y), inv(z, x). c_3: inv(x, y) :- inv(z, y), edge(x, z). c_5: inv(x, y) :- edge(x, y).	1.0	**Minimize Arguments** on c_1 to create c_1' (z $\rightarrow$ y).
$R5$	c_1': scc(x, y) :- inv(y, y), inv(x, y), inv(y, x). c_3: inv(x, y) :- inv(z, y), edge(x, z). c_5: inv(x, y) :- edge(x, y).	1.0	**Minimize Literals** on c_1' to create c_1''.
$R8$	c_1'': scc(x, y) :- inv(x, y), inv(y, x). c_3: inv(x, y) :- inv(z, y), edge(x, z). c_5: inv(x, y) :- edge(x, y).	1.0	

Figure 2: Sequence of mutations by GENSYNTH in the accretion ($A0$-$A5$) and reduction ($R0$-$R8$) phases for the SCC example.

Finally, the reduction phase is crucial for interpretability, as illustrated in Figure 2. While in generation $A5$ we have derived a correct program, it is difficult to understand, has vestigial code, and may even overfit the example. The reduction phase, by syntactically and possibly semantically modifying the program, aims to reduce the size of the candidate solution without compromising on its correctness.

In summary, these insights together make GENSYNTH very effective at quickly synthesizing highly expressive, interpretable programs without language bias.

2 Algorithm

Formally, GENSYNTH takes as input a set of relation schemas R which is divided into the input relations $R_{in} \subsetneq R$, and an output relation $r_{out} \in R$. The schema of each relation $r(T_1, T_2, \ldots, T_k)$ describes its arity k and the types of each column T_i. The training data consists of a set of input tuples I which populate the input relations, a set of desirable output tuples O^+, and a set of undesired output tuples O^- such that $O^+ \cap O^- = \emptyset$. Finally, it also takes as input the fitness threshold $0 \leq f_T \leq 1$. If successful, it returns a Datalog program with the desired fitness value on the training data. We note that the synthesized program may reference invented relations $r_{inv} \notin R$.

As discussed in Section 1, GENSYNTH consists of an accretion phase where it discovers an initial target program with the desired fitness score, followed by a reduction phase in which it attempts to reduce the size of the learned program. We describe these algorithms in Algorithms 2 and 3 respectively. Informally, both procedures are instances of evolutionary algorithms (Fogel 2006) which repeatedly apply mutations to a population of candidate programs, until they discover a program with the desired properties—with adequate fitness score, and with minimal size, respectively.

Throughout the algorithm, we ensure that all programs in the population remain valid programs. Each clause in a valid program must be *well-typed*, such that the arguments respect the schema of the relations, *grounded*, such that all arguments that appear in the head must appear at least once in the body, and *connected*, where all literals must have at least one argument which can be chained, directly or indirectly to some argument of the head.

Algorithms 1, 2, and 3 are designed to maintain these invariants throughout execution.

2.1 Clause Generation, Accretion, and Reduction

Recall that the accretion algorithm repeatedly mutates the programs in the population until it achieves the desired fitness score. It starts with a list of c seed programs, each of which is a small valid program generated by an invocation of the $\mathrm{CreateClause}$ method, formally defined in Algorithm 1. In each generation, it selects the best-performing $s \cdot c$ programs, where $0 < s < 1$, and repeatedly mutates each selected program to restore the population size. Each mutation is itself a sequence of n elemental mutations, described in Section 2.3.

The $\mathrm{CreateClause}$ procedure is a three-phase process: It starts with the schema of the output relation, and fixes the list of relations appearing in the body of the clause by greedily picking input relations which can bind as many output variables as possible. It then walks through the list of literals, and randomly assigns variable names while ensuring that all conditions for a valid program are met. This algorithm is used to generate the seed programs, in Step 2 of Algorithm 2, as well as in the **Append Clause** mutation as described in Section 2.3. While it is possible that the seeds generated by the $\mathrm{CreateClause}$ procedure may be isomorphic, subsequent mutations in Algorithm 2 will cause them to diverge.

Next, observe that the reduction algorithm closely follows the structure of the accretion phase, with a few notable differences. First, while the initial programs of Algorithm 2 are randomly generated by calls to the $\mathrm{CreateClause}$ method, the reduction algorithm initializes its population with c copies of $\widehat{p}$. It follows that the population of programs is therefore a list with possible duplicates rather than a classical set. Second, it sorts the programs by size rather than by fitness score in Equation 2, with the condition that all programs have fitness scores surpassing the threshold. The purpose of the reductive mutations is therefore to reduce the size of the learned program, rather than necessarily improve fitness. Third, at each step, it applies the reductive mutations to generate an offspring program that has never been included in the population before. Finally, in contrast to the accretive mutations, which maintain or increase the size of the program, the reductive mutations reduce or maintain the size of the program to which they are applied. We catalog these mutations in Section 2.3. As a result, it is a self-limiting process guaranteed to terminate in Step 2c, when the 1-step reductions are unable to discover any as-yet-unseen offspring.

2.2 Population-Specific Fitness Functions

One curious aspect of Algorithm 2 is that different populations use different values of β to track the programs under consideration. More precisely, for each population, we sample $\beta' \sim (0, 1)$ uniformly at random between 0 and 1. Then with probability 0.5, we choose $\beta = \beta'$, and with probability 0.5, we choose $\beta = 1/\beta'$.

Recall that the training data consisted of the input tuples I, desired output tuples O^+, and undesired output tuples O^-. Consider a program p which, when applied to the input tuples I, produces the output tuples $p(I) = O$, with $TP = |O \cap O^+|$ true positives. In this case, its fitness score $F_\beta(p)$ is defined as the β-weighted harmonic mean of its precision $TP/|O|$ and recall $TP/|O^+|$:

$$F_\beta(p) = \frac{(1+\beta^2) * TP}{|O \cap (O^+ \cup O^-)| + \beta^2 * |O^+|} \tag{3}$$

As different populations are using slightly different fitness functions, it reduces the chance of all populations simultaneously getting stuck in local maxima. Regardless of this, Step 3c of Algorithm 2 allows the procedure to terminate only if the F_1 score of the program exceeds the cutoff.

Algorithm 1 CreateClause(R_{in}, r_{head}). Given the set of input relations R_{in}, and the output relation r_{head}, produces a valid clause C that is as short as possible and includes only input relations in the body.

1. Let C have head r_{head} and an empty body. Introduce fresh arguments for r_{head}. Let A_{head} contain these arguments.
2. **Literal phase:**
   (a) Let A_{ug} be the set of arguments of r_{head} that cannot be grounded by any literal in the body of C. Initially, $A_{ug} := A_{head}$.
   (b) Repeat while $A_{ug} \neq \emptyset$:
      i. Select a relation $r \in R_{in}$ where r allows the largest possible number of arguments in r_{head} to be grounded (breaking ties at random). Let A be a maximal set of arguments that r can ground in A_{ug}.
      ii. Add r to the body of C without setting the arguments and update $A_{ug} := A_{ug} - A$.
3. **Argument phase:**
   (a) Let A_{body} contain all the arguments of all the literals in the body of C, initally all unset arguments. Note that A_{head} only contains fresh arguments that are therefore set. While there exists an unset argument $a_i \in A_{body}$:
      i. If there exists a previously set argument $a_j \in (A_{body} \cup A_{head})$ such that a_i and a_j are of the same type, with probability 0.5 set $a_i := a_j$.
      ii. If Step 3(a)i does not set a_i, fix a fresh argument in a_i.
4. **Validity phase:**
   (a) While there exists a literal r_i unconnected with r_{head}, select arguments a_i from r_i and a_j from $(A_{body} \cup A_{head})$ uniformly at random such that their types match and a_j is not in r_i. Update $a_i := a_j$.
   (b) While there exists an ungrounded argument $a_i \in A_{head}$, select an argument a_b of the same type uniformly at random from the body. Update $a_b := a_i$.

2.3 Mutations

In this section, we describe the six accretive mutations and six reductive mutations used by Algorithms 2 and 3, respectively. Crucially, the mutations are designed such that the offspring produced by any mutation is necessarily a valid program as defined in the introduction to Section 2.

A candidate program is a collection of Datalog clauses of

Algorithm 2 $\mathrm{Accrete}(R, I, O^+, O^-, f_T)$. Given a set of relation names R and training data (I, O^+, O^-), returns a program $\widehat{p}$ with fitness score $F_1(\widehat{p}) \geq f_T$.

Run b independent populations in parallel. Within each, do:

1. Choose the fitness function F_β as described in Section 2.2.
2. Initialize the list of seed programs P with c calls to the randomized $\mathrm{CreateClause}(R_{in}, r_{out})$ method.
3. Repeat forever:
   (a) **Selection event:** Sort the programs $p \in P$ in descending order of their fitness scores $F_\beta(p)$, and update:
   $$P \coloneqq [P_1, P_2, \ldots, P_{\lfloor s \cdot c \rfloor}], \tag{1}$$
   where s is the fraction of programs which survive each selection event, and c is a user-provided limit on the population size.
   (b) **Proliferation sub-phase:** Produce $(1-s)/s$ offspring for each program $p \in P$:
      i. Select the number of mutations n to be applied to p by sampling from a distribution, $n \sim B$ (defined in the supplementary material).
      ii. Initialize $p_0 = p$, and for each $i \in \mathbb{N}$, let $p_{i+1} \coloneqq Mutate(p_i)$.
      iii. Update: $P \coloneqq P \cup \{p_n\}$.
   (c) **Termination:** If there is a program $\widehat{p} \in P$ such that $F_1(\widehat{p}) \geq f_T$, terminate all populations and return $\widehat{p}$.

Algorithm 3 $\mathrm{Reduce}(R, I, O^+, O^-, f_T, \widehat{p})$. Returns a reduced program p^* such that $F_1(p^*) \geq F_1(\widehat{p})$.

Run b independent populations in parallel. Within each, do:

1. Initialize the list of seed programs P with c copies of $\widehat{p}$.
2. Repeat forever:
   (a) **Selection event:** Let $P' = [p \in P \mid f(p) \geq f_T]$ be the list of programs with acceptable fitness scores. Sort the programs in increasing order of their size, and update:
   $$P \coloneqq [P'_1, P'_2, \ldots, P'_k], \tag{2}$$
   where $k = \min(\lfloor s \cdot c \rfloor, |P'|)$, and as before, s is the fraction of programs which survive each selection event.
   (b) **Proliferation sub-phase:** Repeat $(1-s)/s$ times for each program $p \in P$:
      i. Choose a random mutation type m and let $M_{p,m}$ be the set of 1-step mutants obtained by applying m to p.
      ii. Let the set of ancestors, C be the set of all programs which inhabited P at any time.
      iii. If $M_{p,m} \not\subseteq C$, pick a mutant $p' \in M_{p,m} \setminus C$ uniformly at random, and append p' to P.
   (c) **Termination:** If no new programs were added during the proliferation sub-phase, then terminate this population, and return the smallest program $p \in P$.

Let p_i be the program returned by the i-th population. Let p^* be the smallest program in $\{p_1, p_2, \ldots, p_b\}$. Return p^*.

the form $r_0 \texttt{ :- } r_1, ..., r_n$, where r_i is a relation with arguments $(a_1, ..., a_k)$.

Accretive Mutations. Step 3b of Algorithm 2 applies a sequence of accretive mutations to produce offspring in each generation. These mutations aim to increase the size of the candidate program.

1. **Append Clause:** Create a new clause using the $\mathrm{CreateClause}$ method and append this clause to the candidate program.
2. **Append Literal:** Randomly pick a clause. Append a random input, invented, or output literal to the body of this clause. When assigning arguments to the new literal, choose fresh and existing arguments with equal probability such that the clause is valid.
3. **Extend:** Randomly pick a clause $r_0 \texttt{ :- } r_1, ..., r_i, ..., r_n$, and within this clause, randomly pick a literal r_i with arguments $(ai_0, ..., ai_k, ..., ai_m)$. Introduce a fresh argument ai'_k. Append a random input, invented, or output literal r_j to the body of this clause with arguments $(aj_0, ..., ai_k, ..., ai'_k, ..., aj_p)$. Replace argument ai_k with ai'_k such that r_i has arguments $(ai_0, ..., ai'_k, ..., ai_m)$. The resulting clause is $r_0 \texttt{ :- } r_1, ..., r_i, ..., r_n, r_j$.
4. **Swap:** Randomly pick a clause. Swap the location of two randomly chosen arguments in the body of the clause.
5. **Invent:** Randomly pick a clause and randomly select a literal from the body of the clause, where the clause is $r_0 \texttt{ :- } r_1, ..., r_i, ..., r_n$ and r_i is a randomly selected literal. Replace r_i with a new invented predicate r_{inv} that has the same schema and arguments as r_i such that the original clause becomes $r_0 \texttt{ :- } r_1, ..., r_{inv}, ..., r_n$. Add a new clause to the program $r_{inv} \texttt{ :- } r_i$ with head r_{inv} and body r_i.
6. **Recurse:** Randomly pick a clause and randomly select a literal from the body of the clause, where the clause is $r_0 \texttt{ :- } r_1, ..., r_i, ..., r_n$ and r_i is the randomly selected literal. Replace r_i with a new invented predicate r_{inv} that has the same schema as r_i such that the original clause becomes $r_0 \texttt{ :- } r_1, ..., r_{inv}, ..., r_n$. Then add two new clauses:
   (a) One "base case" clause where $r_{inv} \texttt{ :- } r_i$.
   (b) One "recursive step" clause where $r_{inv} \texttt{ :- } r_i, r_{inv}$ such that r_i contains at least one argument appearing in the head and r_{inv} and r_i share a newly introduced argument that does not appear in the head.

Observe that the **Invent** mutation can only synthesize invented predicates whose schemas coincide with that of an input or output relation. While this is indeed a limitation, we have never encountered a task in practice that has required an invented predicate with a distinct schema.

Note also that the accretive mutations are designed such that the algorithm will eventually reach a consistent solution with probability 1 if such a solution exists, given a large enough choice of the peak mutation length. This follows from the observations that: (a) any clause which is currently producing undesired output tuples can be deactivated by appending sufficiently many literals, and (b) any target clause

can be created by a suitable combination of the Append Clause and Append Literal mutations.

Reductive Mutations. Step 2b of Algorithm 3 applies a sequence of reductive mutations to produce offspring each generation. These mutations aim to simplify the candidate program by decreasing its size.

1. **Remove Repeating Clauses:** If the candidate program contains two identical clauses, remove one of the clauses.
2. **Remove Repeating Literals:** If there exists some clause with two identical literals with identical arguments, remove one of the literals.
3. **Reduce Invented Predicate:** Randomly pick a clause $r_0 :- \ r_1, ..., r_{inv}, ..., r_n$ such that r_{inv} is a non-recursive, one-clause invented predicate where $r_{inv} :- \ ir_1, ..., ir_k$. Replace r_{inv} in the body of the clause with the body of r_{inv} so that the original clause becomes $r_0 :- \ r_1, ..., ir_1, ..., ir_k, ..., r_n$. Update arguments in the new clause appropriately so that the original and new programs are semantically equivalent.
4. **Minimize Clauses:** Randomly pick a clause and remove it from the candidate program.
5. **Minimize Literals:** Randomly pick a clause. Within the body of the clause, randomly pick a literal and remove it from the clause.
6. **Minimize Arguments:** Randomly pick a clause. Randomly choose two arguments that appear in the clause, a_i and a_j, where $a_i \neq a_j$. Replace all instances of a_j with a_i throughout the clause.

The first three mutations above are equivalence-preserving and therefore do not alter the overall fitness score of the candidate programs. The remaining mutations, which remove clauses, literals, and arguments, may alter the fitness score of the candidate programs. However, Algorithm 3 ultimately only applies mutations such that the fitness score is either preserved or improved.

3 Evaluation

In this section, we experimentally evaluate GENSYNTH with respect to the following criteria:

1. **Effectiveness:** How does GENSYNTH compare to existing approaches that use different kinds of language bias?
2. **Generality:** How does GENSYNTH perform on diverse tasks compared to a state-of-the-art approach?
3. **Robustness:** How does GENSYNTH perform on noisy data compared to a state-of-the-art approach?
4. **Scalability:** How does GENSYNTH scale with the size of the data and the amount of available parallelism?

All experiments were run on a Ubuntu 18.04 server with an 18 core Intel Xeon 3 GHz processor and 394 GB memory. We use the following hyperparameters in our experiments:

1. Number of populations: $b = 32$.
2. Population size: $c = 50$.
3. Selection ratio: $s = 0.2$.
4. Number of mutations in each step: $n \sim B$, where $B = \text{Bin}(n, p)$ is a binomial distribution with $n = \lfloor 15 c_1 c_2 \rfloor$ and $p = 0.3$. Both c_1 and c_2 are sampled uniformly at random between 0 and 1.

3.1 Effectiveness

We study the effectiveness of GENSYNTH at learning non-trivial Datalog programs compared to three contemporary approaches: Metagol, a meta-interpretive learning system using a top-down Prolog interpreter; ProSynth, a program synthesizer using a bottom-up Datalog interpreter; and ILASP3, an inductive Answer System Program learning system.

Setup. We compare these tools on **Andersen**, a popular program analysis for statically reasoning about pointer aliasing in programs written in languages like C and Java. The task consists of 4 input relations and 19 input-output tuples. Since **Andersen** is noise-free, we require a solution with an F1 score of 1.0. We choose **Andersen** as a representative from the 42 tasks used in Section 3.2 as its solution consists of multiple recursive clauses, making it a challenging task:

```
pt(x,y) :- addr(x,y).
pt(x,y) :- assgn(x,z), pt(z,y).
pt(x,y) :- load(x,z), pt(z,w), pt(w,y).
pt(x,y) :- store(z,w), pt(z,x), pt(w,y).
```

As previously stated, Metagol and ILASP3 require a choice of metarules and are further influenced by either the choice of orderings of rule bodies or mode declarations. So we use a single representative benchmark for this comparison as it would be difficult to fairly set up these tools across 42 tasks.

Methodology. We compare the time taken by GENSYNTH, Metagol, ProSynth, and ILASP3 on **Andersen**. We describe each tool's instantiation using as (n, r, t) where n is the number of templates, r is the number of times the tool was run, and t is the number of runs that timed out in 1 hour.

Metagol's runtime depends on the ordering of the templates. We thus provide it with the exact four templates needed to learn the solution but order the predicates of each template differently. We run ProSynth with the 64 templates used in (Raghothaman et al. 2020). We also run it with a more natural set of templates generated using the algorithm from (Si et al. 2018), which constructs them by mutating a small number of chain rule templates. Lastly, ILASP3 requires a search space of templates induced via mode declarations that specify how many times each predicate can occur in a rule's body. We run it with 28,237 templates—the minimum number possible via mode declarations. The templates used by ProSynth and ILASP3 were grounded, whereas the metarules used by Metagol were not.

Results. The results are shown in Figure 3. GENSYNTH does not time out on any of its 8 runs and synthesizes the solution within 5 minutes on average. On the other hand, Metagol times out on 54 out of the 72 runs, despite providing it with the minimum set of templates. ProSynth is able to synthesize the solution quickly when using 64 templates, but its performance suffers with the larger choice of templates. ILASP3 solves the benchmark in 48 minutes on average.

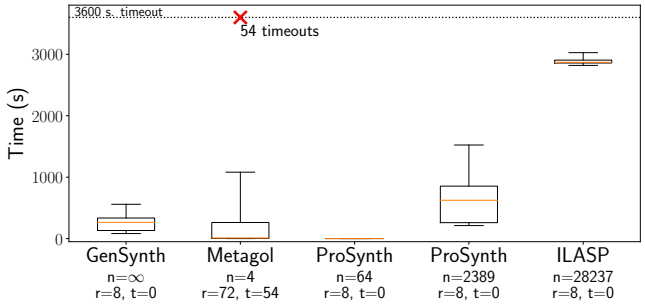


Figure 3: Results of the effectiveness experiment using n templates over r runs, of which t runs timed out in one hour. Observe that Metagol times out on 54 out of 72 runs.

Figure 3 also shows that the running time of template-based approaches is heavily influenced by the choice of templates, and effectively requires the user to tune them. For instance, the running time of Metagol varies by two orders of magnitude based on the ordering of templates, and that of ProSynth increases by three orders of magnitude in going from the smaller to the larger choice of templates.

3.2 Generality

A key benefit of language bias mechanisms is the ability to tailor them to tasks in different application domains. In this section, we investigate how GENSYNTH performs on diverse tasks in the absence of such mechanisms, compared to a state-of-the-art approach. We choose ProSynth as this baseline since it is faster than Metagol and ILASP3, as demonstrated in Section 3.1. Since all tasks in this section are noise free, we require solutions with an F1 score of 1.0. We run both GENSYNTH and ProSynth using the same Datalog interpreter, Souffle (Jordan, Scholz, and Subotić 2016).

Setup. We compare GENSYNTH and ProSynth on 42 tasks from three different domains: 17 knowledge discovery tasks frequently used in the artificial intelligence and database literature, 11 common program analysis tasks for statically reasoning about C or Java programs, and 15 relational query tasks from (Wang, Cheung, and Bodik 2017) based on Stack Overflow posts and textbook examples. Of these 42 tasks, 13 are recursive, and 12 require invented predicates.

Methodology. We overcome the differences in dependencies between ProSynth and GENSYNTH as follows. In addition to requiring templates, ProSynth requires the signatures of invented predicates, unlike GENSYNTH, which synthesizes them automatically. So we provide ProSynth with a number of advantages: we enumerate all well-typed templates up to a certain bound, we provide ProSynth with correct signatures for invented predicates, and we hand-craft settings for the template enumeration algorithm for each task so as to produce the minimum number of templates that allow to synthesize the intended solution. Finally, we simulate parallelizing ProSynth by taking the minimum of 32 runs.

Results. Figure 4 compares GENSYNTH and ProSynth in terms of (a) running time and (b) quality of synthesized programs. We observe, from Figure 4a, that GENSYNTH synthesizes programs faster than ProSynth on all 42 tasks. Most notably, GENSYNTH, which never times out, has a clear advantage once the tasks become more difficult, as ProSynth times out on 11 out of the 42 tasks.

Interpretability is a major advantage of program synthesis approaches; producing small and easily readable programs is a large part of their usefulness. We observe from Figure 4b that GENSYNTH always produces a program with fewer than 10 predicates, and always returns a smaller solution than ProSynth. Note that we define program size as total number of atoms that appear in the body of each rule in the program. This shows that ProSynth often overfits on the data given to it and produces uninterpretable programs. GENSYNTH's reduction phase is a large part of the reason why it produces such interpretable programs, and, on average, it accounts for a 43% decrease in the size of programs.

For instance, compare GENSYNTH's program for **SCC**:

```
inv(x,y) :- edge(x,y).
inv(x,y) :- inv(x,z), edge(z,y).
scc(x,y) :- inv(x,y), inv(y,x).
```

an easily interpretable solution, with that of ProSynth's:

```
scc(x,z) :- scc(x,y), inv(x,z).
inv(z,x) :- scc(x,y), inv(z,y).
inv(x,z) :- edge(x,y), inv(y,z).
scc(y,x) :- edge(x,y), inv(y,x).
scc(x,y) :- edge(x,y), scc(y,x).
inv(z,x) :- edge(x,y), edge(z,x).
scc(y,z) :- scc(x,y), inv(x,z).
```

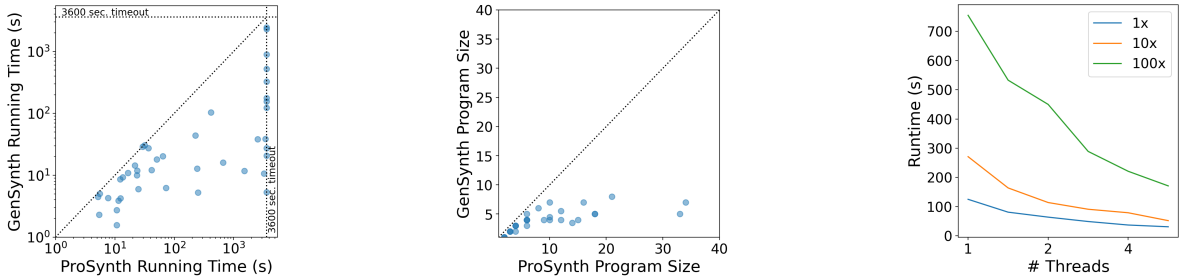
which is nearly triple in size and highly overfits the task.

Thus we see that GENSYNTH not only produces programs more efficiently, but produces higher quality programs. Despite a lack of templates, it is able to solve a diverse range of tasks. On the other hand, template-based approaches often timeout when too many templates are provided, and even when a program is synthesized, it is potentially of poor quality due to high syntactic bias.

3.3 Robustness

We investigate whether GENSYNTH is resilient to noise and how its resilience compares to existing approaches. Neural approaches naturally handle noise, so we compare it to a state-of-the-art neural approach, the Neural Theorem Prover (NTP). NTP is a differentiable learning system based on dense vector representations of symbols. We do not compare to Metagol or ProSynth as they are both unable to handle noise.

Setup. We use the **Countries** benchmark as it is the most difficult of the NTP benchmarks (Rocktäschel and Riedel 2017). It consists of 244 countries, 23 subregions, 5 regions, and 1,158 geographical facts (`locatedIn(x,y)` and `neighborOf(x,y)`). The countries are split into 198 training, 24 validation and 24 testing countries. This data was obtained from NTP's GitHub repository, and we use the same sets of present and missing data for both tools. However, since GENSYNTH is type-conscious, we further partition the `locatedIn` relation into `locatedInCR(c,r)`, `locatedInSR(s,r)`, and `locatedInCS(c,s)` where `c` is a country, `r` is a region, and `s` is a subregion. Note that we



(a) GENSYNTH v/s ProSynth running times. (b) GENSYNTH v/s ProSynth program sizes. (c) Results of the scalability experiment.

Figure 4: Results for the generality and scalability experiments.

	NTP		GENSYNTH	
	F1 Score	Time (s)	F1 Score	Time (s)
S1	1.0	245.45	1.0	14.06
S2	0.7586	328.63	0.8936	3.05
S3	0.7547	1660.48	0.8888	684.82

Table 2: Comparison of F1 scores and time taken for solving the **Countries** benchmark by NTP and GENSYNTH.

cannot use any of the 42 benchmarks introduced in Section 3.2, as they have solutions that perfectly fit the example and are therefore noise-free.

Methodology. The **Countries** benchmark contains 3 sub-problems, S1, S2, and S3, that contain increasing amounts of naturally occurring noise as a result of there being no reasonable solution that perfectly fits the data. To increase the amount of noise, increasing numbers of facts are removed from S1, S2 and S3. Hence, for each subproblem, the solvers must fill in larger and larger gaps.

In S1, all ground atoms `locatedInCR(c,r)` where `c` is a test country and `r` is the region are removed. In S2, in addition to S1, all ground atoms `locatedInCS(c,s)` where `c` is a test country and `s` is a subregion are removed. In S3, in addition to S2, all ground atoms `locatedInCR(c,r)` where `c` is a training country neighboring a test or validation country and `r` is a region are removed. In all sub-problems, the positive examples are all pairs (c, r) in `locatedInCR` such that c is a train or validation country and r is a region. The negative examples are all pairs (c, r) not in `locatedInCR` such that c is a train or validation country and r is a region.

For our comparison, we run GENSYNTH and NTP on the same machine as described in Section 3, but additionally use an Nvidia 2080 Ti GPU for NTP's scalable implementation (Minervini et al. 2018). We compare the F1 scores of the results produced by GENSYNTH and NTP on the test countries as well as the time taken for the respective tools. Both GENSYNTH and NTP were run 8 times and we consider the median of those runtimes.

Results. While the F1 score for S1 is expected to be 1.0, problems S2 and S3 only admit solutions with a lower F1 score. Table 2 shows that GENSYNTH outperforms NTP on S2 and S3 while taking less time. A closer look reveals that the difference in F1 scores, especially in S3, is mainly due to the fact that NTP is restricted by templates provided to it:

```
3 #1(X,Y):- #1(Y,X).
3 #1(X,Y):- #2(X,Z),#2(Z,Y).
3 #1(X,Y):- #2(X,Z),#3(Z,Y).
3 #1(X,Y):- #2(X,Z),#3(Z,W),#4(W,Y).
```

These templates, which specify variable bindings and even how often each will be instantiated, were crafted to perfectly match the following expected solution:

```
neighborOf(x,y) :- neighborOf(y,x).
locatedIn(x,y) :- locatedIn(x,z), locatedIn(z,y).
locatedIn(x,y) :- neighborOf(x,z), locatedIn(z,y).
locatedIn(x,y) :- neighborOf(x,z),
                  neighborOf(z,w), locatedIn(w,y).
```

However, the expected solution is not, in fact, globally optimal. Since GENSYNTH is not dependent on templates, it finds the following more optimal solution, which also scores a higher F1 score on the test dataset:

```
locatedInCR_out(x,y) :- neighborOf(z,x),
                locatedInCS(z,w), locatedInSR(w,y).
locatedInCR_out(x,y) :- locatedInCR(x,y).
```

3.4 Scalability

We next investigate how GENSYNTH's running time is affected by the size of the input-output data and the number of threads. Again, since we test on a noise-free benchmark, we require a solution with an F1 score of 1.0.

Setup. We consider the **SCC** benchmark from the set of 42 tasks described in Section 3.1. This benchmark contains one relation `Edge` with 10 tuples. We use **SCC** since it is easier to control its size while still remaining a complex benchmark requiring recursion and invented predicates.

Methodology. We create three variants of the **SCC** benchmark: 1x, 10x, and 100x, containing 10, 100 and 1,000 tuples respectively, the latter two variants representing unions of multiple disjoint graphs. We then run each of these variants using different numbers of threads, each 8 times, and take the median of these 8 runs. We require that all runs simulate the same number of populations so that the quality of result is not affected. Note then that runs with fewer threads must simulate some populations in sequence.

Results. Figure 4c shows the result of this experiment. We observe that GENSYNTH scales very well over size of input-

output data, with only about a 5x slowdown in synthesis time for an 100x increase in input-output data size. Almost all of this slowdown occurs in the Datalog interpreter, Souffle, which generally accounts for over 90% of the running time of GENSYNTH. Since GENSYNTH only interacts with the output of the interpreter, it is possible to use faster interpreters than Souffle to better handle large input-output data.

We also observe that GENSYNTH benefits from its parallelism immensely; since populations can be run independently of one another, we are able to consider many more candidate programs than non-parallelizable approaches.

3.5 Limitations

We discuss some limitations of GENSYNTH in aspects of expressiveness, termination, and efficiency. First, GENSYNTH does not support aggregation operations (e.g., sum and $count$) nor negation, although such operations could be incorporated as carefully crafted mutations with some effort. Second, as Algorithm 2 indicates, it runs until it finds a solution with an F1-Score above the desired threshold. This means that GENSYNTH is potentially non-terminating, especially in cases where a solution above the threshold does not exist. However, we have not experienced such non-termination in practice. Third, GENSYNTH incurs heavy resource consumption due to its significant use of parallelization. Moreover, since GENSYNTH interacts with a Datalog solver, a significant amount of time is spent in I/O processing.

4 Related Work

Cropper, Dumancic, and Muggleton (2020) provide a comprehensive survey of the relevant literature over the last three decades. We briefly discuss and compare representative works in ILP, ASP, program synthesis, and neural learning.

Genetic Approaches. The idea of using genetic approaches for program synthesis has been explored in previous works. For example, (Wong and Leung 1997) alters the derivation tree of the current candidate program at each step with cross-over being the primary genetic operation. (Tamaddoni-Nezhad and Muggleton 2002) starts with a seed clause and considers mutations which merge variables. This can be seen as a more sophisticated version of our minimize arguments mutation. On the other hand, both these approaches require some form of background knowledge and lack a reduction phase, which GENSYNTH uses as a regularization mechanism to prevent the synthesized program from overfitting. Finally, (Wu 2019) describes several directions for future research, such as learning of existential rules, rules with negation and aggregation, and selection of the fitness function.

ILP and ASP. ILP techniques take besides input-output examples the background knowledge in the form of a logic program. They target Prolog which is more expressive than Datalog. Older ILP systems such as FOIL and Progol work by bottom clause construction (Muggleton 1995) and struggle to synthesize recursive programs, especially from few examples. Modern ILP systems such as Metagol overcome this limitation by using meta-interpretive learning (Muggleton, Lin, and Tamaddoni-Nezhad 2015) but require the user to provide templates. Lastly, compared to GENSYNTH, Metagol supports higher-order programs, but cannot handle noise.

ASP programs are declarative akin to Datalog programs but more expressive. Modern ASP systems such as ILASP (Law, Russo, and Broda 2020) and FastLAS (Law et al. 2020) can handle noise, but still require language bias in the form of mode declarations, which also specify a *recall*—the maximum number of times that declaration can be used in each rule. Popper (Cropper and Morel 2020), a more recent system which combines ILP with ASP, requires predicate declarations for invented predicates and cannot handle noise.

Program Synthesis. These techniques are based on enumerative search, such as ALPS (Si et al. 2018), or constraint solving, such as Zaatar (Albarghouthi et al. 2017), or hybrid, such as ProSynth (Raghothaman et al. 2020). ALPS and ProSynth search for the target program as a subset of templates whereas Zaatar encodes the templates as an SMT formula whose solution yields the target program. Besides the language bias, they cannot handle noise, and cannot exploit parallelism as easily as GENSYNTH. GENSYNTH also produces smaller and more interpretable programs. On the other hand, these techniques are more efficient at learning from failures and pruning the search space than GENSYNTH.

Neural Learning. Recent works cast logic program synthesis as a neural learning problem in order to handle tasks that involve noise or require subsymbolic reasoning. These works differ from GENSYNTH in a few key aspects.

NeuralLP (Yang, Yang, and Cohen 2017), NLM (Dong et al. 2019), and ∂ILP (Evans and Grefenstette 2018) model relation joins as a form of matrix multiplication, which limits them to binary relations. NTP (Rocktäschel and Riedel 2017) constructs a neural network as a learnable proof (or derivation) for each output tuple up to a predefined depth (e.g. ≤ 2) with a few (e.g. ≤ 4) templates, where the network could be exponentially large when the depth or number of templates grows. The predefined depth and a small number of templates could significantly limit the class of learned programs. In contrast, GENSYNTH can synthesize programs with relations of arbitrary arity, and supports rich features like recursion and predicate invention. Lastly, neural approaches face challenges of generalizability and data efficiency.

Difflog (Si et al. 2019) overcomes the above hurdles but scales poorly by reasoning about all candidate programs simultaneously, which not only overwhelms the Datalog solver but also requires MCMC-based random sampling to avoid being stuck in local minima in the complex search surface.

5 Conclusion

We proposed a technique and tool, called GENSYNTH, to learn Datalog programs from input-output examples. GENSYNTH overcomes the need for the user to tune language bias mechanisms or restrict expressiveness. It employs an evolutionary search strategy that effectively navigates the unconstrained space of programs by mutating them and evaluating their fitness on the examples using an off-the-shelf Datalog interpreter. We demonstrated the ability of GENSYNTH to learn correct programs in diverse domains from few examples, including for tasks that require recursion and invented predicates, and in the presence of noise.

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References

Abiteboul, S.; Hull, R.; and Vianu, V. 1994. *Foundations of Databases: The Logical Level*. Pearson, 1st edition.

Albarghouthi, A.; Koutris, P.; Naik, M.; and Smith, C. 2017. Constraint-based synthesis of Datalog programs. In *Proceedings of the International Conference on Principles and Practice of Constraint Programming (CP)*.

Cropper, A.; Dumancic, S.; and Muggleton, S. H. 2020. Turning 30: New ideas in inductive logic programming. In *Proceedings of the International Joint Conference on Artificial Intelligence (IJCAI)*.

Cropper, A.; and Morel, R. 2020. Learning programs by learning from failures. *CoRR* abs/2005.02259.

Dong, H.; Mao, J.; Lin, T.; Wang, C.; Li, L.; and Zhou, D. 2019. Neural logic machines. In *Proceedings of the International Conference on Learning Representations (ICLR)*.

Evans, R.; and Grefenstette, E. 2018. Learning explanatory rules from noisy data. *Journal of Artificial Intelligence Research* 61.

Fogel, D. 2006. Foundations of evolutionary computation. In *Modeling and Simulation for Military Applications*, volume 6228. International Society for Optics and Photonics, SPIE.

Jordan, H.; Scholz, B.; and Subotić, P. 2016. Soufflé: On synthesis of program analyzers. In *Proceedings of the International Conference on Computer Aided Verification (CAV)*.

Law, M. 2018. *Inductive learning of answer set programs*. Ph.D. thesis, Imperial College London.

Law, M.; Russo, A.; Bertino, E.; Broda, K.; and Lobo, J. 2020. FastLAS: Scalable inductive logic programming incorporating domain-specific optimisation criteria. In *Proceedings of the 34th AAAI Conference on Artificial Intelligence (AAAI)*.

Law, M.; Russo, A.; and Broda, K. 2020. The ILASP system for inductive learning of answer set programs. *CoRR* abs/2005.00904.

Minervini, P.; Bosnjak, M.; Rocktäschel, T.; and Riedel, S. 2018. Towards neural theorem proving at scale. In *ICML Workshop on Neural Abstract Machines and Program Induction (NAMPI)*.

Muggleton, S. 1991. Inductive logic programming. *New Generation Computing* 8(4).

Muggleton, S. 1995. Inverse entailment and Progol. *New Generation Computing* 13(3).

Muggleton, S.; Lin, D.; and Tamaddoni-Nezhad, A. 2015. Meta-interpretive learning of higher-order dyadic Datalog: Predicate invention revisited. *Machine Learning* 100(1).

Raghothaman, M.; Mendelson, J.; Zhao, D.; Naik, M.; and Scholz, B. 2020. Provenance-guided synthesis of Datalog programs. In *Proceedings of the Symposium on Principles of Programming Languages (POPL)*.

Rocktäschel, T.; and Riedel, S. 2017. End-to-end differentiable proving. In *Proceedings of the Advances in Neural Information Processing Systems (NeurIPS)*.

Si, X.; Lee, W.; Zhang, R.; Albarghouthi, A.; Koutris, P.; and Naik, M. 2018. Syntax-guided synthesis of Datalog programs. In *Proceedings of the Joint Meeting on European Software Engineering Conference and Symposium on the Foundations of Software Engineering (ESEC/FSE)*.

Si, X.; Raghothaman, M.; Heo, K.; and Naik, M. 2019. Synthesizing Datalog programs using numerical relaxation. In *Proceedings of the International Joint Conference on Artificial Intelligence (IJCAI)*.

Tamaddoni-Nezhad, A.; and Muggleton, S. 2002. A genetic algorithms approach to ILP. In *Proceedings of the International Conference on Inductive Logic Programming*.

Wang, C.; Cheung, A.; and Bodik, R. 2017. Synthesizing highly expressive SQL queries from input-output examples. In *Proceedings of the Conference on Programming Language Design and Implementation (PLDI)*.

Wong, M. L.; and Leung, K. S. 1997. Evolutionary program induction directed by logic grammars. *Evolutionary Computation* 5(2).

Wu, L. 2019. Evolutionary learning of existential rules. In *Proceedings of the International Joint Conference on Artificial Intelligence (IJCAI)*.

Yang, F.; Yang, Z.; and Cohen, W. 2017. Differentiable learning of logical rules for knowledge base reasoning. In *Proceedings of the Advances in Neural Information Processing Systems (NeurIPS)*.