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Parallel Pattern Discovery

Master's Thesis Draft

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Contents

Chapter 1

Introduction

1.1 Motivation and background

Collecting new data has been increasing more rapidly than algorithms and computer processing power. The average size of each dataset has also been increasing. This suggests that the only way to keep up with analysis is to parallelize algorithms.

One of main drivers of such large datasets is analysis of genomic and proteomic sequences. Regularities in such data can give new insights into how these patterns form and how they are related to the other features of the data.

More on importance

In this thesis we explore an algorithm for finding patterns and show how abstractions can make it scalable and flexible, and simpler both in theory and implementation compared with non-abstract version.

1.2 Pattern Discovery

Pattern discovery is a research area aiming to discover unknown patterns in a given set of data structures that are frequent and interesting according to

some measure.

Since the discovery algorithms are highly dependent on the data structures, that are being searched, the algorithm must be minimal in the requirements on the dataset to be applicable as wide range as possible. This also means that the patterns found must be dependent on the initial data.

1.3 Structure of the thesis

Basic idea is to select a basis algorithm. Abstrify away concretness of implementation to support flexibility. Use the flexibility to substitute concretness with parallel implementations.

Fix when structured

First we introduce definitions of our data and patterns in Chapter 2. In Chapter 3 we describe the pattern discovery algorithms. In Chapter 4 we generalize the SPEXS algorithm to get a flexible algorithm. In Chapter 5 we swap out the abstract parts with parallel implementations. The actual implementation of SPEXS is described in Chapter 6. In Chapter 7 we show how the algorithm can be used and analyse the speed behavior.

Chapter 2

Definitions

Pattern discovery is a problem of finding interesting patterns in some dataset. We discuss the algorithm in terms of DFAs and show how this can help to discover patterns in sequences.

2.1 Sequence

We use Σ to denote the set of tokens in the dataset, an *alphabet*. The *size* of the alphabet is $|\Sigma|$. *Tokens* can be numbers, letters, words or sentences - any symbol.

Any *sequence* $S = a_1 a_2 ... a_n, \forall i \in \Sigma$ is called a *sequence* over the token set Σ. If the length of the string is 0, it is called an empty sequence or ϵ.

2.2 Pattern

A *pattern* is a structure that defines a set of structures Γ. We denote the set that a pattern defines as $x(\Gamma)$. If a structure α *matches* a pattern Γ, it means that $\alpha \in x(\Gamma)$.

better definition

The most common form of such structures are regular expressions.

2.3 Dataset

A *dataset* is a set of NFAs. In practice it may be more comfortable to view it as a set of sequence because of it's simpler structure.

example

2.4 Query

A *query* is a compound structure that has information about a pattern and it's matches in a dataset. The information about a match is the ending states where a pattern matches a DFA.

On sequences this means the ending positions of the pattern in the sequence.

example

2.5 Query features

Query feature is a function of the query. It gives information about the query such as the pattern representation, length, number of matches in the dataset.

example

Query interestingness is a function of the query whose results are well-ordered. This functions result allows to say whether one query is more interesting than the other. For convenience it is useful to represent that value in $\Re$.

example

Query filter is a function of the query whose result is a boolean.

example

2.6 Pattern discovery problem

Pattern discovery problem is a process of finding most interesting queryies according to some interestingness measure, and use the pattern they reflect.

Chapter 3

Algorithms

There are many itemset discovery algorithms, but only few are general and can discover more complex patterns.

3.1 SPEXS

SPEXS is an pattern discovery algorithm described by Vilo et al. This algorithm finds patterns from a sequence. We take this as our basis for developing a new parallel algorithm. In this chapter we describe original algorithm so that we can later show the changes made to this algorithm.

We describe the general representation of the SPEXS algorithm. The original algorithm was as follows:

Algorithm 1 The SPEXS algorithm

Input: String S, pattern class $\mathcal{P}$, output criteria, search order, and fitness measure $\mathcal{F}$

Output: Patterns $\pi \in \mathcal{P}$ fulfilling all criteria, and output in the order of fitness $\mathcal{F}$

```
1: Convert input into sequences into a single sequence
2: Initiate data structures
3: Root ← newnode
4: Root.label ← ϵ
5: Root.pos ← (1, 2, ..., n)
6: enqueue(Q, Root, order)
7: while N ← dequeue(Q) do
8:     Create all possible extensions P ∈ P of N using N.pos and S
9:     for extension P of N do
10:        if pattern P and position list P.pos fulfill the criteria then
11:            N.child ← P
12:            calculate F(P, S)
13:            enqueue(Q, P, order)
14:            if P fulfills the output criteria then
15:                store P into ouput queue O
16: Report the list of top-ranking patterns from output queue O
```

The main idea of the algorithm is that first we generate a pattern and a query that match all possible positions in the sequence. We then put this query into a queue for extending.

Extending a query means finding all queries whose patterns length is longer by 1. If any of the queries is fit by some criteria it will be put into the main queue, for further extension, and output queue for possible result.

3.2 TEIRESIAS

write about it

Chapter 4

Abstractification

In this chapter we show how to make the algorithm more abstract by allowing flexibilty through functions as parameters and finding minimal requirements for the data-structures.

4.1 Algorithm

The algorithm in a more convetional view is:

Algorithm 2 The SPEXS2 algorithm

Input: *dataset*, *in* pool, *out* pool, *extender*, *extendable* filter, *outputtable* filter, *postprocess* function
Output: Patterns satisfying filters and *extender* are in *out* pool

```
1: ε ← NewEmptyQuery(dataset)
2: in.put(ε)
3: while q ← in.take() do
4:     extended ← extender(q, dataset)
5:     for qx ∈ extended do
6:         if extendable(qx) then
7:             in.put(qx)
8:         if outputtable(qx) then
9:             out.put(qx)
10:    postprocess(q)
```

When the algorithm starts we create an empty pattern query and put into the in pool. The in pool contains queries whose patterns should be further examined.

We pick a query from the in pool for extending. The extending means generating all queries whose pattern is larger by one. There can be several such queries.

If any of the queries should be further examined as defined by the extendable filter, it will be put into the in pool.

If the query is fit for output we as defined by the outputtable filter, it will be put into the out pool.

If we extend each pattern at each step by one we guarantee that we examine the all patterns that conform to our criteria.

4.2 Pools

Pool is an abstract datatype for a collection of queries. The pool allows queries to be put into it and taken from it, also we can ask whether the pool is empty or not.

It has no guarantees on how the queries are stored internally and in which order they are taken out.

In practice this means we can use any collection such as list, set, queue as a pool. This gives us different performance characteristics.

This also means that pools can persist the queries if necesssary.

4.3 Filtering

Filtering allows us to dramatically reduce the number of queries we have to look at. It also allows to select only interesting patterns by some criteria.

If we have interestingness measure we can create filter from it by defining

it's minimum or maximum value. One very usefule example would be a filter for limiting the pattern length.

By separating the extension and output filter, as opposed to SPEXS, we can still limit output without affecting the extension process. For example if we wish to see only patterns of length 3 we cannot do it with one filter. Since we need to extend patterns of length 0, 1 and 2.

4.4 Extending

The extending process is at the core of the algorithm. We shall look at how we can deal with different types.

The extending method is:

Algorithm 3 SPEXS2 extender

Input: q query, *next* function
Output: result contains queries that have been extended by one

```
1:  nexts ← new collection
2:  for pos ∈ matches(q) do
3:      (token, pos) ← next(pos)
4:      nexts.put((token, pos))
5:  matches ← new map of token to position set
6:  for (token, pos) ∈ nexts do
7:      if matches[token] doesn't exist then
8:          matches[token] ← {}
9:      matches[token] ← matches[token] + {pos}
10: result ← new collection
11: for (token, positions) ∈ matches do
12:     qx ← new query
13:     qx.pattern ← q.pattern + token
14:     qx.positions ← positions
15:     result.add(qx)
```

This extender depends on how next is implemented, we shall look at different ways how to implement it.

4.4.1 Sequences

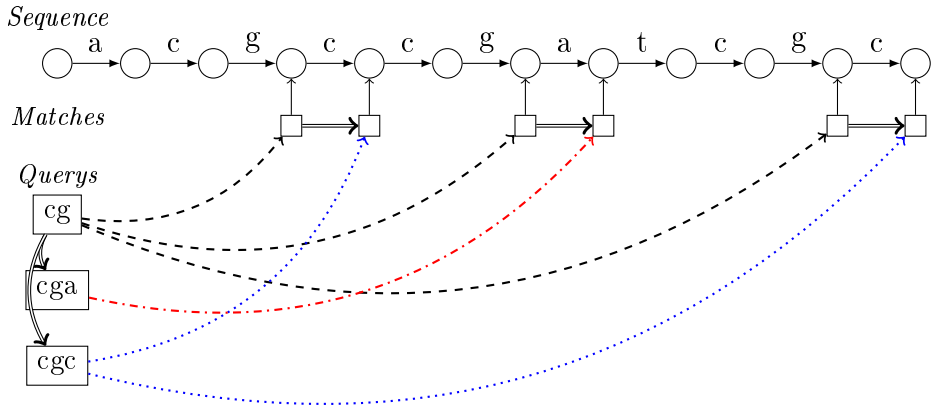
The simplest case how the next function behaves is when we are only looking for simple sequences.

Let's consider a sequence ACGCCGATCGC and a pattern CG.

Diagram of the ACG.CCG.ATCG.C and query for that pattern.

Next positions step is finding ACG.[C]CG.[A]TCG.[C].

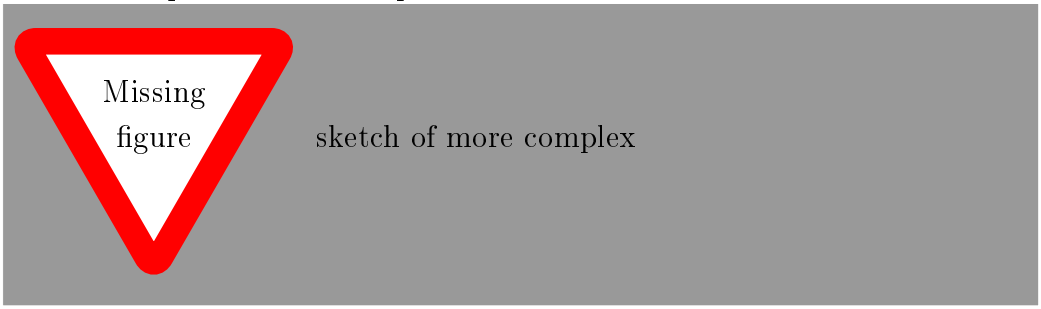
Grouping is [C] ==> CGC, [A] => CGA.



4.4.2 Groups and Stars

Since we want to find more interesting patterns we can add more information to the sequence DFA. Such as a star expression.

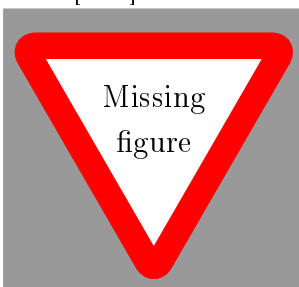
Same sequence with star paths.



4.4.3 Optimizations

Although we can add the group information to the DFA, it is more performant to use the information gathered from the extension of non-groups.

A[CG].Positions = AC.Positions union AG.Positions



sketch of possible optimizations

4.4.4 Other

There maybe several other extensions to the regular expressions.

Questionable position:

AC?.Positions = A.Positions + AC.Positions

sketch of questions

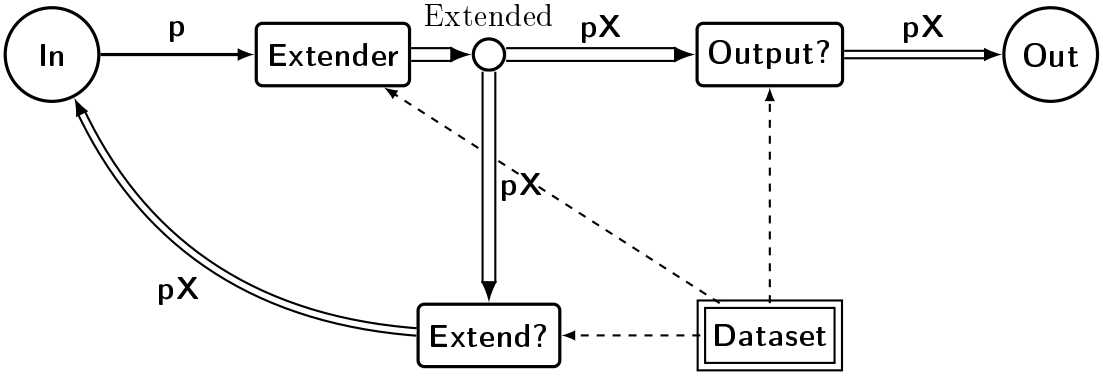
Chapter 5

Parallelization

Here we describe parallel implementations of the parts of the algorithm. A proof of concept for fully parallelized code can be seen in appendix A.

5.1 Process

The main process of the algorithm as described by dataflow.[?, ?]



The easiest thing here to parallelize is the extender since it's interaction can be seen as a separate unit.

5.2 Adding Nodes

If instead of in/out pool we had several the algorithm can still work, if we have single take / put process to decide which actual pool to use.

We can use several extenders that work in parallel without problems since they do not need information about other queries nor input/output pools.

5.3 Extending

We still can also do the extending process in parallel:

Algorithm 4 Parallel Extender

Input: Query q, function $next : \mathcal{I} \to [(\mathcal{I}, \mathcal{P})]$
Output: Set of querys that have been extended by one step

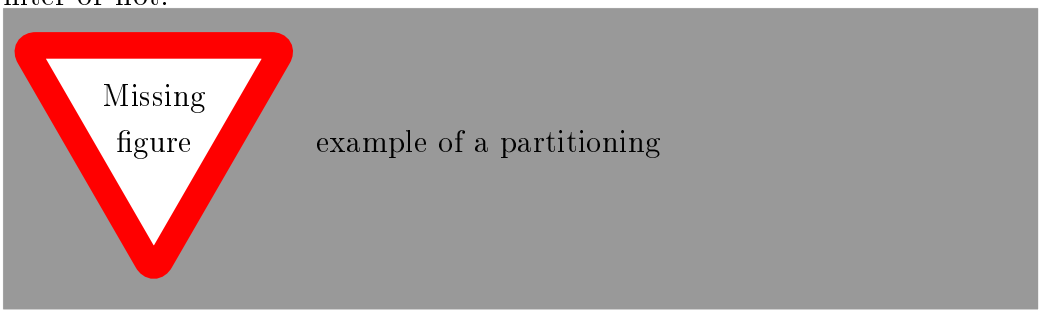
1: $nexts \leftarrow map(next, q.pos)$
2: $matches \leftarrow groupBy(snd, nexts)$
3: $result \leftarrow map(mkQuery(q), matches)$
4: $optimized \leftarrow map((x) \to (union(matches(x))), groups)$
5: $returnunion(result, optimized)$

```
func extender(query) {
// find all next positions
nexts = (map next query.matches)
matches = (group nexts by token)
result = (map newquery matches)
other = (map #(union (matches %1)) groups)
return result union other
}
```

5.4 Dataset partitioning

If we look at where we need synchronization points if we partition the dataset. Whole parts of extension still apply for parts of dataset.

Synchronization is only needed for filtering. We don't need to know the whole query but just information about parts to make a decision whether to filter or not.



example of a partitioning

5.5 Filtering

This is the only place where we may need the whole information about the query.

Although many operations can be parallelized with map reduce.

example how to do counting

example what cannot be done easily on sharded data

Chapter 6

Implementation

Here we discuss a practical implementation, *spexs2*, for pattern discovery in sequences.

The actual implementation may need to diverge from the abstract definition for several reasons; mainly practicality, simplicity and performance. Many of the operations can be optimized for some particular type of datasets and configuration.

In this chapter we will discuss parts of program that the author considers non-trivial in it's design decisions. Information about the full source code is in the Appendix B and C.

6.1 Architecture

The main criteria for designing program have been described in D. Parnas paper On the Decomposition of Programs. It suggests decomposing into isolated units and parts that are likely to change together. [**?**]

We chose the following decomposition:

Configuration structure for holding the configuration data

Setup based on the configuration initializes data-structures and functions for the algorithm

Reader reads in the data from files

Database a collection of datasets

Algorithm the SPEXS2 algorithm

Pattern represents a pattern

Query stores the pattern with database and pattern

Set stores matching positions

Pool stores queries

Extender drives algorithms extending step

Feature computes a value from the Query

Filter filters some queries

Printer prints the result queries

Debugging utilities for the program

It is a trivial decomposition for the algorithm part, since a lot of is derived directly from the algorithm definition.

The main criteria was to decompose things based on their behavior, whether there is a commonality between them or whether they change independently from the other parts.

6.2 Configuration

One problem with flexible algorithms is that they a lot of ways to be run. This often would need having tens or hundereds of program flags. To avoid this problem we decided to use a json file for the program configuration.
Short example of a configuration file.

To properly represent configuration in a static language we marshal this file directly to the data-structure. This means we can be less worried about parsing when setting up our algorithm.

The problem with only using a json file is that when running from command line it may be more comfortable using flags. To solve this problem we added replacement strings into the json files that can be given in as a program argument.

```
"Datasets" : {
"fore" : { "File" : "$inp$"
...
```

When using spexs2 –conf conf.json input=filename the input will be replaced by filename. Also there is optional default value if one wasn't given.

6.3 Setup and Database

Setup consumes the configuration and based on the values initializes pools; creates and combines features and filters; reads in the data; and creates the printer.

Database

6.4 Reader and Printer

One problem with data is that it comes in many different forms. For example reading in words and single letters requires different behaviors.

One thing that may be helpful is supporting different binary formats.

6.5 Sets

Since we need a collection how to store the matching positions it suggests the need for a set datatype.

If we have predictable distribution we can pack the sets better.

Although such optimizations can be avoided, if during storing pools the sets are packed using some compression algorithm.

6.6 Pools

There can be different performance characteristics when using a particular implementation. Most importantly to support parallelism they should be ideally lock-free, but we can use locked version as well.

For the pools we have several choices: lifo, fifo or priority.

If we use a fifo queue as the in pool the algorithm does a breadth first search of patterns. This can be problematic since we would need a lot of memory to hold all the patterns in memory.

A lifo queue for in pool is a more reasonable choice for memory problems since we need to hold less patterns in memory.

A priority queue suits for the out pool since we can easily then use some feature to sort the queue and choose only a limited amount. A lock-free priority queue would be preferred but it has many details to work correctly.

link to lock-free queues

One simple solution to make priority queue concurrent is to use mutexes when storing or retrieving values. This would mean that many processes can get locked.

We can use some knowledge about the priority-queue behavior. We know that it usually has limited-size and the amount of patterns suitable for putting into the output queue is several magnitudes larger; this means most of the queries put into the result queue are discarded.

We know that if the query is worse than the worst in the priority queue, it can be discarded immediately without doing push/pop. If we allow for that check to fail once in a while - we can make it mostly lock-free.

```
worst := current-worst
if worst > new-query {
```

```
exit
}

mutex.lock
pqueue.push(new-query)
current-worst = pqueue.pop()
mutex.unlock
```

Although the worst may already have changed after line 1, the algorithm still only keeps the best results.

6.7 Features and Filters

One problem is that the amount of possible filters it's useful to construct them from some other features. Or if we wish to use multiple filters we can combine them.

We can use these features to find out something about the query. They each feature is defined as:

```
type Feature func(q *Query) (float64, string)
```

Most of features are in $\Re$, but for some there is some extended information that we may wish to know - hence the need for additional string value. One of the simplest is Pattern representation.

Also many of the features are defined in terms of multiple datasets. We can use a closure to easily define a more generic feature.

Example:

```
func Matches(dataset []int) Feature {
return func(q *Query) (float64, string) {
matches := countf(q.Pos, dataset)
return matches, ""
}
}
```

Here the Matches function creates a feature function defined for dataset.

We can use the name in the configuration file as "Matches(fore)".

If a feature returns a floating point value we can easily turn that into a filter by specifying a minimum or/and maximum value.

For example to give a lower and higher limits to some feature:

```
func featureFilter(feature Feature, min float64, max float64) Filter {
return func(q *Query) bool {
v, _ := feature(q)
return (min <= v) && (v <= max)
}
}
```

Of course there are some filters that cannot be defined by features hence there is still possibility to make separate filters. Such as disallowing star symbol in the beginning of the pattern.

6.8 Debugging

Debugging is a important part of development process hence the need for more information how the algorithm is working.

Often this is resolved by adding some debug statments:

```
for i := 0; i < 100; i += 1{
printf("picking")
a := pick()
printf("picked %v", a)

printf("picking")
b := pick()
printf("picked %v", b)

out.put(a + b)
}
```

This can be harmful to the readability of the code. To fix this debugging problem we use closures.

```
type PickFunc func()Thing
func debuggable(fn PickFunc) PickFunc {
return func() Thing {
printf("start picking")
p := fn()
printf("picked %v" p)
return p
}
}

pick = debuggable(pick)
for i := 0; i < 100; i += 1{
a := pick()
b := pick()
out.put(a + b)
}
```

As we can see the algorithm implementation is much more readable and we can inject different debugging statements without actually changing the algorithm.

Also we can now change the ways how to add debug info. One of would be a full stepwise debugger.

```
func debuggable(fn PickFunc) PickFunc {
return func() Thing {
mutex.lock()
p := fn()
while not continue
interact with user
mutex.unlock()
return p
```

```
}
}
```

Chapter 7

Applications and experimental results

Here we show examples for the program:

7.1 DNA sequences

make an example

7.2 Protein sequences

make an example

7.3 Text mining

make an example

7.4 Code mining

make an example

Chapter 8

Conclusions

results 1
results 2
context, compare
strength + limitations
so what? why is it important
what is next?
strong conclusions
take home message

In this thesis we showed how by making an algorithm more abstract and general we can also make it parallel. We showed that this algorithm can find patterns from sequences and also NFAs.

Although we showed that we can apply this algorithm on NFAs we did not analyze the performance characteristics. This suggests that this algorithm may be able to work on trees and graph, but would require slight modifications.

We also demonstrated how to make the algorithm more concrete and work well on some particular datasets. This also took into consideration further development and flexibility of the algorithm.

The SPEXS2 implementation currently is already used in biosequenceing

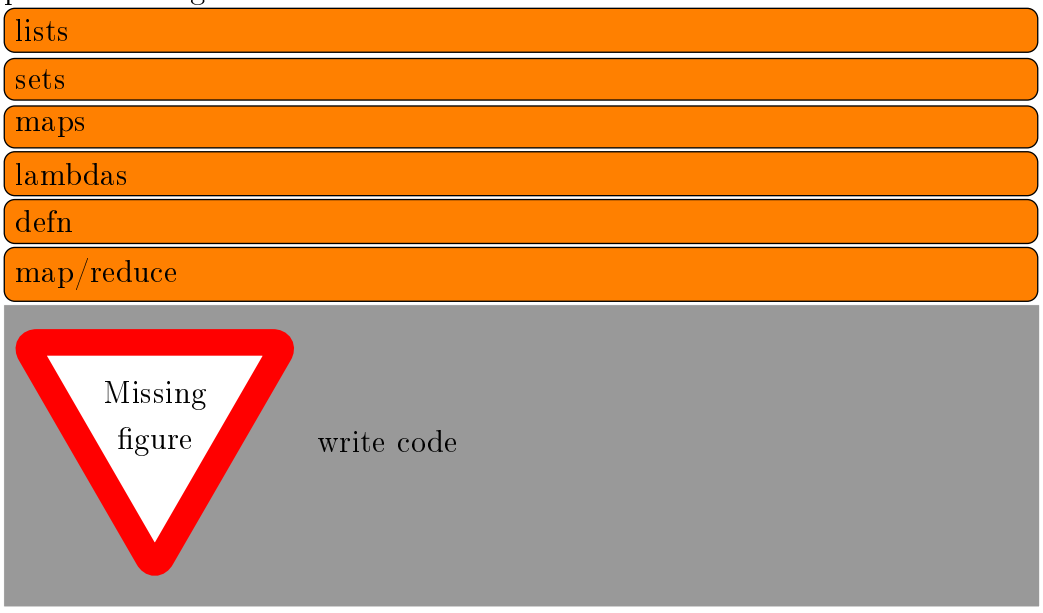
and text mining.

Appendix A

Exhaustive Parallel Pattern Search

This part assumes knowledge of *lisp* like languages. The code here is presented in Clojure and for an introduction see `clojure.org/getting_started`.

First we show reader macros that are different from other lisps. Then we present the algorithm with comments.



Appendix B

SPEXS2 Command Line Utility

Write

B.1 Configuration

Write

B.2 Running

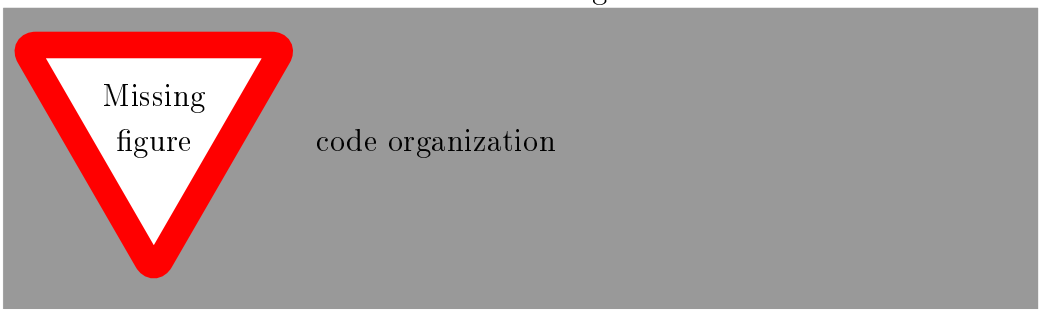
Write

Appendix C

SPEXS2 Source Code

The source code for the implementation of *SPEXS2* is available at `github.com/egonelbre/spexs`.

The source folder "src" has the following structure:



code organization