DTU Compute
Department of Applied Mathematics and Computer Science

02122 Software Technology Project

Detecting Structural Breaks in Time Series via Genetic Algorithms

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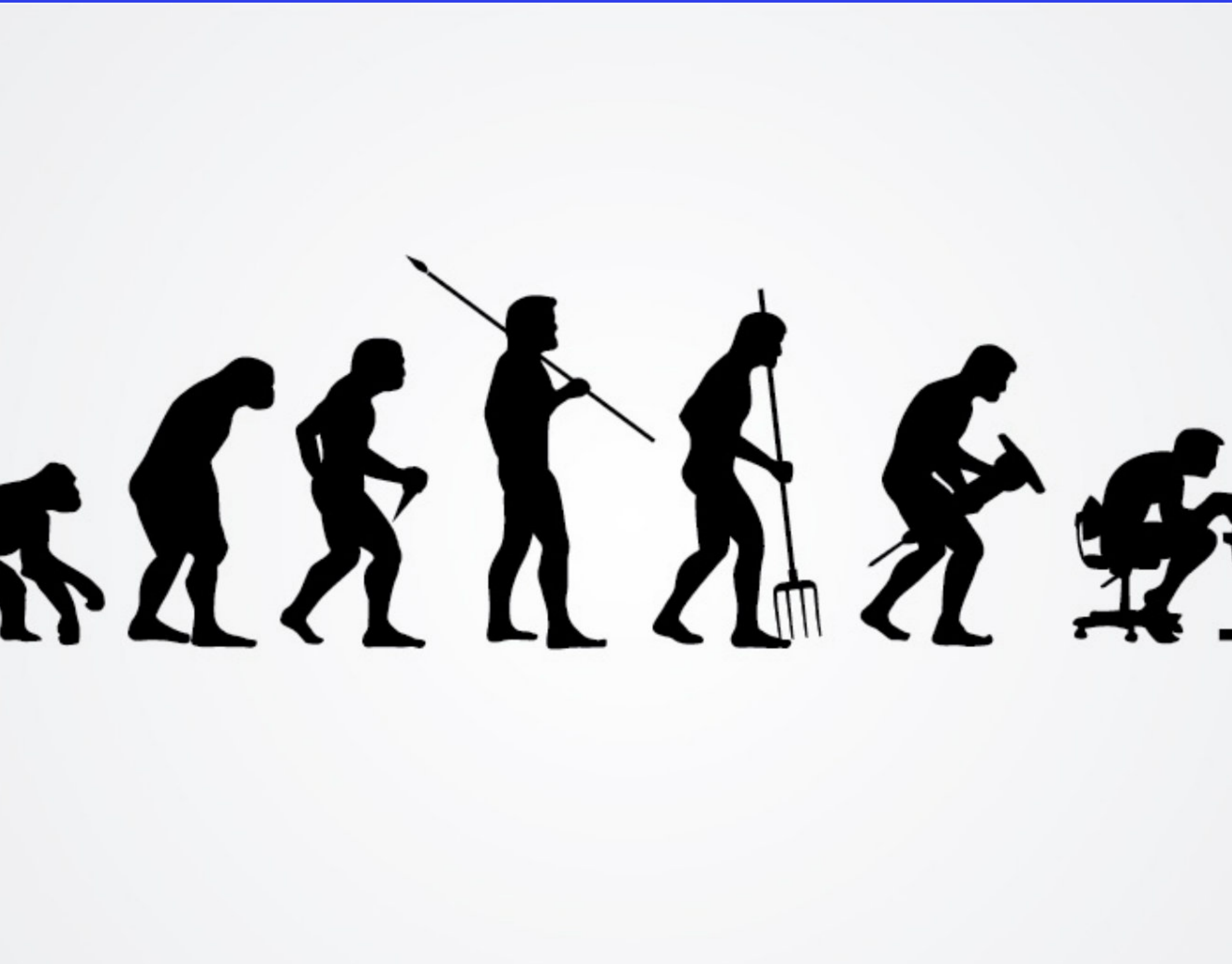

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1 Introduction

Detecting structural break points is an essential tool in analyzing time series. Structural break points are points on a time series where the pattern of the time series measurements changes in the amplitude. A simple example is shown in figure 1a where the break point is easily detected at $t = 500$. Structural breaks are where the pattern of a time series changes.

In the example above, the break point is easy to detect. As usual, the real world is far more messy. In figure 1b, which shows the number of patients hospitalized in Denmark due to Covid19, the break points are less obvious. This is where detecting break points is important: Being able to recognize when the pattern changes, so that a pandemic does not run amok or looking for fluctuations in the stock market.

Please find another example than the stock market

In this project, the break points are found by using a so-called genetic algorithm. This algorithm mimics natural evolution: A number of individuals (solutions that indicate the positions of break points) mutate and mate during generations where survival of the fittest is the rule. In the end, the best solution will (hopefully) have found all the break points.

This project will focus on implementing the algorithm in the programming language Java and make a simple application. The application will give the user the ability to tweak some of the algorithm's parameters and see the break points directly on the time series graph. Further improvements to the speed of the algorithm will also be implemented "under the hood".

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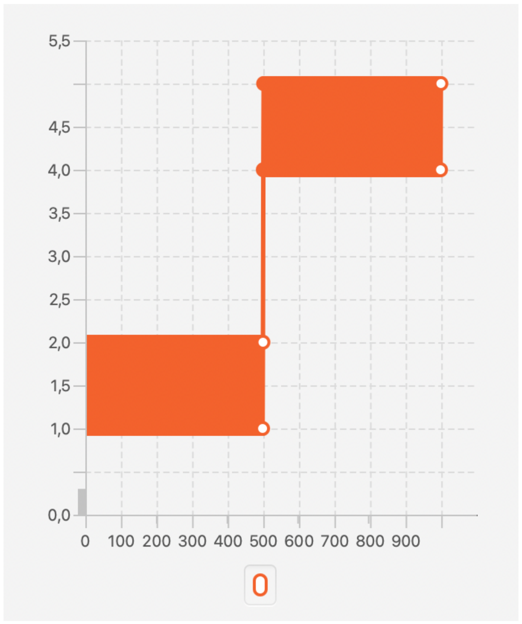
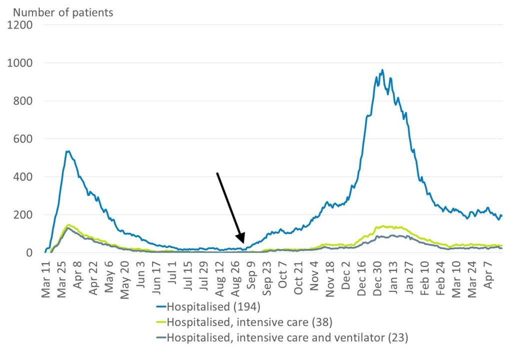


(a) Graph with break point at $t = 500$



(b) Number of people hospitalized due to Covid19 in Denmark. The arrow indicates a break point. Source: the Danish regions

Figure 1: Two figures illustrating break points in time series

2 Goals

A prioritized list of the functional goals for the project is listed below. While adding a lot of features seems very appealing, I will in this project focus on usability, stability, and speed. This leads to a somewhat conservative list of potential features, but the quality of the final product will reflect this decision.

1. Implement the algorithm using the rectangle-method from [Doerr et al., 2017] in Java.
2. Visualize two-dimensional time series graphs together with the rectangles produced by the algorithm in a simple graphical user interface (GUI). This GUI will allow user to load a time series data file and see the output of the algorithm on the time series. The user will also be able to tweak certain parameters of the algorithm.
3. Make the algorithm more flexible by allowing the user to alter the values of algorithm-parameters in the GUI.

A previous goal was also to implement further fitness functions (see explanation for *fitness functions* in section 3). Since this project ended up being a one-man-project, this goal was removed. In stead, a priority is to design the project so that it is easy to implement other fitness methods. This will be discussed further in section 4.

2.1 Non-project goals

As for non-project goals, there are a few:

- Learn the Maven project structure for Java. While previous courses have dealt with Maven a little bit, it has never been fleshed out. It seems to be a structure that is widely used and thus a good system to learn.
- Working on big project. This is the first big project I am working on. A big focus here is on the project management, report writing workflow and keeping track of sources in a bibliography. Especially the report writing workflow can become crucial, as I have a tendency to postpone it to the very last minute. Here, I will make it a part of my weekly work.

My ambition level is quite high; I am a perfectionist to the core. While I will attempt to keep the perfectionism to a minimum, I like working on bigger projects and making it work well. This will probably result in me working a lot on this project, purely because it will be fun, and I like improving my less-than-optimal solutions. I am aware that this course is only 5 ECTS points and will thus keep track of my hours spent on the project as to not overdo it.

3 Terminology

The terminology used in this report is specified below. The terminology differs a bit from [Doerr et al., 2017]. It takes inspiration from other sources ([Thede, 2004, Point,]) and follows a more biological narrative.

Individual An individual consists of a solution string. It is one possible solution to the problem.

Genome An individual consists of a genome. A genome is an array of genes. The genome *is* the solution string.

Allele A gene's value is called an allele. In this project, the allele is thus responsible for holding the information of whether or not a certain gene is a break point. An allele is the value at a certain gene in the genome/solution string.

Population A group of individuals.

Fitness function A function that measures how well the solution from an individual fits with the data. This can be any function relevant for a particular problem.

Parent and offspring individual Since genetic algorithms mimic evolution, procedures must include parent and offspring individuals. A parent individual is a parent to the offspring individual, meaning that any procedure must take one (or two) parent individual(s) and the procedure creates an offspring.

Crossover (Procedure) Crossover-procedures takes two parent individuals and creates an offspring from the genomes of the two parents. This project will incorporate *one-point crossover* and *uniform crossover*.

One-point crossover extracts the genes in the interval 0 to a random gene $i - 1$ from the first parent. Then, it appends the genome with the genes i to the last gene $n - 1$ from the second parent. Thus, the offspring's genome consists of the first i genes from parent one and $n - i$ last genes from parent two.

Uniform crossover is more simple. For each gene in the offspring's genome, there is a fifty-fifty chance whether it will be the gene from parent one or the gene from parent two.

Mutation (Procedure) Just like the corona virus, the genome of an individual can mutate. It means, that for any gene, there is a random chance that the allele will change. In this case, the change will be either creating break points or removing them.

4 Problem analysis and design

The main challenges are already hinted at in section 2. All these goals pose different problems. These problems (and especially their solutions) is best analyzed when also discussing the chosen design.

4.1 Genetic Algorithm Design Paradigm: General vs. Specific

A genetic algorithm is a very general tool. In the most simple of cases, the individuals manipulated are simple solution strings containing 1s and 0s - or other simple characters. The individual is thus a simple entity, and the value of it only becomes meaningful in the context of a given problem.

In the context of finding structural break points with the rectangle fitness method, the genome of the individuals contains two types of alleles: `0` meaning no break point and `1` meaning a break point. Thus, the genome has T genes, where each gene can contain one of two types of alleles.

The *general paradigm* is alluring due to its simplicity. This is especially the case within the biological narrative of the genetic algorithm: A genome of fixed length and a small set of alleles matches the narrative. But for this problem, where the number of breakpoints is potentially miniscule compared to the length of the time series, there is a more efficient approach. The specific approach.

4.1.1 Specific Paradigm: The Optimized Approach

The *specific paradigm* is made specifically for the problem at hand. For detecting structural break points, the biggest modification is this: The genomes no longer contain genes with non-break-point-alleles. The genome is in stead a list-structure G. At each gene g is an allele a_g, $G(g) = a_g = (b_g, B_g)$. The value b_g is itself an index representing the index of the break point, $b_g \in [0, T]$. The term B_g is a more abstract value containing information relevant for the fitness model.

4.2 Modified Genetic Algorithm Procedures

Going from a general approach to a specific approach changes how the genome-altering procedures work. In the following, each individual will be represented by only its genome. This might not be the case for the actual implementation, but it will now serve as a mean to simplification. The sentence "An individual I" will actually mean "An individual with genome I".

4.2.1 One Point Crossover

The most simple to adapt is the `one point crossover procedure`: A random index $i \in [1, T-1]$ is chosen as the splitting point. From the first parent P, the offspring O gets all genes p with alleles $a_p = (b_p, B_p)$ where $b_p < i$. From the second parent Q, O gets all genes q with alleles $a_q = (b_q.B_q)$ where $b_q \geq i$.

4.2.2 Mutation

The mutation procedure is also simple, or at least *made* simple. A single index i is randomly selected in the interval $[1, T-1]$. With a probability p_m a break point is placed at i. Else, with a probability $1 - p_m$, the point will become at non-break-point. This means that if a break point already exists with index i, the break point is removed. If no break point exists at i, then no action is performed.

For the mutation procedure it might be possible that there exists multiple break points at one index. This is allowed and in stead affects the fitness score. If a break point is removed at index with multiple break points, only one of the break points is removed.

Explain the fitness thing somewhere else and link to that from here

4.2.3 Uniform crossover

The final procedure, uniform crossover, is a bit more complex in the new context. The uniform crossover takes two parents P and Q. In a single for loop, the two genomes are both traversed by maintaining two iteration parameters. i traversing P and j traversing Q. The two parameters are initialized to $i = j = 1$. The break point indexes at the genes p_i and q_j are compared: The allele storing the lowest break point index is added to the offspring with a fifty-fifty chance. The iteration parameter for that genome is incremented. If the two break point indexes are the same, a coin toss decides which allele is added to the offspring. Both counters are incremented afterward. This is repeated until both genomes are traversed.

Figure 2 shows an example. The two parents P and Q have three and two break points in the interval respectively. The diagram contains four scenarios:

1. For $i = j = 1$, the break point index $p_1 < q_1$. Thus, the allele storing p_1 is added to the offspring with a fifty-fifty chance. Now i is incremented so $i = 2$
2. $q_1 < p_2$. Allele storing q_1 is selected and j is incremented $j = 2$.
3. $p_2 < q_2$: Allele storing p_2 is selected and i is incremented to $i = 3$.
4. $p_3 = q_2$: A random allele of the two is selected and both i and j are incremented to $i = 4$ and $j = 3$.

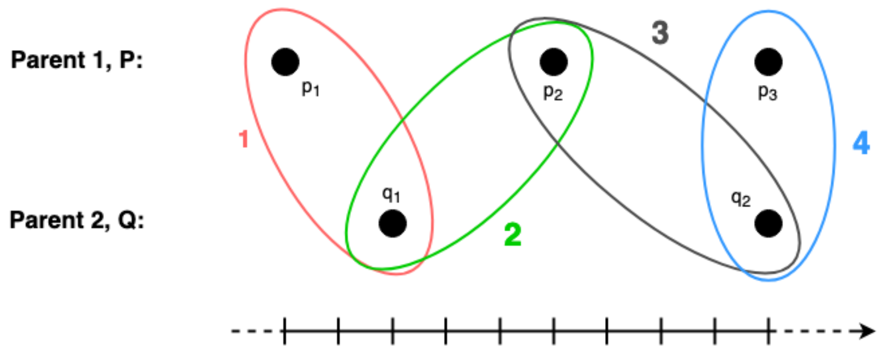


Figure 2: A diagram showing multiple cases when calculating uniform crossover.

4.3 Model-View-Controller

4.3.1 Observer pattern

The observer pattern is not implemented here as the application is very small. A more simple approach is simply to allow the controller and the business logic to exchange information. The business logic can, in this application, never change if no changes are performed in the GUI. This makes observer pattern rather useless.

The absence of the observer pattern will result in the controller having direct access to the business logic. This is not inherently bad and will make the controller easier to follow. It will possibly result in a bit more cluttered controller class. But hopefully the simplicity will outweigh potential negatives.

5 Implementation

6 Test

6.1 Running time

For testing running times, a simple class `runTimeTimer` was made. It has two methods `start()` and `stop()`. `start()` must be called before the code chunk to be examined. `stop()` must be called just after. The running time will appear in milliseconds in the console.

7 Project Management

8 Conclusion

References

[Doerr et al., 2017] Doerr, B., Fischer, P., Hilbert, A., and Witt, C. (2017). Detecting structural breaks in time series via genetic algorithms. *Soft Computing*, 21(16):4707–4720.

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[Thede, 2004] Thede, S. (2004). An introduction to genetic algorithms. *Journal of Computing Sciences in Colleges*, 20.