Speeding Up the Simulation Animals Diseases Spread: A Study Case on R and Python Performance in PDSA-RS Platform

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Abstract: The control and prevention of livestock diseases play a crucial role in safeguarding business continuity, simulating disease prevention and control measures are vital to mitigate future epidemics. In this sense, modelling systems can be an effective tool that allows the simulation of different ways of spreading diseases by configuring parameters allowing testing of different prevention measures. This work investigates enhancing a system that simulates disease spread processes in animals. The stochastic model system was developed in R; however, given a large amount of data and intense processing of stochastic functions that simulate spreading and control actions, it required optimization. We focused on translating and modifying it to Python using packages focused on data analysis, aiming to speed up the system execution time. We conducted experiments comparing high computational cost functions executed in the actual model R with the new proposal implemented in Python. The results showed that rewriting the code in Python has advantages such as performance in time execution, which in Python is more than four times faster than R, memory usage consumption in R uses 460 MB and 315 MB in Python.

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1 INTRODUCTION

With the advancement of technology in the current times, the use of data for decision making has become increasingly important. This data is generated through various digital channels, such as mobile devices, the Internet, social media, e-commerce sites, among others. Using the data has proven to be of great use since its inception, as companies began to realise its importance for various business purposes. With this amount of data it is possible now, with the increase of processing power to develop intelligent systems that can help to make decisions, create simulation about critical situations. In this sense, several applications are using real data to create intelligent systems in different areas with different

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applications, such as healthcare, transportation, and sustainable ecosystems that can help to avoid economical loss in any kind of business (Omolbanin et al.,2017).

An example of intelligent systems is the control and prevention of animal diseases. It is important for public health, and may include measures such as vaccination of animals, vector control, good hygiene and food handling practices, as well as monitoring of diseases in animals. In addition, globalization and international trade in animals and animals' products have increased the spread of zoonotic disease worldwide. It is essential that effective prevention and control measures are implemented to minimize the risk of epidemics. The dynamics of farms pose some risks for the spread of diseases, such as isolation

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of animal lots, human traffic, truck traffic, the useful area of the farm or farm can influence possible transmission of diseases (Jason et al., 2022). In this area, one intelligent system using real data was proposed by Descovi et al, 2022, which uses data from farms to simulate the spread of diseases in animals (e.g. cattle, swine, and small ruminants). The system also allows researchers to test different actions to control these diseases. As for livestock, it is possible to control and isolate animals with disease, so all animal transport is controlled. With this, it is possible to develop a system that can simulate the impact of a disease that spreads when an infected animal is transported and create scenarios about the life cycle of the disease and the impact on the farm or production of the region (Jason et al., 2022).

This system was developed in R Language, using real data collected from farms in Rio Grande do Sul state (Brazil) and used in PDSA-RS platform (Descovi et al, 2021, Perlin et al., 2023). It is noteworthy that the R language was developed specifically for statistical analysis and data visualization, but, when it comes to data handling performance, it is important to consider factors including: dataset size, data format, hardware processing power, and the efficiency of the libraries used to read and manipulate data (Ioannis,2020). As the volume of input data increases, the existing system developed in R faces performance challenges. To address this, we decided to reimplement some computationally intensive functions into Python. This shift enables us to conduct a comparative analysis of performance and processing speed between the two implementations (R and Python). By migrating to Python, we aim to enhance the system's efficiency and efficacy, ensuring it can handle the everexpanding data landscape more effectively and deliver optimal results. This transition allows us to explore the potential benefits of Python performance capabilities and adapt our system accordingly.

The methodology for developing the performance improvement initiated by testing Python and R functions used in the implementation of the system. Firstly, we investigated different libraries to speed up reading the dataset. After this, we analyzed the different ways to update the dataset cells values, as many functions include situations that are necessary to change these values based on specific conditions. In the second phase of the study, we will improve the performance rewriting the code in Python programming language, all the functions of the model, all the functions work with update in values in the data frame, change the information when the day moves across the disease spread process, this needs for update in values in the data frame has better performance in Python.

The present paper is structured as follows. The next section presents the related work on intelligent systems applied to disease spread problems, showing R and Python performance comparison studies. Section 3 describes the disease spread and control system, highlighting the functions targeted in this work. Section 4 describes our evaluation and results comparing the execution time of the original functions implemented in R and their version in Python. Section 5 outlines the conclusions and research opportunities that emerged from this work.

2 MOTIVATION AND RELATED WORK

This section presents about the digital system, that we are working to improve performance and time execution and some related papers about the programming language R and Python, and its primary characteristics.

2.1 Compartmental Stochastic Model

Stochastic modelling is a mathematical technique used to model systems or processes that involve randomness or uncertainty. The term "stochastic" refers to randomness, and stochastic modeling involves describing the behavior of systems or phenomena in probabilistic terms. Common techniques in stochastic modeling include stochastic differential equations, Markov chains, queuing theory and Monte Carlo. These methods provide ways to simulate, analyze, and make predictions about complex systems affected by randomness (Shah, 2022).

Infectious diseases are known as one of the most critical threats to global health today. Climate change and the accelerated growth of population are some causes of the disease spread among humans. This leads to increased infection at the global level; some systems use water waste to control the level of infection in some areas, which can be monitored in real-time at the community level can help to avoid or control some diseases and infections and act to prevent the spread of the disease (Nathalie & Barbara, 2021). Several disease transmission systems were developed and used to examine control strategies (Rohit et al., 2020). Some systems to control the spread were developed based on cell phone location, using data from the geolocation of the cell phone to understand the movement of the population and study the spread of the disease process (Sachi et al., 2021).

The system in the scope of this work is a model that simulates the spread of disease in animals cultivated for human consumption, so controlling the disease and the spreading process is important because it can have an economic impact in the region. Even if we can isolate the animals that are infected, the animal transport, circulation of employees in the farm, the logistics to deliver product and material can impact the spread process. The system created to prevent and simulate the disease spread uses a stochastic model developed in R, this digital system was created considering real data collected for the transporting process of the animals between farms located in Rio Grande do Sul, Brazil (Manuel et al., 2021)..

2.2 R and Python Comparison

As stated before, in this work we implemented in Python an intelligent disease spread and control system for the spread, originally implemented in R. Python and R are programming languages used in data analysis, and efforts have been made to support our research practices using these two computational programming languages. However, an important focus has been given to the visualization of researchoriented studies and their comparable efficiencies in analyzing large fragmented datasets. While Python is a general-purpose language with an easy-to-understand syntax, R's functionality was designed with statisticians in mind, providing fieldspecific advantages such as great data visualization capabilities, but R lacks performance and speed process (Anupam et al., 2021).

The R programming language is a free, powerful, open-source software package with extensive statistical computing and graphics capabilities due to its high-level expressiveness and multitude of domain specific packages. R prioritizes ease of use and data exploration, which can lead to less efficient memory management compared to languages like C or Java, which prioritize performance and memory efficiency (Weijia, et al., 2016).

The Python language is a general-purpose, opensource tool for web, internet, and software development applications; education and academia; and numerical and scientific tasks, among others. In the field of data analysis, some of the common packages are: Pandas and Polars, ideal for data manipulation; Statsmodels, for modelling and testing; scikit-learn, for classification and machine learning tasks; NumPy (Numerical Python), for numerical operations and vectors; and SciPy (Scientific Python), for scientific tasks, other libraries like Dask to huge amount of data. One big advantage of Python language is that for data extraction and data analysis is the possibility to use the API Apache Spark and use Pyspark to work with big data and with Spark Streaming that is data near real time (S Saabith et al., 2021).

Python is favoured for data science, AI and machine learning due to its concise code, enabling easy testing and focusing on actual programming. It uses significantly less code compared to other languages, Python ranks second after Ruby in lines of code required for projects, making it a top choice for ML and AI. It boasts simplicity, fewer keywords, and a clear syntax, making it accessible for students and newcomers. Python prioritizes readability, fostering collaboration and rapid open-source project development (Abhinav et al., 2019).

One library used in this proposal of a new model in this digital system is Pandas, that is used for data extraction and analysis, which in the current version 2.0, has implementations such as the use of PyArrow, which in turn is possible to accelerate the process and make operations more efficient in terms of memory, using the C++ implementation of Arrow. Arrow allows sharing data between processes without the need to copy them, which improves performance and reduces memory consumption. In this sense, PyArrow is a library that provides a bridge between Python and Apache Arrow, offering resources to work with data in a columnar format in an efficient way and interoperable with other programming languages (Pantelis et al., 2019). For the R language, the two libraries we use in the tests are data.table and tidyverse, the tidyverse package is a collection of R packages that were developed to facilitate the manipulation, analysis and visualization of data. Within it we will use dplyr which is one of the packages used in tidyverse, offering a consistent and intuitive syntax to perform data manipulation operations. The dply package also has the advantage of having a more readable and intuitive syntax, and its philosophy is based on "data manipulation grammar", this package is used a lot in data analysis and exploration in conjunction with ggplot. In the model the data manipulation and data visualization process are created using the tidyverse package. The data.table, that is used for data reading in the digital system, is known for its efficiency and speed in processing large data sets, it is fast in process of filtering, grouping, modifying data, there are several reasons why data.table is fast, but one of the main ones is that, unlike many other tools, it allows you to modify the information in your table by reference, i.e. it changes in place rather than requiring the object to be recreated with the modifications. This means that when using data.table you need to use the <- operator less often.

Python at the moment is the first choice of even the topmost companies in the world such as Amazon, Facebook, Spotify and Instagram, that have the challenge to deal with enormous amounts of data, for their needs, and for their clients' needs, for data processing and data analysis (Sebastiaan et al., 2021).

3 DISEASES SPREAD AND CONTROL SYSTEM

The digital system proposed by the author (CARDENAS et al., 2022). It was designed to demonstrate the potential for the spread of infectious animals, considering transmission through animal movements. The system also implements the simulation of control actions. These control actions can, for example, prevent farms from receiving or shipping infected animals such as culling, isolation of animals, increased hygiene measures, or vaccination.

As the present work aims at improving the most computational intensive functions, they will be detailed in the next subsections. For a comprehensive understanding of the system, please refer to the original paper (CARDENAS et al., 2022).

3.1 Animal Movement Representation

The system uses Social Network Analysis (SNA) methods to characterize animal trade patterns, and the between-farm total of animals moved is represented in the system as a directed graph, where each farm is represented as a "node" and the movements among farms are represented as "edges". Each edge connects a specific node origin to a specific node destination, maintaining also the type and number of animals that are being moved. The system maintains an event dataset with data on origin, destination, type, and number of animals, used to construct the movement graph. The between-farm movements among farms of different species, therefore considering a real multihost contact network of movement data collected from (CARDENAS et al., 2022).

3.2 Disease Spread Dynamics

The system applies a stochastic simulation algorithm (SSA) to simulate the disease spreading, as well as, vital dynamics (birth and deaths) of animals inside each farm. The system incorporates within farm and between farm dynamics through a susceptible infectious model using the temporal animal movement data explicitly with a higher effective

contact rate to ensure an efficient disease transmission over the simulations.

The within-farm dynamics is represented by a state machine composed of four states. Transition from susceptible (S), to exposed (E), to infected (I), to recovered (R). Every state is represented as compartments for each farm, at a rate proportional to a frequency dependent transmission parameter (β).

3.3 Control Action Zones

After an initial silent spread where animals on some farms became infected, control and containment of the disease agent is essential for eradication and recovery. Quarantine and movement control are examples of actions to protect animal health, helping to prevent the disease from being transmitted to noninfected populations (James, 2007). These actions are applied to specified control zones, which are defined through specific user parameters.

This function defines control action zones in geographic locations, classified or designated according to specific disease or disease-free status criteria. These designations help to associate specific response activities with specific locations.



Figure 1: Control zone representation.

Figure 1 shows the control action zones defined as outbreaks for farms containing infected animals, the infected zone containing farms within a 3 km area around the outbreak, the buffer comprising farms in a region considering 7 km, and the surveillance zone was defined as 15 km from the outbreak.

3.4 Vaccination

This function simulates the animal vaccination process. The process occurs during the disease spread where vaccinated animals are moved from SEIR compartments to a V (vaccinated) compartment, according to the vaccination efficacy and specific rate conversion day by day, specified by the user when defining the control actions. This implies changing values in the dataset row by row, which can be a problem in R when the model grows in size.

4 EVALUATION AND DISCUSSION

This section reports the experiments carried out, showing the comparison time between the different tested approaches and discussing the results obtained. It is divided in two subsections, where the first shows functions implemented in the languages libraries and the function call itself while the second presents the execution time of complex functions developed to simulate different aspects of the disease spreading. All results presented through this section were measured in seconds.

The tests were performed on a computer with the following specifications. CPU Intel(R) Core(TM) i7-8650U, 8 cores, 1.90GHz, 16Gb RAM, Linux Debian 5.10.162-1 (2023-01-21) x86_64 operating system. There are some functions that were developed in the digital system. One is to create a simulation about movement of animals from one farm to another farm, that is a root of some disease spread process, this process occurs during 15 days. The data reading of events is using data.table, we will compare with Pandas and Polars in Python. Using two csv files, one with 65Mb and other with 225MB, the reading process will test 100 times and we will use the mean.

4.1 Reading Datasets and Function Calling

The first test was performed for reading two datasets with sizes 65MB and 225MB. For Python, we tested two different libraries (Pandas and Polars), while Tidyverse and data.table were used to read the same datasets in R. The test was repeated 100 times and the average execution times are shown in Table 1.

Figure 2 and Figure 3 show the distribution, through boxplots, of the time for reading the datasets. We can see some outliers in the boxplot distribution, but in this case, we will consider them as special cases, and they do not change our test results.

Table 1: Mean time for reading process.

Dataset	Pandas	Polars	Tidyverse	Data.table
65MB	0.526396	0.257375	1.093194	0.20933
225MB	4.377422	0.480025	15.98519	2.59795



Figure 2: Boxplot graph distribution times for reading for 65 MB dataset.



Figure 3: Box plot graph distribution times for reading the 225 MB dataset.

It is possible to observe that in the process of reading the small dataset, the Polars library in Python and the Data.table in R have equivalent reading speeds, with a slight advantage for Data.table, plus increasing the size of the dataset to Polars stands out and becomes the fastest in the reading process, in our case is good, because the system can grow with more data and bigger datasets, Polars is around 5 times faster than Data.table, mainly due to its construction in Rust, which is a low-level language that in turn is more efficient, and in Polars it is possible to work in parallel and scale the system and maintain the performance, if the digital system grow (Ruizhu et al.,2018).

For the R language, data.table proves to be very efficient due primarily to being built in C, the data.table package is more performant than the Tidyverse package, which includes the Dplyr package, the data.table in several operations does not copy it, filters and selects in the object itself, which saves memory and time in the process and can improve the performance of the model, but in some situations it is necessary and practical using the tidyverse package (Matt & Joshua, 2016). As the datasets are passed as arguments to the functions, we compare the time just for calling the previous function in both languages. On average, the time in Python was 0.000001533 seconds, while calling a function in R took 0.2811756256 seconds. In terms of

function calls, Python code is converted to the machine code before being executed, while R code is interpreted line by line, thus making it more performative in this process. When the function grows with more parameters, the difference in performance in both languages also grows (Yi Lin et al., 2016).

4.2 Spreading and Control Functions for the Digital System

This section compares the digital system's most computationally intensive functions model implemented in R and Python. This study uses the three most complex computational performance functions to improve the performance.

4.2.1 Animal Movements

The first function simulates the animal movement across the farms. It uses an event dataset containing farm-to-farm animal movements and number of animals being moved. We defined 15 days for moving animals from the dataset of 65Mb, which contains 337.600 farms. This simulation creates the disease spread situation in the moving process.



Figure 4: Distribution for function simulating animal's movements for 15 days.

As we can see in Figure 4, Python is around eight times faster than R for this function. This can be explained as the Python version using an index on the farm's IDs, speeding up the search procedure for modifying the dataset's number of animals.

4.2.2 Disease Spread Dynamics

The function simulates the spatial disease spread driven by the geographic distance between farms. It uses statistical methods based on the initial parameters to update the number of infected animals near infected farms. In this simulation, there were 52 infected farms and during the execution, 48.530 farms had their status modified from this function. The execution times for this update process in both languages are presented in Figure 5.



Figure 5: Graph distribution for the local transmission dynamics.

4.3 Control Zones

In this section we will study and improve the performance and time execution from the functions that simulate the vaccination process and control zone simulation, that is control and isolate farms that

the disease is already vaccinated or isolated in the process to control the infection, this function receives data from the vaccination function and inserts and updates the data in the data frame. The results are presented in Figure 6.



Figure 6: Graph distribution for function simulating the update and data in the function that controls the infected zone.

4.3.1 Vaccination

The next function simulates the animal vaccination process. The results shown in Figure 7 represent a vaccination occurring between 6 and 14 days after the disease spreads.



Figure 7: Graph distribution for function simulating the vaccination process from day six until day 14.

In the system, when the animal is vaccinated, the dataset is updated row by row, updating the vaccination status of each animal. This explains why using Python language is four times faster than R in this application. Finally, Table 2 summarizes the function's average results previously seen in this section.

Table 2: Average execution time of computationally intensive functions.

	Move Function	Animal Vaccination	Control Infected Farms	Spread disease
Python	10.12597	14.34065	0.32091214	3.046755
R	83.05695	60.686126	6.42530646	4.128237

In terms of memory usage, the process of the digital system using the R language is 460 MB, and the Python language with the same application has 315 MB of memory usage. Python has a feature called function memorization, where you can cache the results of a function for specific inputs, improving performance for expensive computations, which helps to control memory usage (Xing Cai et al., 2005). As an overview, the Python implementation exhibited remarkable performance and significantly faster processing speeds, presenting a promising avenue for enhancing the overall system, aiming to achieve responsiveness and reducing the execution time.

5 CONCLUSIONS

Based on the tests carried out, it is possible to verify that in a model with many functions and a lot of data processing, data reading, and update in dataset, the optimized solution would be Python, because of the advantage in functions (time execution and speed process) and the use of Polars for data analysis. The implementation in Python proved to be more efficient than in R, mainly due to its constructive characteristics and objectives, with some great advantages in performance, speed process and memory usage. In terms of reading speed of large datasets, Polars is more efficient in reading than Pandas using the Python language. Polars is built in Rust which guarantees more speed than Pandas, the great advantage of Polars is that it works in parallel, so even with an increase in data volume it maintains its performance, in addition Polars is considered a library that has Lazy operation, that is, only perform the function, when necessary, that is, it saves memory, Polars can work in parallel, which can improve speed process. Even though Python is slower in runtime and has some design restrictions as compared to compiled languages like C or C++. Python is preferred by scientists and developers in the field of data analytics, numerical computations and almost all technical domains, like AI and Deep Learning. The best approach for work in the model, according with the test, is to rewrite in Python, using Polars in data reading (files .csv) and data manipulation files, mainly because some digital system grow and the question about memory usage in Python, in R all objects are stored in memory and when the system grows, we can have a problem. Polars, have the lay attribute to save memory and if necessary, in long term work in parallel, which can be an advantage in this model, because it's possible to to speed up the simulation work with more simulation in parallel.

For future work it could be important to try to implement Rust, as Rust is compiled directly to the machine code, has high performance, works in parallel and has better memory control management, which is for some authors the next step in data analysis (Bugden & Alahmar, 2022).

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