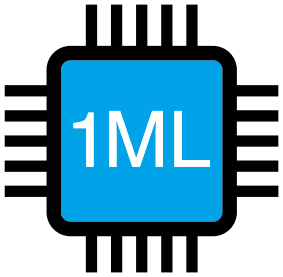
The 1chipML library



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Chapter 1

What is 1chipML?

1.1 Introduction

The Internet of Things (IoT) and Edge Computing (EC) are, nowadays, topics of high interest since it is becoming clear that important advantages could emerge from this new sort of technologies. What kind of hardware will be in use in this context is still work in progress since many different directions are currently being explored.

In more details, one can consider the IoT as an ensemble of computing objects with sensors, embedded software, etc., which can connect and exchange data with other devices over the Internet (or, equivalently, other communication networks). A continuously growing number of IoT devices are already being created for connected vehicles, home automation, wearable technology, and all sort of appliances with remote monitoring capabilities. For instance, in industry, we are witnessing the creation of a growing number of IoT devices to acquire and analyze data from connected equipment, operational technology, locations, and people. Combined with monitoring devices, this new technological paradigm is helping to regulate and monitor industrial systems. The same approach can be applied for automated record updates of asset placement in industrial storage units. Another important example of IoT is represented by the Internet of Medical Things (IoMT) which can be considered as an application of the IoT for medical and health related purposes. This novel technology can help in the creation of a digitized healthcare system, connecting available medical resources and healthcare services.

Edge computing is a growing and relevant approach as well, but very different than the IoT. In practice, the aim of edge computing is to move the computation away from data centers towards the edge of the network, exploiting smart objects, mobile phones, or network gateways to perform tasks and provide services on behalf of the cloud. Therefore, it also can be considered as a distributed computing paradigm that brings computation and data storage closer to the sources of data. In other words, one can consider the EC as any

type of computer program which can deliver low latency nearer to the requests. Thus, this new computing approach is expected to speed up response times and save bandwidth since it is possible to provide content caching, service delivery, persistent data storage, and IoT management resulting in better response times and transfer rates.

Obviously, the sort of hardware needed to implement these two approaches cannot solely rely on classical computing devices such as servers, Beowulf clusters, etc. since they require those devices to be fast, low power demanding and in small packages. One technology approach that seems to be currently emerging is based on the use of microcontrollers (MCUs). While this seems to be a promising direction, it obviously comes with new challenges which needs to be addressed. Among these open problems, one that seems to be relevant nowadays is the lack of a available software infrastructures for the fast development of such technologies. 1chipML is a library which purpose is to bridge this gap.

1.2 1chipML in a nutshell

In order to make a technology take off, it is important to have a fast and reliable way to develop (and evolve) it. Without such infrastructure and tools, it is hard to imagine how to develop something that can have a real impact on society. In fact, the availability of such infrastructure can become the very reason for the success (or failure) of an invention, no matter what the field is. Obviously, this is valid for the fields of IoT and EC too. At the time of writing this manual, one quickly realizes (unfortunately) that such development tools are practically unavailable, especially if the goal is to run relatively sophisticated algorithms on MCUs such as number crunching and machine learning (ML) methods. Of course, there are some available libraries but they are either proprietary (or incomplete), which is known to slow down the development of technology (a great example is provided by the GNU/Linux operating system which has, eventually, allowed the development of the Android operating system). The goal of 1chipML is to bridge this gap so that IoT and EC can become quickly mainstream.

The target of the 1chipML team of volunteers is to develop and maintain a library which can provide relevant computational capabilities on MCUs related to number crunching and ML. For example, one could need to run the Gauss elimination method to solve a relatively small system of linear equations. The only option for now is to develop everything from scratch which can be time consuming and error prone. With the 1chipML library, this problem is solved. One simply needs to download it and use it right away. A practical example is reported in a section below.

At the time of writing this manual, there are relevant main families of MCUs available on the market such as the ones produced by ARM and AVR. While, in the past, these MCUs used to be very limited (with very limited amount of memory and computational power), nowadays they have features which allow to run relatively complex algorithms on such devices which used to be practically

impossible previously. This is one of the reasons why 1chipML has been created.

1.3 Development paradigms

How to use 1chipML? There are essentially two ways:

- It is possible to include the whole library into a code so that all methods implemented are available at once.
- It is possible to include only the algorithm that is needed. In this case, only the relevant methods are included.

A first practical example is discussed below.

1.4 A first example

The Gauss elimination method, also known as row reduction method, is an algorithm to solve systems of linear equations. This method consists of a sequence of operations performed on the matrix of coefficients corresponding to the system at hand. To perform the computation, a sequence of elementary row operations which modifies the matrix until the lower left-hand corner of the matrix is filled with zeros, as much as possible.

This method is available in the 1chipML library and it is very simple to use it. The user does not need to implement anything related to number crunching beyond the definition of the linear system itself.

```
#include<stdio.h>
#include<stdlib.h>
#include<math.h>

#include "../src/1chipml.h"

int main(void){
 /* Variables and pointers declarations */
 int i;
 int N;
 gauss_real A[2][2];
 gauss_real B[2];
 gauss_real *sol; /* pointer towards the solution */

 /* The following parameters define a system of 2 linear equations A*X=B */
 N=2;
 A[0][0]=+1.; A[0][1]=+1.;
 A[1][0]=+1.; A[1][1]=-1.;
 B[0]=0.;
 B[1]=1.;
```

```
 /* Apply gauss elimination method to solve the system */
 sol=gauss_elimination(N,A,B);

 /* Print solution on screen */
 for(i=0;i<N;i++) printf("sol[%d] = %0.3f\n",i,sol[i]);
 return(0);
}
```

Chapter 2

Numerical crunching

This chapter introudces and discusses the various numerical methods that are already implemented in the current version of the library. The Reader should bear in mind that this is still work in progress at the moment.

2.1 Random number generators

The generation of random numbers is a process used to create a sequence of numbers which cannot be reasonably predicted. Two main methods are used to generate random numbers. In the first approach, one measures some physical phenomenon that is expected to be random and then compensates for possible biases in the measurement process. For instance, sources of randomness include measuring atmospheric noise, thermal noise, and other external electromagnetic and quantum phenomena. In the second approach, one uses computational algorithms that can produce long sequences of apparently random results, which are in fact completely determined by a shorter initial value, known as a seed value or key. This type of random number generator is often called a pseudorandom number generator and it is the method used in the 1chipML library.

While a pseudorandom number generator based solely on deterministic logic can never be regarded as a true random number source in the purest sense of the word, in practice they are generally sufficient even for demanding security-critical applications. In fact, carefully designed and implemented pseudorandom number generators can be certified for security-critical cryptographic purposes. Many computational methods exist for pseudorandom number generation. In the following we present two of these pseudorandom number generators.

2.1.1 The linear congruential generator

This method is implemented in the file "src/linear_congruential_random_generator.c" of the library.

A linear congruential generator is an algorithm that yields a sequence of

pseudo-randomized numbers computed with a discontinuous piecewise linear equation. This method represents one of the oldest and best-known pseudorandom number generator algorithms. The theory behind them is relatively easy and, consequently, allow a fast and easy implemention.

The main idea behind this generator is to use the following recursive relation:

$$X_{(n+1)} = (aX_n + c) \pmod{m},$$

where $X_{(n+1)}$ and X_n are values in the sequence of pseudorandom numbers, and X_0 is called the seed or start value of the sequence. The constants a, c and m are known as the multiplier, the increment and the modulus respectively with $m > 0$, $0 < a < m$ and $0 \leq c < m$. In our particular implementation of this method, the values for these constants are $a = 1027$, $c = 0$ and $m = 1048576$. The initial seed X_0 is set to 38467 by default. The user can modify it by using the following command:

```
ISEED = some_value;
```

For clarity, an extract of the file "tests/test_linear_congruential_random_generator.c" is reported below:

```
/* Variables and pointers declarations */
int i,n=100;

printf("linear congruential random generator\n");
for(i=0;i<n;i++) printf("%1.3f ",linear_congruential_random_generator());
```

2.1.2 The Mersenne twister

Work in progress. This method is not implemented in the library yet.

2.2 Systems of linear equations

A system of linear equations is simply a collection of one or more linear equations involving the same variables. The theory of linear systems is the basis and a fundamental part of linear algebra, a subject which is used in most parts of modern mathematics. Computational algorithms for finding the solutions are an important part of numerical linear algebra, and play a prominent role in engineering, physics, chemistry, computer science, and economics. In the following we present the methods implemented in the library.

2.2.1 The Gaussian elimination method

This method is implemented in the file "src/gauss_elimination.c" of the library.

The Gaussian elimination method, also known as row reduction, is an algorithm used to solve systems of linear equations. It consists of a sequence of

operations, i.e. row reductions, performed on the corresponding matrix of coefficients. This method can also be used to compute the rank of a matrix, the determinant of a square matrix, and the inverse of an invertible matrix.

To perform row reduction on a matrix, one uses a sequence of elementary row operations to modify the matrix. There are three types of elementary row operations, i.e. *1)* swapping two rows, *2)* multiplying a row by a nonzero number, and *3)* adding a multiple of one row to another row. Using these operations, a matrix can always be transformed into an upper triangular matrix, and in fact one that is in row echelon form. Once all of the leading coefficients are equal to 1, and every column containing a leading coefficient has zeros elsewhere, the matrix is said to be in reduced row echelon form. This final form is unique, i.e. it is independent of the sequence of row operations used, and it is this form that is utilized to find the solutions of the system at hand.

To better understand how to use this method implemented in the library, an extract of the file "tests/test_gauss_elimination.c" is reported below:

```
/* Variables and pointers declarations */
int i;
int N;
gauss_real A[2][2];
gauss_real B[2];
gauss_real *sol; /* pointer towards the solution */

/* The following parameters define a system of 2 linear equations A*X=B */
N=2;
A[0][0]=+1.; A[0][1]=+1.;
A[1][0]=+1.; A[1][1]=-1.;
B[0]=0.;
B[1]=1.;

/* Apply gauss elimination method to solve the system */
sol=gauss_elimination(N,A,B);

/* Print solution on screen */
for(i=0;i<N;i++) printf("sol[%d] = %0.3f\n",i,sol[i]);
return(0);
```

2.2.2 The LU decomposition method

Work in progress. This method is not implemented in the library yet.

2.3 Interpolation and extrapolation

Work in progress.

2.3.1 Polynomial-based approach

Work in progress.

2.3.2 Spline-based approach

Work in progress.

2.4 Optimization problems

Work in progress.

2.4.1 The gradient descent method

The gradient descent method is an optimization algorithm to find a local minimum of a given function using it's gradient.

Many variations of the gradient descent algorithm exist, the simplest one probably being the steepest gradient descent method. However, this naive implementation of the algorithm tends to converge too slowly on the minimum as it approaches it using only right angle turns.

The variation implemented here is the conjugate gradient method, which seeks to reach the local minimum faster by approaching it using series of direction conjugate to the previous direction traveled.

Here is a pseudo-code of the algorithm optimizing $f(x)$:

Algorithm 1 Conjugate Gradient Descent Algorithm

$x_0 \leftarrow$ Initial guess point
$g_0 \leftarrow -\nabla f(x)$ ▷ g is the gradient vector
$h_0 \leftarrow g_0$ ▷ h is the conjugate vector
$i \leftarrow 0$
while $g_i \neq 0$ **do** ▷ Continue until the gradient is 0
    $\lambda_i \leftarrow$ LineSearch(f, x_i, h_i)
    $x_{i+1} \leftarrow x_i + \lambda_i h_i$
    $g_{i+1} \leftarrow -\nabla f(x_{i+1})$
    $\gamma_i \leftarrow \frac{(g_{i+1} - g_i) \cdot g_{i+1}}{g_i \cdot g_i}$ ▷ Adjustment factor for the gradient
    $h_{i+1} \leftarrow g_{i+1} + \gamma_i h_i$
    $i \leftarrow i + 1$
end while
return x_i

At each iteration, the conjugate gradient descent algorithm travels to the minimum of the function in the direction of the current conjugate. It then computes the gradient at that new point. Using the previous and current gradient, we can calculate the adjustment factor to get the new conjugate. We then continue to the next iteration until we find a local minimum.

In order to find the minimum of the function in the direction of the conjugate we use a the line search strategy.

We start by broadly bracketing the minimum between three points by using a succession of quadratic interpolation.

Quadratic interpolation relies on the assumption that the minimum of a one dimensional function resembles a parabola. In order to approach this minimum, we can take three points on our function and move to the abscissa at the minimum the parabola passing by these 3 points. By applying this interpolation multiple times we can eventually arrive to a local minimum.

Here is the formula for the interpolation using three points $f(a)$, $f(b)$ and $f(c)$:

$$x = b - \frac{1}{2}\frac{(b-a)^2(f(b)-f(c)) - (b-c)^2(f(b)-f(a))}{(b-a)(f(b)-f(c)) - (b-c)(f(b)-f(a))} \tag{2.1}$$

Once the minimum is broadly bracketed by three points, we can use Brent's algorithm to find the exact abscissa and value of the minimum. This algorithm uses a combination of parabolic interpolation and golden section search to reach the minimum.

It is possible for the gradient descent method to not be able to find a minimum if for example such a minimum does not exist or the initial guess starting point provided does not allow to converge to a minimum. In order to differentiate between successful an unsuccessful descent, a status of either GRADIENT_SUCCESS or GRADIENT_ERROR is returned by the function.

2.4.2 The genetic approach

The genetic algorithm is a probabilistic global optimization metaheuristic. That means that it can be used to optimize solutions with many local optimums. It does this by simulating the genetic evolution of a population. The algorithm consists of a sequence of operations that can be run continuously until a solution presenting a sufficient accuracy has been created.

1. The first step is to randomly initialize a population of solutions
2. We then evaluate all of the solutions present in the population and the algorithm returns a solution if its fitness value is small enough
3. Each set of parents for the next generation are chosen based off of a tourney approach (a fixed amount of solutions are randomly selected and the best two solutions are chosen to be parents)
4. Each parent is then encoded into a table (Each parameter is condensed together to form a string)
5. Two children are then created by a uniform crossover method between both encoded parents
6. Each child then has a chance to have one value of its table mutated

7. The two children are then decoded and added to the next generation
8. Steps 3-7 are repeated until the next generation is the same size as the original generation
9. The original generation is replaced by the new generation
10. Steps 2-9 are repeated until a certain amount of generations has been created or a valid solution has been found.
11. The best solution is returned

There are many methods for selecting the parents. One of the most popular methods is the roulette wheel solution where a solutions chance of being chosen is decided by its fitness divided by the sum of the fitnesses of the whole population. Another popular approach is the tournament selection where we randomly select a certain amount of solutions and pick the two with the best fitness. There are also many crossover approaches. The one we have chosen is a uniform crossover that means that each character of the encoded parents has an equal chance to be present in a child. The simplest approach is a one-point crossover in which an index is chosen for both parents and both encoded arrays representing the parents are swapped around those points to create the children.

Genetic algorithms present a few problems such as premature convergence. This means that the algorithm can sometimes converge towards a point which is not the global optimum. We have implemented a variant of the genetic algorithm called "elitist selection" in order to reduce the likelihood of this happening. This means that the best solutions from a population are directly transferred to the next generations without undergoing any genetic operations. This algorithm is not guaranteed to find the global optimum but will generally head in the good direction. They can also consume a lot of memory in order to store all of the population and the fitnesses which is why we have also developed a low-memory version of this algorithm where the fitnesses are not stored and are calculated each time they are needed. This slows down the execution time but can let us initialize larger populations which could mean better solutions.

2.5 Numerical derivation and integration

Work in progress.

2.5.1 First and second order finite differences approach

The file "src/finite_difference.c" implements a function allowing to approximate the gradient of a multivariate function by implementing a first and second order finite difference approximation. Three different approximations are available depending on the function for which we want to know the gradient.

The first order forward finite difference approximation uses the following formula to compute the partials derivatives of the function needed for the gradient :

$$\frac{\partial f(x_0, x_1, ..., x_n)}{\partial x_0} = \lim_{h \to 0} \frac{f(x_0 + h, x_1, ..., x_n) - f(x_0, x_1, ..., x_n)}{h}$$

The first order backward finite difference approximation uses the following formula to compute the partials derivatives of the function needed for the gradient :

$$\frac{\partial f(x_0, x_1, ..., x_n)}{\partial x_0} = \lim_{h \to 0} \frac{f(x_0, x_1, ..., x_n) - f(x_0 + h, x_1, ..., x_n)}{h}$$

The second order central finite difference approximation uses the following formula to compute the partials derivatives of the function needed for the gradient :

$$\frac{\partial f(x_0, x_1, ..., x_n)}{\partial x_0} = \lim_{h \to 0} \frac{f(x_0 + h, x_1, ..., x_n) - f(x_0 - h, x_1, ..., x_n)}{2h}$$

The central finite difference approximation will usually lead to better gradient approximations, however it is possible that this method is not suited for certain functions if they are not smooth.

2.5.2 The Monte Carlo approach

The file "src/mc_integration.c " describes the function of doing integration with Monte Carlo approach. One can examine the expected value of an integral using the Monte Carlo approach. Traditionally, the expected value of a function $g(x)$ can be calculated by first multiplying by its probability density function, $f(x)$, and taking the integral over the desired region:

$$E[g(x)] = \int_a^b g(x) f(x) dx$$

Alternatively, we can use a Monte Carlo approximation for the expected value by repeatedly sampling a uniform distribution between the limits of integration.

$$E[g(x)] = \frac{1}{n} \sum_{i=1}^{n} f(x_i)$$

where $x_i \in [a, b]$. As noted, x_i is a value that is sampled from a uniform distribution between the limits a and b for each unique $n = 1, 2, 3$, etc. This approach samples the $f(x)$ function and uses the law of large numbers to find a converged expected value. As an aside, the multiplicative factor of $1/n$ is sometimes given as $1/(n-1)$ because there are truly $n-1$ degrees of freedom

with n-samples, but when n is large enough the difference between $1/n$ and $1/(n-1)$ is negligible.

Given the form of the estimator for the expected value, extending to the estimate of the integral is simple. The expected value formula is multiplied by the range of the integration limits, as shown below.

$$F = (b-a)\frac{1}{n}\sum_{i=1}^{n} f(x_i)$$

where $x_i \in [a, b]$.

The file "src/mc_std.c" describes how to calculate variance using the Monte Carlo approach. The variance of the Monte Carlo integration scheme follows a traditional process of calculating variance around some random variable. By continuing with the notation of taking the integral of a function $g(x)$, and the expected value of the integral being $E[g(x)]$, the relationship for standard deviation can be given as:

$$\sigma_n = V\sqrt{\frac{E[g(x)^2] - E[g(x)]^2}{n-1}}.$$

Here the additional V term represents the total volume of the integration limits. If we were to evaluate a one-dimensional integral between the limits of a to b then the equation could be written as:

$$\sigma_n = (b-a)\sqrt{\frac{E[g(x)^2] - E[g(x)]^2}{n-1}}.$$

Using this format, we can easily calculate standard deviation or variance (standard deviation^2 = variance) along with the integration estimate.

The file "src/mc_stratified_sampling.c" is concerned with stratified sampling which is an approach to variance reduction by which the integration volume is divided into subdomains that are each evaluated separately. The estimates from each subdomain are then combined with a weight depending on their subdomain integration volume. Stratified sampling has the benefit of always reducing the sample variance, without any prior knowledge of the function's shape. Optimized stratified sampling routines may recursively divide the function into regions with comparable values by grouping specific peaks or values. Just as well, the naive approach of parsing the integration volume into uniformly large works without any prior knowledge of the function's structure. The stratified sampling estimate of an integral over a function $g(x)$ is given as:

$$E[g(x)] = \sum_{j=1}^{k} \frac{V_j}{n_j} \sum_{i=1}^{n_j} g(x_{ij})$$

where $x_i \in V_j$.

2.6 Eigenproblems

Work in progress.

2.6.1 The Jacobi method

The Jacobi method is an iterative algorithm for approximating the eigenvalues and eigenvectors of a symmetrical matrix.

It works by applying multiple orthogonal similarity transformations to the original matrix. These transformations, called *Jacobi* rotations are chosen so that, over time, the sum of the squares of the off-diagonal elements is minimized. The algorithm accumulates these transformations until the resulting matrix is diagonal. The product of all transformations gives then the eigenvectors of the matrix.

The algorithm starts by choosing an element to annihilate. To choose that algorithm, two variants are given in the library. First, the *cyclic Jacobi method* chooses the elements in the order that they are given in the matrix starting with the first off diagonal element ($S_{0,1}$, $S_{0,2}$, ...). The other variant simply chooses the element that has the highest absolute value in the matrix.

Once the element a_{pq} to annihilate is chosen, a rotation matrix P_{pq} is then created using the following formulas :

$$\tau = \frac{a_{qq} - a_{pp}}{2a_{pq}}$$
$$t = -\tau + / - \sqrt{1 - \tau^2}$$

Then, choosing the root with the biggest absolute value :

$$c = \frac{1}{\sqrt{1+t^2}}, \quad s = ct$$
$$P_{pq} = \begin{bmatrix} 1 & & & & & & \\ & \cdots & & & & & \\ & & c & \cdots & s & & \\ & & \vdots & 1 & \vdots & & \\ & & -s & \cdots & c & & \\ & & & & & \cdots & \\ & & & & & & 1 \end{bmatrix}$$

Once the matrix P_{pq} is computed, the element can be annihilated by multiplying P_{pq} with the input matrix A. The algorithm is be described in the following pseudo-code where A is the input matrix:

Algorithm 2 Jacobi Algorithm

1: $V \leftarrow$ Identity Matrix
2: **for** $i = 0; i \leq$ numberOfIterations; $i++$ **do**
3: $p, q \leftarrow$ chooseElementToAnnihilate() ▷ Cyclic or classical method
4: $P_{pq} \leftarrow$ createRotationMatrix(p, q)
5: $A \leftarrow P_{pq}^T \cdot A \cdot P_{pq}$
6: $V \leftarrow V \cdot P_{pq}$
7: **end for** ▷ V will contain the eigenvectors and A the eigenvalues

Multiple optimizations are made in the library to take into account the machine's precision. To do that, the concept of a *sweep* is defined. Given a matrix of size n x n, a *sweep* is defined as $n(n-1)/2$ Jacobi rotations. To optimize the algorithm to skip useless rotations, in the first three sweeps, the rotation matrix is carried out only if :

$$|a_{pq}| > \frac{1}{5}\frac{\sum_{r<s}|a_{rs}|}{n^2}$$

After that, the algorithm sets a_{pq} to 0 if $|a_{pq}| < 10^{-(D+2)}|a_{pp}|$ and $|a_{pq}| < 10^{-(D+2)}|a_{qq}|$ where D is the machine's precision (number of decimal digits).

2.6.2 The Lanczos method

The lanczos method is an iterative algorithm for approximating the eigenvalues and eigenvectors of a symmetrical, sparse matrix.

The algorithm generates a sequence of orthonormal vectors, called the Lanczos basis, that form an approximation of the eigenvectors of the matrix. At each iteration, the algorithm computes values forming a tridiagonal matrix that is similar to the original matrix and has the same eigenvalues.

The basic idea behind the Lanczos algorithm is to generate an orthonormal basis for the subspace spanned by the approximate eigenvectors of the matrix and then use this basis to construct the tridiagonal matrix.

Here is a pseudo-code of the algorithm :

Algorithm 3 Lanczos Algorithm

1: $x_0 \leftarrow$ Random unit vector
2: $\beta_0 \leftarrow 0$
3: **for** `i = 1; i ≤ k; i++` **do** ▷ k is the number of iterations
4: $v_i \leftarrow Ax_{i-1} - \beta_i v_{i-1}$
5: $\alpha_i \leftarrow v_i^T \cdot x_{i-1}$
6: $v_i \leftarrow v_i / ||v_i||$
7: $x_i \leftarrow v_i$
8: $\beta_i \leftarrow ||v_i||$
9: **end for**

$$T = \begin{bmatrix} \alpha_1 & \beta_1 & \dots & 0 \\ \beta_1 & \alpha_2 & \beta_2 & \vdots \\ \vdots & \beta_2 & \ddots & \beta_k \\ 0 & \dots & \beta_k & \alpha_k \end{bmatrix}$$

$$V = \begin{bmatrix} v_0 & v_1 & \dots & v_n \end{bmatrix}$$

The Lanczos algorithm is useful for solving large sparse eigenvalue problems since it generates a small, dense tridiagonal matrix that can be solved efficiently, rather than solving the entire matrix. It can also be used to compute a few eigenvalues and eigenvectors of the matrix, rather than all of them.

Due to the rounding error caused by the IEEE-754 standard, the Lanczos algorithm is vulnerable to numerical instability. When applying the algorithm, Lanczos bases tend to loose their orthogonality. To overcome this issue, the Gram-Schmidt algorithm is applied after every iteration to reorthogonalize the vectors v_i.

The Lanczos algorithm does not directly outputs the eigenvalues and the eigenvectors associated with the original matrix. Further steps are needed to compute those values. However, the Lanczos algorithm does help finding those values by providing a tridiagonal matrix T which is much easier to compute.

The eigenvalues and eigenvectors of T can be calculated using standard methods such as the Jacobi algorithm.

Once the eigenvectors and eigenvalues of T are known, the eigenvectors of the original matrix can be approximated by linear combinations of the Lanczos basis vectors. For example, given an eigenvector of T, say γ, corresponding eigenvector of the original matrix, say λ is given by $\lambda = V\gamma$

2.7 Statistical approaches

Work in progress.

2.7.1 Analysis of variance

Work in progress.

2.7.2 Correlation

Work in progress.

2.7.3 Cluster analisys

Work in progress.

2.7.4 Regression

Work in progress.

2.8 The Fast Fourier Transform

The Fast Fourier Transform (FFT) is an algorithm that computes the discrete fourier transform (DFT) of a set of complex values. More specifically, the FFT is often used to convert a set of values from its original domain to a representation in the frequency domain.

The DFT equation can be seen in 2.2:

$$X_k = \sum_{n=0}^{N-1} x_n \exp\left(-\frac{2\pi i}{N} nk\right) \tag{2.2}$$

where N is the size of set of values, k ranges from 0 to $N-1$ and i is the imaginary part. The equation shown in 2.3 represents the twiddle factor.

$$\exp\left(-\frac{2\pi ik}{N}\right) \tag{2.3}$$

The Cooley–Tukey FFT algorithm is used to find the FFT of a set of values. This algorithm uses a strategy similar to divide-and-conquer, allowing it to have a time complexity of O(n log n).

The algorithm is implemented in a function that takes in two separate arrays to represent complex values. The first array consists of real numbers, while the second array holds imaginary numbers. This algorithm overrides the arrays passed as arguments and replaces them for the result of the FFT. Furthermore, the radix-2 decimation-in-time (DIT) method was used, meaning the arrays must have a length equal to a power of 2. If this is not the case, an error code will be returned by the function.

The first step of the algorithm is to execute bit-reversal permutation on the incoming arrays, as it uses the iterative approach. Then, the divide-and-conquer strategy starts. For the first set, the algorithm iterates over the elements that require the same twiddle factor. It then iterates over each group and uses the same twiddle factor for each one. After that, the twiddle factor is updated using the trigonometric recurrence formula and the next elements are selected. The same steps are repeated for the second set and so forth. By using this strategy, we end up with the result of the FFT.

Given the context of microcontrollers and their lack of memory, multiple design choices were made, which are summarized here:

- The FFT takes in two arrays of the same size (real and imaginary)
- The FFT only takes in arrays that have a length equal to a power of 2

- The FFT overrides the incoming arrays with the result
- The FFT returns 1 in case of an error, 0 otherwise
- The FFT has a space complexity of O(1) and a time complexity of O(nlogn)
- The FFT uses the iterative approach
- The FFT uses bit-reversal for the iterative approach
- The FFT does not calculate the twiddle factors in advance
- The FFT uses the trigonometric recurrence formula to reduce the number of sin and cos calculated

Chapter 3

Machine learning

The various already implemented machine learning methods are described here.

3.1 Neural networks

3.1.1 Migration of pre-trained neural networks

3.2 Reinforcement Learning

3.2.1 The multi-arm bandit problem

ϵ-greedy method, UCB (upper confidence bound) method, gradient bandit method.

3.2.2 Monte Carlo methods

The Monte Carlo algorithm learns which action is best to execute next in a certain environment. It iterates through an action tree, playing out random episodes and receiving rewards based on how well it has performed. The algorithm can iterate until the value of a following action reaches a certain threshold, chosen by the user. Once it reaches that threshold, it returns the next action with the best value depending on the rewards received and it's number of visits.

The Monte Carlo method is divided into 4 steps :

The first step is to select the node to expand. The selection traverses the tree and selects the node based on it's value. The node with the highest value will be selected to be expanded next.

Next comes the expansion of the selected node. From the selected node, the algorithm expands the children of the selected node.

The next step is the random playout of an episode. From the expanded node, the algorithm playouts an episode, choosing randomly the next action to execute. The playout finishes once the tree reaches a terminal node. When it is done, it returns the result of the episode. The result can be WIN, LOSS or DRAW.

The last step of the Monte Carlo algorithm is to backpropagate the result of the episode. The result is thus propagated to the parent of the current node, until it reaches the root node.

The algorithm executes these 4 steps iteratively until the value of a following action reaches a certain threshold chosen by the user, or a maximum number of simulations.

The UCB method was chosen to calculate the value of the node depending on the number of visits and the value returned from the simulations.

Here is a pseudo-code of the method :

Algorithm 4 Monte Carlo Method

```
1: rootNode ← Initial state
2: while UCBScore < k do                ▷ k is the threshold for the UCB score
3:     childNode ← selectChild(rootNode)
4:     expandChild
5:     score ← mcEpisode
6:     backpropagate(score)
7: end while
```

The biggest limitation of the execution of this method on an MCU is the size of the tree of actions and rewards. Indeed, the number of nodes that can be expanded is limited to the size of the memory of the MCU. Therefore, the nodes have been optimized such that a maximum of them can be expanded, resulting in a limited number of simulations. While executing this method, keep in mind the memory size of the MCU on which the method is used.

The Monte Carlo method has been written in order for it to be as configurable as possible by the user. To accomplish this goal, many functions must be written by the user and passed as argument to the method.

The methods that must be implemented by the user are the ones specific to the context and environment in which the Monte Carlo method is applied.

Chapter 4

Hardware applications

Chapter 5

How to contribute

Chapter 6

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