Accelerator for Event-based Failure Prediction

Acceleration of an Extended Forward Algorithm for Failure Prediction on FPGA

Master's Thesis submitted to the

Faculty of Informatics of the *Università della Svizzera Italiana*

in partial fulfillment of the requirements for the degree of

Master of Science in Informatics

Embedded Systems Design

presented by

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Janaury 2014

I certify that except where due acknowledgement has been given, the work presented in this thesis is that of the author alone; the work has not been submitted previously, in whole or in part, to qualify for any other academic award; and the content of the thesis is the result of work which has been carried out since the official commencement date of the approved research program.

Simon Maurer
Lugano, 29. Janaury 2014

Abstract

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Chapter 1

Introduction

In today's live it becomes increasingly important, that computer systems are dependable. The reason being, that computer systems are used more and more in areas where the failure of such a system can lead to catastrophic events. Banking, public transportation and medical engineering are only a few examples of areas employing large and extremely complex systems. The increasing complexity of computer systems has a direct impact on their maintainability and testability. It is simply impossible to guarantee that a piece of software comes without any faults. On top of that, the same problematic arises with the hardware components which also may contain faulty parts but also get increasingly prone to failures due to decay of material.

In the event of a system failure it is of course desirable to fix the system as soon as possible in order to minimize the downtime of the system (maximize the availability). This can be accomplished by using different types of recovery techniques, e.g. Check-pointing (create checkpoints to roll back/forward), system replication (switch to a redundant system), fail over (reboot). All these techniques require a certain amount of time to complete the recovery process, time that is very expensive. In order to minimize this time, techniques have been developed to anticipate upcoming failures. Such a technique is described in [20].

The work presents a new algorithm to predict failures and compares the results with other techniques. The accuracy of the presented algorithm to predict failures proves to be better compared to the other techniques, has however the drawback of increased complexity and hence increased computation time. It is very important to keep the computation overhead very low in order to maximize the time between the prediction of a failure and the actual event of the failure. One way to decrease the computation time is to design a hardware accelerator for the prediction algorithm. The design of such an accelerator is outlined in this document.

1.1 Problem Statement

1.2 Motivation

The email of Felix left some doubts to whether the acceleration of the algorithm is useful. The following list will give some arguments to justify the work.

Too many parameters to be identified, estimated and set
Considering an embedded system, this is usually not a problem because the parameters

are defined during the design phase and will never be changed afterwards.

Limited performance scalability
There are studies available claiming otherwise. The discussion of Neumanns work will provide some arguments against this statement.

Industry trends point towards cloud
In embedded systems it will still be beneficial to predict failures of single nodes. It is however important to keep the power and computational footprint low. This will be one of the major challenges. On the other hand, I think it would also be possible to also use this algorithm to monitor a distributed system and predict failures. It is only a matter of getting defining the events to feed to the algorithm.

1.3 Contributions

1.4 Document Structure

Chapter 2

State of the Art

This section provides an overview of the state of the art in the different fields of research that are relevant for the thesis. This includes failure prediction methods, existing solutions to accelerate failure prediction algorithms and acceleration techniques in general.

2.1 Failure Prediction

A very detailed overview of failure prediction methods is given in [21]. The survey discusses i.a. the techniques used as comparison in the main reference [13, 12, 23, 6] as well as the technique described in the main reference [20].

More recent work uses hardware counters of a general purpose CPU and combines them with software instrumentation to analyze failures of single processes (e.g grep, flex, sed) [27]. As industry heads more and more towards cloud computing, it has been proposed to use information of interaction between nodes (instead of analyzing single nodes) in order to analyze and predict failures of a distributed system [22, 17].

2.2 Accelerator

The main goal of this master thesis is to accelerate an adaptation of the forward algorithm. Proposals for a GPU based accelerator for the classic forward algorithm are described in [16, 14]. Further, several proposals to accelerate the Viterbi algorithm (which is closely related to the forward algorithm) have been published: [2] presents an architecture for a lightweight Viterbi accelerator designed for an embedded processor datapath, [7, 15, 18] describe a FPGA based accelerator for protein sequence HHM search and [24] describes i.a. an approach to accelerate the Viterbi algorithm from the HMMER library using GPUs.

Focusing on a more general approach for acceleration, [9] proposes an FPGA implementation of a parallel floating point accumulation and [26] describes the implementation of a vector processor on FPGA.

Quite some research has been done on the question what type of technology should be used to accelerate certain algorithms: [4] presents a performance study of different applications accelerated on a multicore CPU, on a GPU and on a FPGA, [8] discusses the suitability of FPGA and GPU acceleration for high productivity computing systems (HPCS) without focusing on a

specific application and [11] also focuses on HPCS but uses the Basic Linear Algebra Subroutines (BLAS) as comparison and also takes CPUs into account.

It may be interesting to also think about an acceleration of the model training. Similar work has been done by accelerating SVMs (Support Vector Machines): [3] describes a FPGA based accelerator for the SVM-SMO (support vector machine - sequential minimal optimization) algorithm used in the domain of machine learning and [1] proposes a new algorithm and its implementation on a FPGA for SVMs.

Chapter 3

Event-based Failure Prediction

This section provides a brief overview of the computational steps done by the proposed algorithm [20].

brief description of the idea behind the algorithm, HSMM, Events, etc

To be able to understand the formal expression of the algorithm, first a definition of the used parameters is provided.

- N: number of states
- M: number of observation symbols
- L: observation sequence length
- R: number of cumulative probability distributions (kernels)

The delay of the event at time t_k with respect to the event at time t_{k-1} is described as

$$d_k = t_k - t_{k-1} \tag{3.1}$$

3.1 Data Processing

3.2 Model Training

One part of the algorithm is the model training. This part is not described here. The features to be trained by the model training are however important in this context because they are used by the adapted forward algorithm. Following the features:

- π_i, forming the initial state probability vector π of size N
- $b_i(o_j)$, forming the emission probability matrix B of size $N \times M$
- p_{ij}, forming the matrix of limiting transmission probabilities P of size $N \times N$
- $\omega_{ij,r}$, the weights of the kernel r
- $\theta_{ij,r}$, the parameters of the kernel r

3.3 Sequence Processing

The following description will provide a complete blueprint of the extended forward algorithm, that allows to implement it, but without any explanations or proofs related to the formulation. The adapted forward algorithm is defined as follows:

$$\alpha_0(i) = \pi_i b_{s_i}(O_0) \tag{3.2}$$

$$\alpha_k(j) = \sum_{i=1}^{N} \alpha_{k-1}(i) v_{ij}(d_k) b_{s_j}(O_k); \quad 1 \leq k \leq L \tag{3.3}$$

where

$$v_{ij}(d_k) = \begin{cases} p_{ij} d_{ij}(d_k) & \text{if } j \neq i \\ 1 - \sum_{\substack{h=1 \\ h \neq i}}^{N} p_{ih} d_{ih}(d_k) & \text{if } j = i \end{cases} \tag{3.4}$$

with

$$d_{ij}(d_k) = \sum_{r=1}^{R} \omega_{ij,r} \kappa_{ij,r}(d_k | \theta_{ij,r}) \tag{3.5}$$

forming the matrix of cumulative transition duration distribution functions $D(d_k)$ of size $N \times N \times L$.

For simplification reasons, only one kernel is used. Due to this, the kernel weights can be ignored. Equation 3.5 can then be simplified:

$$d_{ij}(d_k) = \kappa_{ij}(d_k | \theta_{ij}) \tag{3.6}$$

Choosing the Gaussian cumulative distribution results in the kernel parameters μ_{ij} and σ_{ij}:

$$\kappa_{ij,gauss}(d_k | \mu_{ij}, \sigma_{ij}) = \frac{1}{2}\left[1 + \operatorname{erf}\left(\frac{d_k - \mu_{ij}}{\sqrt{2}\sigma_{ij}}\right)\right] \tag{3.7}$$

explain difference to the non-extended forward algorithm and introduce a standard notation for the transition probabilities (eg v: extended a: basic, tp: general) stick to this in the whole document

The last set of forward variables α_L are then summed up to compute a probabilistic measure for the similarity of the observed sequence compared to the sequences in the training data set. This is called the sequence likelihood:

$$P(\boldsymbol{o} | \lambda) = \sum_{i=1}^{N} \alpha_L(i) \tag{3.8}$$

where $\lambda = \{\pi, P, B, D(d_k)\}$.

To prevent α from going to zero very fast, at each step of the forward algorithm a scaling is performed:

$$\alpha_k(i) = c_k \alpha_k(i) \tag{3.9}$$

with

$$c_k = \frac{1}{\sum_{i=1}^{N} \alpha_k(i)} \tag{3.10}$$

By applying scaling, instead of the sequence likelihood (equation 3.8), the sequence log-likelihood must be computed:

$$\log(P(\boldsymbol{o}|\lambda)) = -\sum_{k=1}^{L} \log c_k \tag{3.11}$$

where $\lambda = \{\pi, P, B, D(d_k)\}$.

3.4 Classification

explain classification

and finally the classification is performed:

$$\text{class}(s) = F \iff \max_{i=1}^{u} \left[\log P(\boldsymbol{s}|\lambda_i) \right] - \log P(\boldsymbol{s}|\lambda_0) > \log \theta \tag{3.12}$$

with

$$\theta = \frac{(r_{\bar{F}F} - r_{\bar{F}\bar{F}})P(c_{\bar{F}})}{(r_{F\bar{F}} - r_{FF})P(c_F)} \tag{3.13}$$

classification without scaling

Multi-class classification without scaling?

To calculate θ, the following parameters need to be set:

- $P(c_{\bar{F}})$: prior of non-failure class
- $P(c_F)$: prior of failure class
- $r_{\bar{F}\bar{F}}$: true negative prediction
- r_{FF}: true positive prediction
- $r_{\bar{F}F}$: false positive prediction
- $r_{F\bar{F}}$: false negative prediction

Chapter 4

Theoretical Analysis of the Forward Algorithm

introduction to the chapter

- serial implementation and complexity
- find available options for parallelization
- floating points vs fixed points
- implementation of exp and log function (LUT, Taylor, ...)
- choice of accelerator (Type, Model)

4.1 Serial Implementation and Complexity

The sequential implementation of the basic forward algorithm is represented in listing 4.1. It consist of three parts: the initialization step, the computation of consecutive forward variables and the final step, where the likelihood is computed. The initial α variable is computed by multiplying the initial state probability with the emission probability of the first observation symbol of the sequence (cf equation 3.2). The computation of the following forward variables consists of three nested loops: the outer loop iterates over the L sets of N α variables, where each variable depends on the prior computed α variable and the k-th observation symbol of a sequence. The first inner loop iterates over the N α variables of one set, where each variable is computed with the most inner loop. The two nested inner loops form the Matrix-Vector-Vector multiplication

$$\alpha_{k+1} = TP * \alpha_k \cdot B(o_k) \tag{4.1}$$

where α_k is a vector of size N of the prior computed α variables, TP a matrix of size $N \times N$ containing the transition probabilities and $B(o_k)$ a vector of size N containing the emission probabilities of the k-th observation symbol. Note that the first multiplication is a Matrix-Vector multiplication that results in a vector, which is then multiplied element-wise with the vector $B(o_k)$. The equation 3.3 describes the formal definition of the forward algorithm. In the last

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% computation of the forward algorithm without scaling
%
% @param N:             number of states
% @param L:             number of observation symbols
% @param PI:            initial state probability vector. size N
% @param B:             matrix of emission probabilities. size N, L
% @param TP:            transistion probabilities. size N, N
% @param oL:            indices of all observed symbols. size 1, L
% @return Ps:           probability likelihood
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
function [Ps] = forward_s_basic(N, L, PI, B, TP, oL)
    % initialize forward variables
    for i=1:N,
        alpha(i) = PI(i)*B(i, oL(1));
    end
    % forward algorithm
    for k=2:L,
        for j=1:N,
            alpha_new(j) = 0;
            for i=1:N,
                alpha_new(j) += alpha(i) * TP(i, j);
            end
            alpha_new(j) *= B(j, oL(k));
        end
        alpha = alpha_new;
    end
    % compute likelihood
    Ps = 0;
    for i=1:N,
        Ps += alpha_new(i);
    end
end
```

Listing 4.1. Forward Algorithm

step the likelihood is computed, by summing up all elements of the last forward variable α_L (cf equation 3.8).

As proposed by the reference work, the forward variables can be scaled, in order to prevent the result from getting very small due to the continuous multiplication of probabilities. The implementation of the proposed scaling method is shown in listing 4.2. The scaling is formally defined by the equations 3.9 and 3.10. Due to the scaling, instead of the likelihood, the log-likelihood is computed. Equation 3.11 gives the formal definition.

The algorithm to compute the sequence likelihood proposed by the reference work is an extension to the forward algorithm presented in the listings 4.1 and 4.2. Instead of constant transition probabilities, the extended algorithm computes a new transition probability matrix (size $N \times N$) for each arriving observation symbol, by considering the delay of the new symbol with respect to the prior symbol. The computation of the transition probability matrix TP is implemented with listing 4.3 and formally defined by the equations 3.4, 3.5, 3.6 and 3.7. As described in chapter 3.3, also here for reasons of simplification, only one kernel is used.

Complexity in space and time

4.2 Available Parallelism

Considering only the basic forward algorithm (listing 4.1), the computation of the likelihood is divided in $L+1$ steps: the initialization, $L-1$ identical intermediate steps and the finalization. Because of the recursive nature of the algorithm, all steps (except the initialization) depend on the previously computed forward variables. For this reason a direct parallelization of the steps is not possible. However, at every arrival of a new observation symbol, the last L elements of the observation symbol sequence are used to compute the likelihood (sliding window of size L over the stream of observation symbols **??**). This can be exploited to pipeline the steps in order to increase the throughput. By building a pipeline of $L+1$ stages, where each step of the forward algorithm corresponds to a pipeline stage, a likelihood is computed at every completion of a step, with a latency of $(L+1) * t_{step_{max}}$, where $t_{step_{max}}$ is the time needed to complete the computation of the most complex step (each stage of the pipeline must take the same amount of clock cycles). The throughput of a pipelined compared to a non-pipelined system is increased by factor L (assuming that L is big or by ignoring the setup time). Another and more important fact, that makes the pipeline architecture very beneficial in this particular case: the configuration allows to load the transition probabilities TP and the emission probabilities $b_i(o_k)$ for all steps at the same time, which reduces the load operations by factor L. This is visualized by the table 4.1. The table shows the pipeline stages with input values that are fed to the stage before the execution (note, that the input values TP and B always depend on the same observation symbol. The parameter d_k of the transition probabilities can be ignored in this case because only in the extended forward algorithm the transition probabilities depend on d_k. This will be discussed further when the extension is considered) and the output values resulting after the execution of the pipeline stage. Figure 4.1 shows a schematic representation of the pipeline.

add figure with sliding window over arriving sequence of observation symbols

By considering all dissimilar steps of the forward algorithm, more parallelization options can be found. In the initial step, N components of the first forward variable α_1 are computed by multiplying independent pairs of an initial state probability π_i and an emission probability of the first observation symbol $b_i(o_0)$. This can be fully parallelized by replicating the multiplication operation N times. Doing this results in a speedup factor of N, assuming that N multipliers are

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% computation of the forward algorithm with scaling
%
% @param N:             number of states
% @param L:             number of observation symbols
% @param PI:            initial state probability vector. size N
% @param B:             matrix of emission probabilities. size N, L
% @param TP:            transistion probabilities. size N, N
% @param oL:            indices of all observed symbols. size 1, L
% @return Ps:           probability likelihood
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
function [lPs] = forward_s_scaling(N, L, PI, B, TP, oL)
    % initialize forward variables
    for i=1:N,
        alpha(i) = PI(i)*B(i, oL(1));
    end
    % scaling
    alpha_sum = 0;
    for i=1:N,
        alpha_sum += alpha(i);
    end
    scale_coeff(1) = 1 / alpha_sum;
    for i=1:N,
        alpha(i) *= scale_coeff(1);
    end
    % forward algorithm
    for k=2:L,
        for j=1:N,
            alpha_new(j) = 0;
            for i=1:N,
                alpha_new(j) += alpha(i) * TP(i, j);
            end
            alpha_new(j) *= B(j, oL(k));
        end
        % scaling
        alpha_sum = 0;
        for i=1:N,
            alpha_sum += alpha_new(i);
        end
        scale_coeff(k) = 1 / alpha_sum;
        for i=1:N,
            alpha_new(i) *= scale_coeff(k);
        end
    end
    % compute log likelihood
    lPs = 0;
    for i=1:L,
        lPs -= log(scale_coeff(i));
    end
end
```

Listing 4.2. Forward Algorithm

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% computation of the extended transition probabilities
%
% @param N:         number of states
% @param dk:        delay of k-th observation symbol
% @param cdf_param: parameters for the cdf
% @return v:        extended transition probabilities
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
function [v] = compute_tp(N, dk, cdf_param)
    % compute all elements of v
    for i=1:N,
        for j=1:N,
            v(i, j) = normcdf(dk, cdf_param.mu(i, j), cdf_param.sigma(i, j));
        end
    end
    % correct diagonal elemnts of v
    for i=1:N,
        for j=1:N,
            v_sum(i) += v(i, j);
        end
    end
    for i=1:N,
        v_sum(i) -= v(i, i);
        v(i, i) = 1 - v_sum(i);
    end
end
```

Listing 4.3. Extension of the Forward Algorithm with only one kernel (Gaussian)

		Pipeline				
Symb	I/O	Init	Step 2	…	Step L	Final
O_1	in	$B(O_1)$	$B(O_1)$, $TP(d_1)$, 0	…	$B(O_1)$, $TP(d_1)$, 0	0
	out	$\alpha_1(O_1)$	0	…	0	0
O_2	in	$B(O_2)$	$B(O_2)$, $TP(d_2)$, $\alpha_1(O_1)$	…	$B(O_2)$, $TP(d_2)$, 0	0
	out	$\alpha_1(O_2)$	$\alpha_2(O_{1,2})$	…	0	0
⋮		⋮	⋮		⋮	⋮
O_L	in	$B(O_L)$	$B(O_L)$, $TP(d_L)$, $\alpha_1(O_{L-1})$	…	$B(O_L)$, $TP(d_L)$, $\alpha_{L-1}(O_{1,\dots,L-1})$	0
	out	$\alpha_1(O_L)$	$\alpha_2(O_{L-1,L})$	…	$\alpha_L(O_{1,\dots,L})$	0
O_{L+1}	in	$B(O_{L+1})$	$B(O_{L+1})$, $TP(d_{L+1})$, $\alpha_1(O_L)$	…	$B(O_{L+1})$, $TP(d_{L+1})$, $\alpha_{L-1}(O_{2,\dots,L})$	$\alpha_L(O_{1,\dots,L})$
	out	$\alpha_1(O_{L+1})$	$\alpha_2(O_{L,L+1})$	…	$\alpha_L(O_{2,\dots,L+1})$	$Ps(O_{1,\dots,L})$
⋮		⋮	⋮		⋮	⋮

Table 4.1. Pipelined Forward Algorithm, with observation symbol O_k and its delay d_k

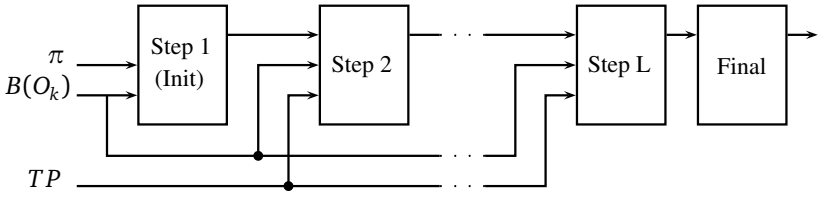

Figure 4.1. Pipelined Forward Algorithm

available and the memory bandwidth is able to provide a data throughput N times higher than in the sequential case.

The computation of the following forward variables α_k, with $k = 2 \dots L$ are similar. To compute the N elements of one step, the Matrix-Vector-Vector multiplication described by equation 4.1 must be performed. Considering first only the Matrix-Vector multiplication, this can be parallelized by decomposing the matrix in to subsets and then use multiple computational units to perform multiplication and/or accumulation operations in parallel on the subsets. The decomposition can be done either by block-striped matrix partitioning (decomposition into subsets of rows or columns) or by checkerboard block matrix partitioning (decomposition in rectangular sets of elements). These partitioning methods are shown in figure **??**. The number of subsets must correspond to the number of available computational units to perform the necessary operations. The choice of decomposition is heavily dependant on the accelerator architecture (e.g. communication between computational units, memory architecture). The resulting vector can then be multiplied element wise by the emission probability vector, which is again the same case as described above. The maximal achievable speedup is a factor of N, assuming that N computational units are available to perform the multiplication and accumulation operation on each subset, N multipliers to compute the final element wise vector-vector multiplication and a memory interface, that can handle a data throughput that is N times higher than in the sequential case.

add figure with different matrix partitioning methods
check maximal speedup in case of checkerboard block partitioning
sources for matrix partitioning methods?

Further parallelization can be done by using a adder tree to accumulate the elements in the matrix-vector multiplication process. Instead of using one adder/accumulator and accumulate the values sequentially, $\frac{N}{2}$ units can be used to add $\frac{N}{2}$ operand pairs in a first step, then consecutively adding resulting pairs until only one value results. This process is visualized in figure **??**. The maximal speedup of this modification can be expressed as $\frac{N}{\log_2(N)}$, assuming that $\frac{N}{2}$ adders are available and the memory interface is able to handle a throughput that is $\frac{N}{2}$ times higher than in the sequential case.

add figure with adder tree

The finalization step of the algorithm consists of calculating the likelihood. This is done by simply accumulating the N elements of the last forward variable α_L. This operation can be parallelized with an adder tree, resulting in a speedup as described above.

The following sections will describe the impact on performance if scaling or the extension of the forward algorithm is implemented. Also the availability of parallelization in both cases will be discussed. Everything will be concluded with an overview of available parallelism and a discussion about the usefulness of each parallelization method in the context of the different algorithm implementations.

4.3 Scaling and Data Representation

Scaling may be applied to prevent that the continuous multiplication of numbers smaller than one (e.g. probabilities) result in zero because of the limited accuracy by digitally representing fractional numbers. Scaling does not influence the order of complexity of the algorithm. By introducing a scaling method as proposed in the reference work, the complexity of calculating one α_k vector goes from N^2 (no scaling) to $N^2 + 2N + 1$ (scaling), which is the same order

$O(N^2)$. However, the introduction of scaling may increase the usage of recourses significantly: In order to scale α_k, the division operation is used to compute the scaling factor. Division is far more complex than multiplication and hence uses more recourses. Additionally, instead of the sequence likelihood (equation 3.8) the sequence log-likelihood (equation 3.11) needs to be computed, with the even more complex log operation.

In order to limit the amount of necessary division operations, it is beneficial to consider the following: Rather than scaling each element of α_k by dividing it by a scaling factor (N divisions), first the inverse of the scaling factor can be computed, which is then multiplied with each element of α_k (one division and N multiplications). Using N multiplication units, this operation can be parallelized.

To compute the log-likelihood, N log and N sum operations are necessary, in comparison to N sum operations for the likelihood. In terms of memory, the log-likelihood is more complex because the scaling coefficients of each α_k are used and need to be stored, while for the likelihood only the last set of forward variables α_L are used. The computation of the log-likelihood can be parallelized by using N units computing the log function and additionally by an adder tree to speed up the accumulation.

Instead of using the proposed scaling method, a simpler scaling may be applied. By analyzing the operands, an average scaling factor can be computed. Using the knowledge, that all the operands are probabilities,

$$\sum_{i=1}^{N} \pi_i = 1, \ \sum_{j=1}^{N} tp_{ij} = 1, \ \sum_{j=1}^{M} b_{ij} = 1 \tag{4.2}$$

and doing the computation of the forward variables,

$$\begin{aligned}
\hat{\alpha}_1 &= \hat{b} \cdot \hat{\pi} = \frac{1}{NM} \\
\hat{\alpha}_2 &= N \cdot \hat{\alpha}_1 \cdot \hat{tp} \cdot \hat{b} = N \cdot \frac{1}{NM} \cdot \frac{1}{N} \cdot \frac{1}{M} = \frac{1}{NM^2} \\
\hat{\alpha}_3 &= N \cdot \hat{\alpha}_2 \cdot \hat{tp} \cdot \hat{b} = N \cdot \frac{1}{NM^2} \cdot \frac{1}{N} \cdot \frac{1}{M} = \frac{1}{NM^3} \\
&\vdots \\
\hat{\alpha}_L &= \frac{1}{NM^L}
\end{aligned} \tag{4.3}$$

it can be computed, that assuming no precision loss at each computational step k, on average a scaling factor of $\frac{1}{M}$ is necessary in each step k. If the intermediate precision of the computational units is high enough to compensate for scaling to much or to few, this method is an easy solution to keep the values in an acceptable range. However, if the precision is not available (eg. if a fixed point data representation is chosen) a fixed scaling factor can cause an overflow (very bad because the result will be wrong) or an underflow (may be acceptable because it is only a loss of precision). In this case, rather than choosing an average scaling factor of $\frac{1}{M}$ it is safer to choose the scaling factor to be equal to the maximal possible scaling factor of all values of a specific event in B (scale $\max\big(B(O_k)\big)$). By doing this, the scaling factor will be to small and if L is big, the forward variables will still approach zero, only slower than without scaling. This is either acceptable because of a high precision, or another scaling factor must be computed to prevent this. The implemented solution will be explained in detail in chapter 5.

Another aspect to consider is the choice of data representation (floating point versus fixed point). This depends on one hand on the necessary precision and on the other hand on the choice of accelerator type. While general purpose hardware such as CPU, GPU and DSP (to some degree) offer an abstraction to make the representation type transparent to the developer, specialized hardware such as FPGA or ASCI offer no such abstraction. For the later devices, floating point operations increase the complexity of the hardware design and the necessary hardware resources considerably. In terms of performance, general purpose devices benefit also from a sparse usage of floating point values. The complexity of the software development however is only marginally or not affected at all by the choice of data representation.

If by choice, scaling is omitted, a fixed point representation will not be possible, due to the rapid convergence towards zero by continuously multiplying probabilities together. This implies, that by omitting scaling to save resources, a floating point representation must be used, which again increases the resource requirements or has a negative impact on performance (or both).

The trade-off between the choice of using scaling or not versus the choice of the precision and the data representation, will be analyzed in more detail in chapter 5, when the technology of the accelerator has been chosen.

4.4 Extension of the Forward Algorithm

The proposed extension uses a transition probability matrix which is not constant. For each arriving observation symbol, the matrix must be recomputed by using the delay (equation 3.1) and the sum of different cumulative distribution functions (equations 3.4 and 3.5). To compute N^2 cumulative distribution functions is very expensive but it only needs to be computed once per dk and can then be stored for later usage. A transition probability matrix can be used for the computation of L forward variables due to the continuous computation of likelihood values (as depicted in figure **??**). This implies, that storage for L such matrices must be available. The computation of the transition probability matrix can be fully parallelized with $R * N^2$ computation units to perform a cumulative distribution function of d_k, where R is the number of different cumulative distribution functions necessary to model the behaviour of the events. The memory interface needs to be able to provide a throughput that is $R * N^2$ higher than in the sequential case (note that each cumulative distribution function takes several parameters as input. Eg. the normal cdf has the two parameters μ and σ). In previous chapters, R was always assumed to be equal to one in order to simplify the problem.

In order to not reduce the throughput of the fully parallelized computation of the forward variables, a small pipeline of two stages must be built, where in the first stage the transition probability matrix is computed and in the second stage the forward variables.

Considering the huge computation power needed to fully parallelize the extension, it may be beneficial to use a very specialized unit (ASIC) just for the computation of the cumulative distribution function.

The degree of necessary parallelization, depending on the choice of architecture will be discussed in the next section.

4.5 Comparison and Scalability

- table presenting an overview of the parallelization options

- discussion on usefulness of each parallelization option

4.6 Choice of Accelerator Type

4.6.1 CPU

- pro
  - fast and easy implementation (availability of /, exp, log, floating points)
  - high precision (double, long double)
  - high frequency (up to 3 GHz)
- contra
  - high power consumption
  - limited parallelization (limited number of cores)
  - large overhead (because of instruction pipeline)
  - fixed architecture (memory, computation units)

4.6.2 GPU

- pro
  - SIMD: a lot of streaming processors for a low price
  - a lot of fast onboard memory
  - high frequency
  - high precision
  - simple implementation (availability of /, exp, log, floating points)
- contra
  - high power consumption
  - overhead for simple instructions (instruction pipeline)
  - fixed architecture (memory, computation units)

4.6.3 FPGA

- pro
  - low power consumption
  - low overhead
  - flexibility
  - optimized floating point representation (small values)
- contra

  - low frequency
  - parallelization is expensive
  - precision is expensive
  - complex implementation

4.6.4 ASIC

- pro
  - very low power consumption
  - no overhead
  - very flexible
  - optimized floating point representation (small values)
- contra
  - very expensive
  - very complex implementation

4.6.5 Conclusion

- target is an embedded system (low power)
- optimize memory hierarchy
- student budget
- -> use FPGA
- only standard forward algorithm
- do not use scaling because of division. Instead use custom FP representation

Chapter 5

Design and Implementation

- parallelization of one of nested for-loop or pipeline the loops
- fully pipelined MACC

To design the accelerator, the top-down approach was applied: the algorithm is broken down into blocks, where each of them is broken down further until the basic functional blocs of the FPGA can be used for the implementation. The implementation follows then the bottom-up approach where each sub-block is implemented and tested. Completed blocks are grouped together to bigger blocks until finally there is only one big block remaining, describing the complete algorithm.

5.1 Precision

Modern FPGAs contain hardware blocks (DSP slices) that are heavily optimized for multiply-accumulate operations as they are often used for DSP applications. These devices only operate on integer values. However, the forward algorithm requires to multiply and accumulate probabilities, i.e. fractional numbers. To being able to use the DSP slices of the FPGA, some hardware must be built around such a slice in order to get a hardware block that can handle the multiplication and accumulation of probabilities. To do this, the choice of data representation must be made (floating point vs fixed point). First the assumption that all operations must be done with floating point numbers is discussed.

the following points need to be explained in more detail

Floating Point Facts: In order to multiply two floating point numbers, the mantissas of both numbers are multiplied and the exponents are added (the sign can be ignored, as probabilities are always positive). For the multiplication of the mantissas the DSP slices can be used. In parallel to this operation, an external adder can add up the exponents. Now the tricky part: to being able to add floating point numbers the exponents of the numbers must be equal. To achieve that, the difference of the two exponents is calculated and then the mantissa of the number with the lower exponent must be shifted by this difference (and possibly rounded/truncated). This process is called normalizing. Then the mantissas can be added. Finally the resulting value needs to be normalized again.

Scaling: By using floating points, scaling becomes superfluous because the exponent allows to represent very small numbers (not respecting IEEE representations).

Truncation: after the multiply accumulate operation the resulting mantissa of 48 bits must be truncated to 25 bits. To achieve better results, a rounding operation can be applied.

Fixed Point Facts: before each multiplication, the operands need to be reduced from 48 to 18 resp 25 bits. This must be done by either truncating/rounding the final value or by scaling or by doing both.

Scaling: The proposed scaling method is not usable in this implementation because of the division operation. Instead, a scaling in base of 2 should be used (shift): In every clock cycle a new value is added to the previous one. The masked result can be compared to a bit stream of zeros. A match directly gives the amount of leading zeros (using the number of times the mask has been shifted). If there is no match, shift the mask and compare in the next cycle. This operation is done with every alpha, while the lowest value of leading zeros is kept. Using this method, in most cases at the end of adding up all the values, the least number of leading zeros of the N alphas will be known. If in the worst case after the addition of the last alpha-component there is a non-match, the pipeline must be stalled and the right leading zeros number must be found by shifting the mask further to the left. To do the masked comparison, the pattern comparing unit of the DSP-slice of the FPGA can be used. The stored values π, B and TP can be preprocessed and scaled, in order to reduce the number of minimal leading zeros to zero. These scaling factors will then be used to recompute the real sequence likelihood.

Truncation: a simple solution is to chop off the leading zeros (as counted) and truncate the value by only using the following 25 bits after the last leading zero. A more precise method would be to use rounding.

5.2 Data Storage Management

the following points need to be explained in more detail

Facts: in each kth step $N^2 * TP$ values and $N * B$ values are necessary. In case of the parallel version, each clock cycle $N * TP$ and one B value must be made available. In case of the serial version one TP or B vale must be made available. By reading directly from the RAM, 16 bits can be read with a bus frequency of 104MHz. Running the pipeline at 52MHz, the necessary data can be provided at each clock cycle in case of the serial implementation. If the parallel implementation should be used, an internal memory must be built.

- real-time (time constraints on every Ps) vs on-line (use buffer to optimize throughput)
- memory hierarchy: at startup copy from flash to ram, then use pipeline to preload values from ram into registers.

5.3 Initialization

Figure 5.1 shows the necessary operation to compute every i-th component of the first forward variable α_1 in the initialization step. The N components of α_1 can be computed one by one when only one such structure is implemented in hardware. Assuming a fully pipelineable multiplier, one component of α_1 appears in the output register at every cycle (with a latency of S cycles, where S is the number of pipeline stages in the multiplier). To compute all N components of α_1 with this structure, $N + S$ cycles are necessary. Alternatively the complete initialization can be fully parallelized if the structure 5.1 is replicated N times. In this case, all N components of α_1

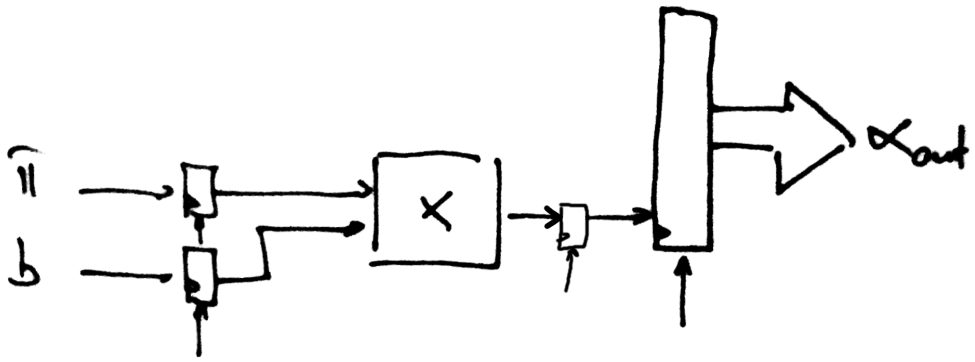

Figure 5.1. Initialisation step with one MACC

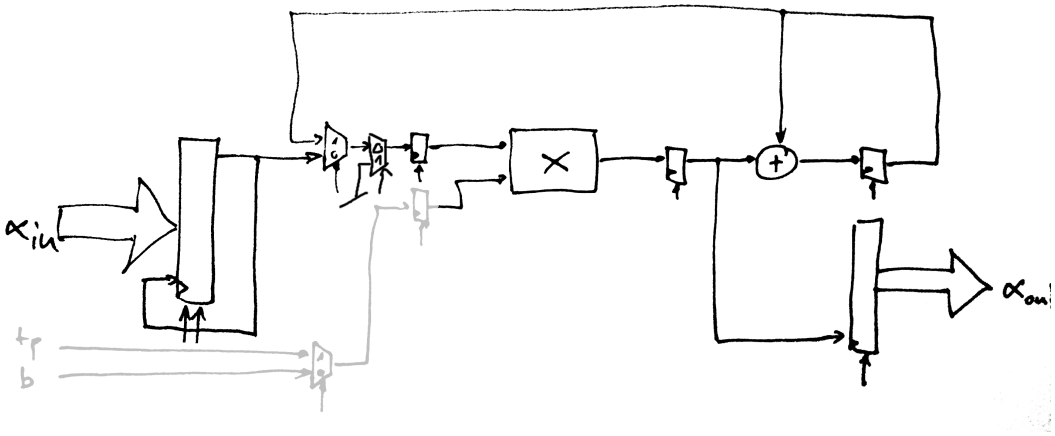

Figure 5.2. k-th step with one MACC unit

appear at the same time, after S cycles in the output registers. If such a heavy parallelization is useful will be analyzed after all stages have been described.

5.4 k-th Forward Variable

better title?

- one pipelined MACC for the computation of all elements
- N pipelined MACC, each computing one α_k
- use optimized Matrix-Vector-Vector multiplication $\alpha_{k+1} = TP * \alpha_k * B(o_k)$ [10, 26]

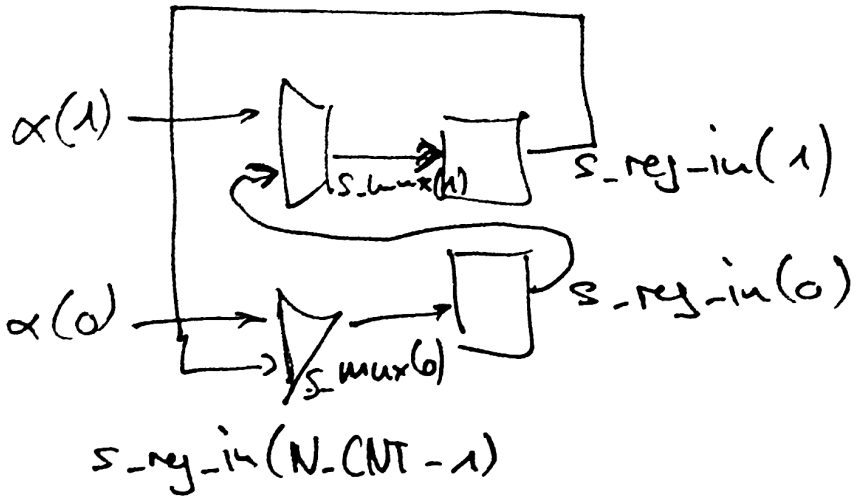

Figure 5.3. Example of input shift register with N=2

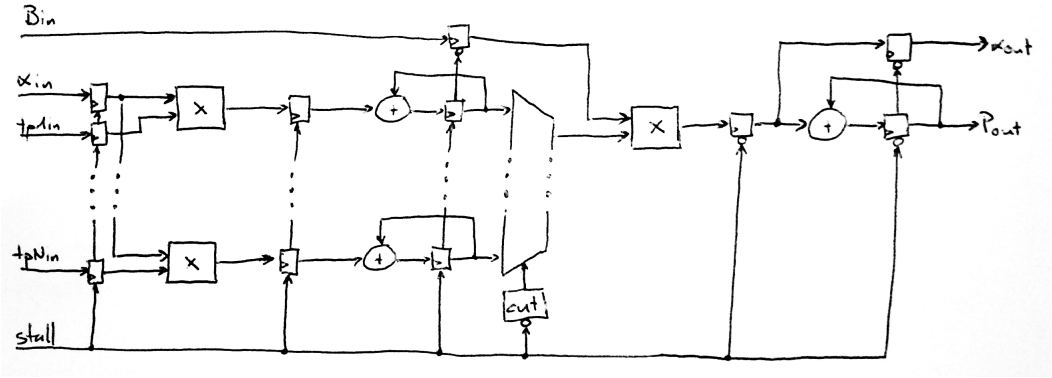

Figure 5.4. k-th step with $N+1$ MACC units and integrated computation of P (which is only needed at the last step)

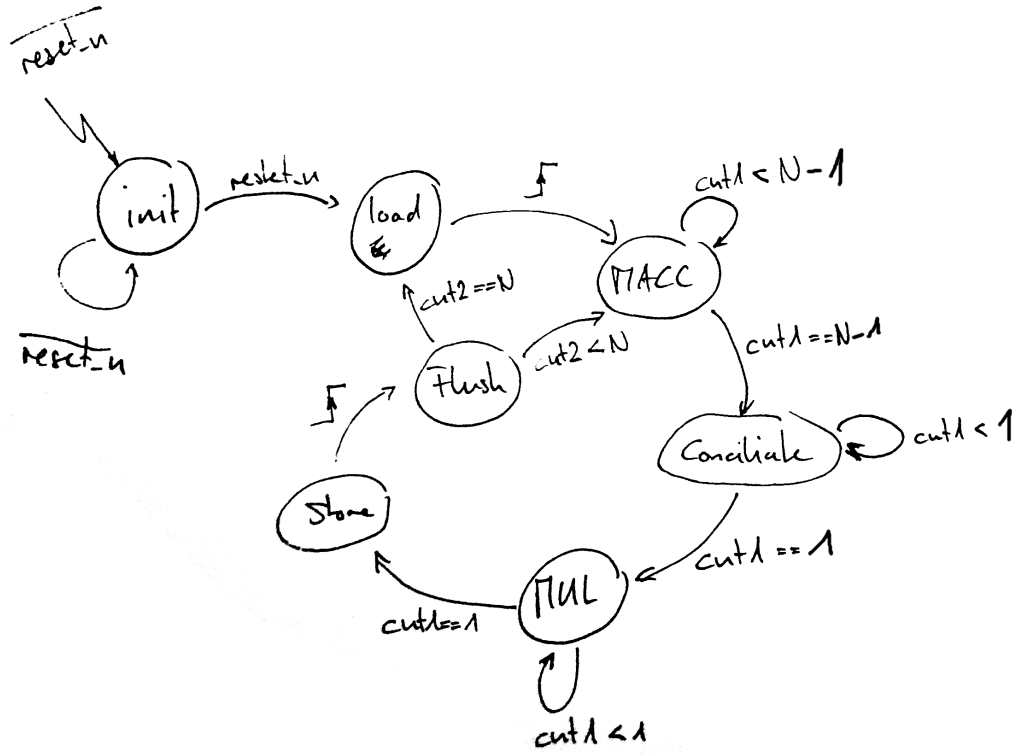

Figure 5.5. Controller of serial implementation

	INIT	SELECT	MACC	CONCILIATE	MUL	STORE	FLUSH
shift_alpha_in	0	0	1	0	0	0	0
shift_alpha_out	0	0	0	0	0	1	0
conciliate	0	0	0	1	0	0	0
enable_init	0	0	0	0	1	0	0
enable_step	0	0	1	1	1	0	0
enable_final	0	1	0	0	0	0	0
flush	0	0	0	0	0	0	1

Table 5.1. Control signals

5.5 Serial Controller

in table 5.1 the signals flush_Ps and load_out are only set in the first iteration. Add a footnote?

5.6 Balancing Pipeline Stages

5.7 Practical Notes

- generic design (change N, L and bit widths in param_pkg)
- if bit widths of op1 is changed, fifo_512x25 must be regenerated

Chapter 6

Testing and Verification

6.1 Device

- Nexys4 board with Artix-7 FPGA
- limited recourses -> proof of concept
- bord hardware for testing

6.2 Relation to Proposed Algorithm

6.2.1 Log Standard

6.2.2 Metrics

Chapter 7

Results

7.1 Speedup

7.2 Accuracy

Chapter 8

Conclusion

8.1 Achievements

8.2 Future Work

Appendix A

Some material

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