# Symbol definitions

- $\cdot$  N = the number of input features,
- $\cdot$  M = the number of hidden neurons (in our case it is always 40),
- $\cdot$  C = the number of output neurons/ number of classes
- $\cdot$  S be the number of samples in the dataset,
- $\cdot$   $x_i$  be the ith input feature,
- $\cdot$   $x_i$  be the  $\mathbf{i}^{\mathit{th}}$  input feature,
- $\cdot$   $D^i$  be the i-th sample of the dataset,
- ·  $D^i_j$  be the value the j\_th\_ input feature takes on the i\_th\_ sample of the dataset,
- $\cdot$   $h_i$  be the i\_th\_ hidden neuron, also used to denote it's output value before binarization,
- $\cdot$   $s_i$  be the i\_th\_ hidden neuron's output after binarization, so  $s_i = h_i \geq 0$  ,
- $\cdot$   $y_i$  be the i\_th output neuron, also used to denote it's output value,
- $\cdot$  W1 = the weight matrix of the first layer,
- $\cdot$  W2 = the weight matrix of the second layer,

Rows represent neurons and columns represent input activations, so  $W1_{i,j}$  is the weight of the first layer that corresponds to the connection between the input feature  $x_i$  and the neuron  $h_i$ .

# Combinatorial fully connected implementations

Two initial approaches for implementing the fully connected BNNs in a fully combinatorial single-cycle datapath are compared. Only the first layer differs between them, the second layer stays unchanged.

## Positive-Negative Sum

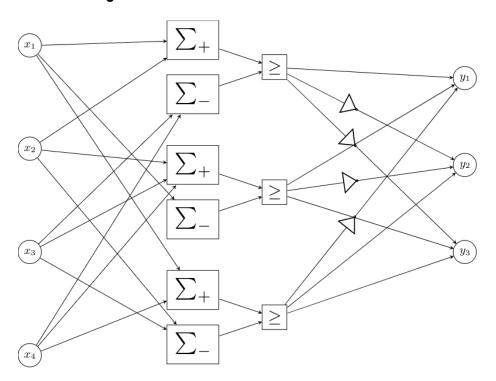


Figure 1: Implementation with positive and negative sums split

For each neuron in the first layer two sums are calculated.  $\Sigma_i^+$  is the sum of the input features for which the connection with the i\_th\_hidden neuron has a positive weight , whereas  $\Sigma_i^-$  the sum of those that have a negative weight associated. The two sums are then compared and if the positive sum is greater than or equal to the negative the output of the neuron is 1, otherwise 0.

$$\Sigma_i^+ = \sum_{j=0}^{N-1} x_j [W1_{i,j} > 0]$$

$$\Sigma_i^- = \sum_{j=0}^{N-1} x_j [W1_{i,j} < 0]$$
 
$$h_i = \Sigma_i^+ \ge \Sigma_i^-$$

Sample code snippet:

The reasoning behind splitting the sums is that keeping the operations to only using unsigned positive numbers and only using addition and not subtraction means simpler operations are required, and that may lead to a smaller footprint.

For each neuron of the output layer it's value is calculated by summing the output of hidden neurons. The binary output of the hidden neuron  $s_j$  is added as—is to the sum of the output neuron  $y_i$  in the case that the weight of their connection  $W2_{i,j}$  is positive and it's binary inverse is added to the sum if  $W2_{i,j}$  is negative. This is equivalent to the sum of the xnor between the output vector of the hidden layer and the weight vector of the output neuron.

$$y_i = \sum_{j=0}^{M-1} \begin{cases} s_j, & \text{if } W2_{i,j} > 0 \\ \neg s_j, & \text{if } W2_{i,j} < 0 \end{cases}$$

Code sample:

## Signed sum

In this version a single sum is calculated for each neuron. If the connection between input feature  $x_j$  and hidden neuron  $h_i$  has weight  $W1_{i,j}=1$  it is added to the sum, otherwise it is subtracted from it. Basically adding the feature multiplied by either 1 or -1 is hard-coded as the resulting addition or subtraction correspondingly. The result is then compared to zero to give the binarized output of the neuron. Since the result is a signed number, this just means taking the sign bit.

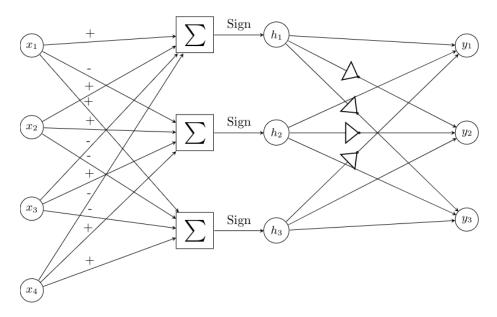


Figure 2: Implementation a single sum per neuron

$$h_i = \sum_{j=0}^{N-1} \begin{cases} +x_j, & \text{if } W1_{i,j} > 0 \\ -x_j, & \text{if } W1_{i,j} < 0 \end{cases}$$

#### Code sample:

The second layer's implementation is not changed from how it is described above.

#### **Discussion**

My prior expectation was that splitting the features into two sums to avoid subtractions would lead to better results than keeping all the operations for a neuron to a single expression by the reasoning summarised previously. In fact it turns out that using a single sum has area and power requirements 20–30% lower than using two.

My explanation for this is that keeping terms in separate expressions prevents the compiler from effectively locating and reducing shared

subexpressions during synthesis. For example, if a neuron's expression contains  $+x_5+x_6-x_7$  and a different neuron contains  $-x_5+x_6+x_7$  then the result of  $x_5-x_7$  can be used for both neurons, but if  $x_5$  and  $x_7$  are not in the same expression, as they would not be in the positive-negative sum implementation, this arithmetic optimization is not used by the compiler. Additionally the two sums need comparators to produce the binarized output of the neuron, whereas in the case the signed sum this corresponds to the sign bit of the sum which means no additional hardware.

## Minimum range bit-width reduction

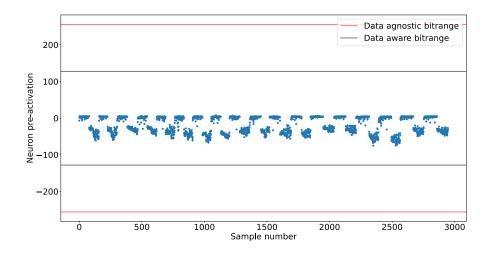


Figure 3: title here

The reasoning goes that if the bitwidth that is demanded for the total sum of the features is reduced, the bitwidth that partial sums it depends on require lower on the adder graph is also reduced. As a consequence, adders need to accommodate less bits and less logic ought to be implemented for them.

At least in theory, the minimal circuit to implement the calculations of the sums of the first layer with reduced widths for the results should be strictly equal or smaller than the one with full widths. This is because given a circuit that implements the full width calculations, the reduced width results can be taken by selecting the bitrange of that width from the least significant bits of the full width result. This is simple wire selection and does not require any additional hardware, therefore reducing neuron widths can never require additional logic.

So far in the first layer the bitwidth of the total sum  $h_i$  of the neuron is set to be large enough to fit any value that may come up as the result of M additions and subtractions of 4-bit unsigned numbers. The assumption is that this range is significantly wider than the range of values the neuron actually takes during evaluation of typical samples. This would mean the bitwidth can be lowered without errors due to overflows or underflows coming up in actual use of the design, and this lowering would improve performance.

To test this the total sum of each neuron  $h_i$  is calculated for each sample in the dataset. I get the minimum and maximum of these values. Since all values for the total sum to take are contained in the range between those two, the arithmetic operations need not accommodate any range larger than that. Let  $H_j^i$  be the value of  $h_i$  when evaluating the j\_th\_ sample of the dataset, and  $wh_i$  be the bitwidth of the i\_th\_ hidden neuron.

$$\begin{split} h_{imax} &= \max_{j=0}^{S-1} H_j^i \\ h_{imin} &= \min_{j=0}^{S-1} H_j^i \\ wh_i &= \lceil \log_2(\max(h_{imax}, |h_{imin}| - 1)) \rceil + 1 \end{split}$$

#### **Discussion**

The results are negligible, in the 1-3% range, and in the case of pendigits they even deteriorate a bit. This deterioration should not be possible in theory if the synthesised circuits are optimal implementations of their description. This is at least evidence that the negligible results on the other datasets can be better if I can get them into a form the compiler can work better with, though I still think the main problem is with the approach itself. It seems that the truncation goes against best practices and blocks the datapath extraction process for some neurons, so certain optimizations do not get applied to them and some would be common resources do not get shared. I have not found a method to work around this limitation at this point.

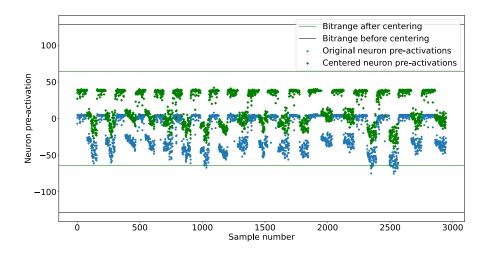


Figure 4: title here

# Range centering

## Rationale

Unfortunately I make a mistake when initialy evaluating the results of limiting the bitwidth of neurons in the previous part. The blunder is accidentaly comparing the results with the positive-negative sums full width circuit instead of the single signed sum version that the reduced width circuits are based on. This causes me to falsely believe that reducing the bitwidths of computations is much more effective than in reality. Based on this misanderstanding I pursue finding ways to further reduce the ranges of values each neuron's total has to support. After realising the mistaken assumption I don't think those efforts were justified. The first of these is the attempt to "center" the range of values so the maximum and minimum values are at an equal distance from zero.

The range of values a neuron of the first layer can take can be significantly unbalanced. What this means is that if for example the feature the hidden neuron tracks occurs infrequently, it will equally infrequently take positive values, and this suggests that the negative values it takes can get much large in an absolute sense than the positive ones get a chance to. If the absolute minimum or maximum value is multiple times larger than the other one, let's say  $h_{imax}=10h_{imin}$ , then the range of values the bitwidth of the neuron must support is up to twice as large as the one of the equivalent range balanced so it's maximum value is as far from zero as it's minimum.

Therefore by subtracting the value that lies at the middle of the range from the result, the bitwidth of the neuron's sum can be further reduced. That requires an additional constant subtraction operation for the calculation of the sum and an additional comparison operation, since the result needs to be compared to the same constant for binarization unlike being compared to zero that needs no additional hardware. However, the hope is that if the width of enough intermediate results of the adder graph and thus the number of full adders is reduced as a result it will be enough to more than make up for the cost.

Example: if the highest value the total of the neuron takes is 300 and the lowest is -100, we need a 10 bit signed integer to fit all values. If we subtract their average(100) the values will be in the range -200 to 200, so they fit in a 9 bit signed integer.

$$\begin{split} h_{imax} &= \max_{j=0}^{S-1} H_j^i \\ h_{imin} &= \min_{j=0}^{S-1} H_j^i \\ h_{imid} &= \lceil \frac{h_{imax} + h_{imin}}{2} \rceil \\ h_i' &= h_i - h_{imid} \\ wh_i' &= \lceil \log_2(\lceil \frac{h_{imax} - h_{imin}}{2} \rceil) \rceil + 1 \end{split}$$

The additional operations are only included in the design for neurons that this method decreases the bitwidth compared the one calculated from the "unbalanced" range. For the rest there is no reason to incur the overhead for no benefit so they are declared the same as they are using minimum range bit-width reduction.

### **Discussion**

The results show that the hardware requirements of the additional operations were not covered by the reduced bitwidths and area and power demands considerably increased. Given the actual results of how much reducing bitwidths helps from above this is not surprising. In fact it seems counter-intuitive that for the winered dataset's model it lead to a 6% improvement.

Notably, this was the model that had the most benefit from the previous bitwidth reduction as well. I estimate this model's operations in the first layer lend themslves less to arithmetic optimizations compared

to the rest, and thus hindering that optimization process is not as rough a sacrifice.

It also seems probable that subtracting a simpler constant than the actual value at the middle of the range  $h_{imid}$ , for example the nearest power of two, would lessen the computational burden of the additional subtraction and comparison, but not enough to be worth implementing.

# Naively reducing bitwidths of intermediate results

#### Rationale

Given the eventual goal of applying approximate computation techniques to the adder graph of the designs a problem, mentioned previously, comes up. If the approximation, whatever it may be, gets applied separately to each neuron's sum, almost certainly blocks the datapath extraction process from performing arithmetic optimizations such as reducing and sharing common subexpressions across neurons. The result is M separate approximate adder trees. Even given that the logic reduction gained from approximate additions for each adder tree is more than enough to offset the lost benefit of intermediate result sharing, that may be an unnecessary concession.

To estimate how large the negative effect of an approximation technique not taking cross-neuron sharing into consideration could be, I reduce the bitwidths of intermediate results of the sum of each neuron. Even though this would reasonably help for a single neuron, I expect it will cause resource sharing to break. Given how large the negative effect is I can check if this is a problem than ought to be fixed before approximation can confidently be applied.

## Implementation

The cumulative sum along the input features multiplied by the weight of their connection with the neuron i is calculated for each hidden neuron and for each sample of the dataset. The maximum and minimum values over all samples at each step of the cumulative sum for a given neuron is then calculated. In a similar fashion to the method described above for reducing the bitwidth of the total result of the neuron's operations, the operations are written sequentially with the result of each having it's bitwidth set based on the range of values for the equivalent step of the sum for all of the dataset.

Let  $h_{i,j}$  denote the result of the pre-activation value of the i-th

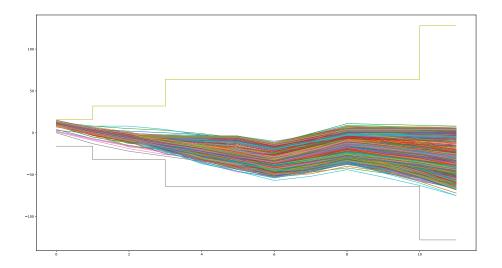


Figure 5: The intermediate sums of the sequential calculation of hidden neuron 28 for all of the Har dataset and the bit range needed to support each step

hidden neuron only taking into account the input features  $x_0$  to  $x_j$ , or equivalently the value of  $h_i$  if  $x_{j+1}$  to  $x_{N-1}$  are masked to zero.

$$\begin{split} h_{i,j} &= \sum_{k=0}^j x_k W \mathbf{1}_{i,k} \\ hmax_{i,j} &= \max_{l=0}^{S-1} \sum_{k=0}^j D_k^l W \mathbf{1}_{i,k} \\ hmin_{i,j} &= \min_{l=0}^{S-1} \sum_{k=0}^j D_k^l W \mathbf{1}_{i,k} \\ wh_{i,j} &= \lceil \log_2(\max(hmax_{i,j},|hmin_{i,j}|-1)) \rceil + 1 \end{split}$$

Sometimes due to the order of additions and subtractions the width needed at a later step is less than the one of an earlier step. This is because every sample for which there would be an overflow in the earlier step with the smaller width would at some following feature underflow back in the range it supports. This has been taken into account. If a width of a subsequent operation's result is smaller, the bitwidth of the previous addition/subtraction is simply set to that smaller value.

$$wh_{i,j}' = \min_{k=j}^{N-1} wh_{i,j}$$

Consecutive operations that have the same result bitwidth are grouped together and expressed in verilog as a single sum. I have not confirmed if this does in fact affect the result of synthesis at all but it seems to conform closer to the recommendations of the best practices guide.

## **Discussion**

The results were positive for two of the models with the smallest count of input features N, which means that this method performed better than the initial expectation. However, the optimization loss from losing shared operations shows clear scaling with the number N of input features. With more elements to sum, more common subexpressions to optimise ought to come up, so this is keeping with expectations.

At the network with the largest N, the one belonging to gasId, which has 128 sensor features, it has gotten bad enough to almost double the area and power requirements. This shows that the issue is indeed considerable when there is more than a handful of inputs, and ways to work around it shall be searched for.