



# VLSI Implementation for DNA Sequencing

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# Outline

- Motivation
- Overview
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- Hardware Architecture
  - Processing Grid
  - Path Tracker
- Validation
- Synthesis
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- Place and Route
- Future Work

# Smith Waterman Algorithm

- Local Alignment DNA Match/Mismatch
- Determine Best possible Match from genome database
- Locate exact position of insertion/deletion/mutation
- Most accurate Bioinformatics algorithm since 1981, but slowest too...

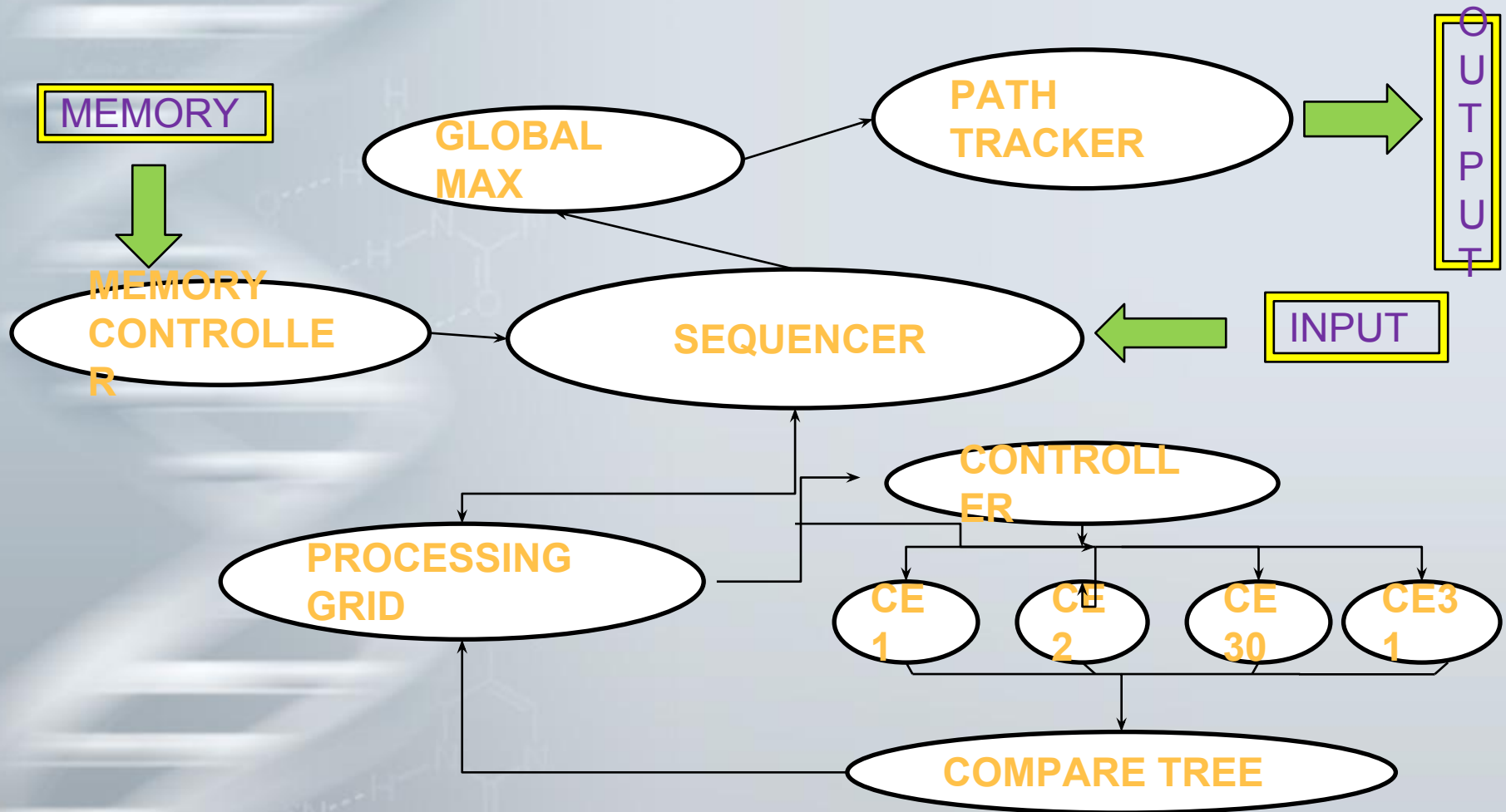
**Demo**

# Math behind...

$$H(i,0) = 0, 0 \leq i \leq m \quad 0$$
$$H(i,j) = \max \left\{ \begin{array}{ll} H(i-1, j-1) + w(a_i, b_j) & \text{Match/Mismatch} \\ H(i-1, j) + w(a_i, -) & \text{Deletion} \\ H(i, j-1) + w(-, b_j) & \text{Insertion} \end{array} \right\}, 1 \leq i \leq m, 1 \leq j \leq n$$

- $a, b$  = Input Sequences (Query + Database)
- $m = \text{length}(a)$
- $n = \text{length}(b)$  ( $m=n$  here)
- $H(i,j)$  - is the maximum Similarity-Score between a suffix of  $a[1...i]$  and a suffix of  $b[1...j]$
- '-' is the gap-scoring scheme
- A, T, C, G sequence elements represented by 00,01,10,11

# Hardware Control Flow



# Verilog Code

## Memory

- Register files
- Latency with 8 bit communication

## Processing Grid

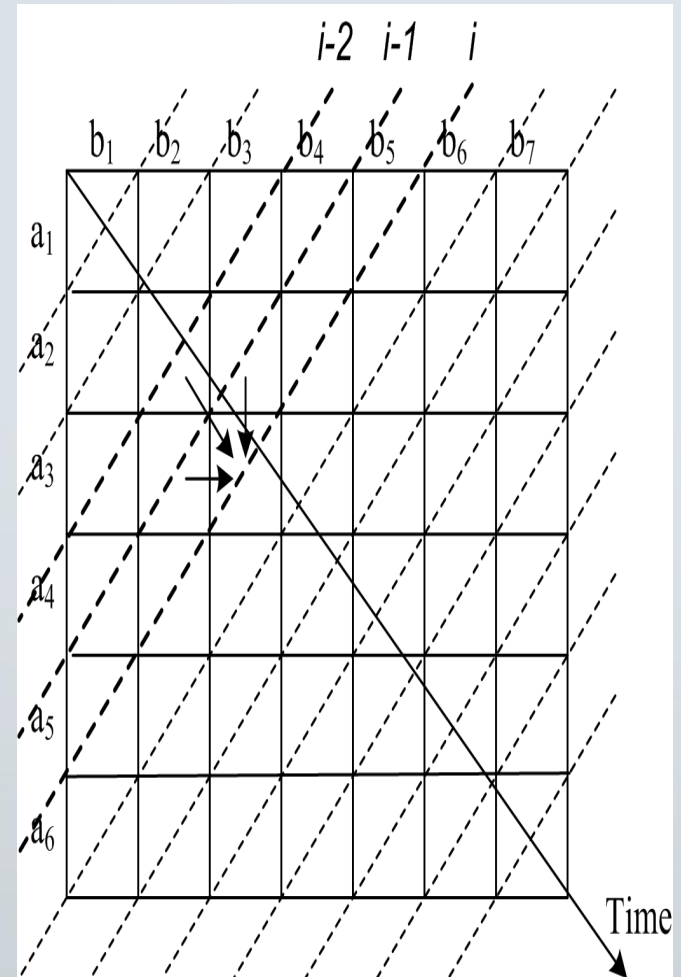
- Diagonal parallelism
- Emphasis on Hardware reuse
- Parallelization and Streaming Techniques
- Optimization of matrix non-storage: mimic FIFO

## Path Tracker

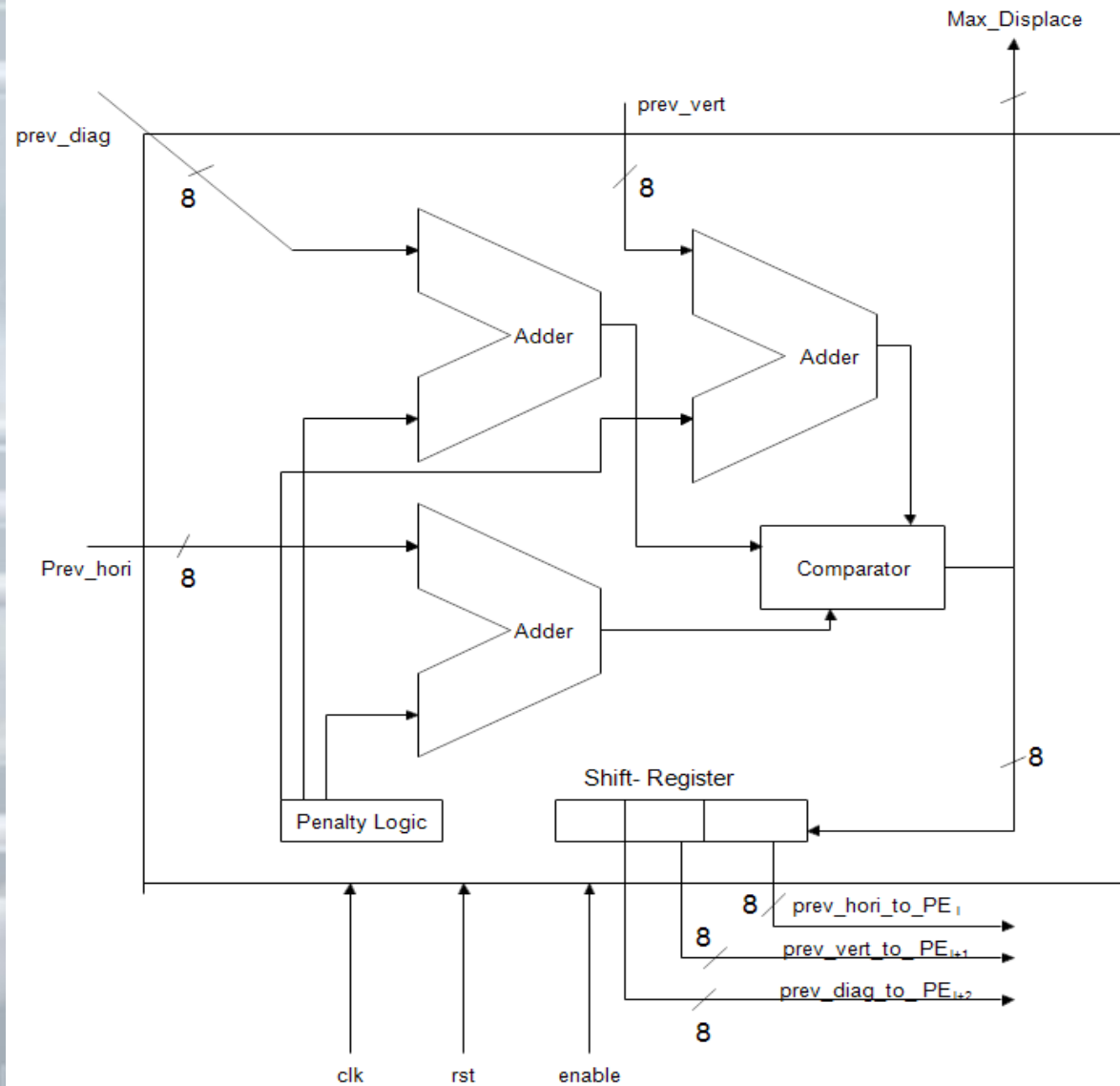
- Computes Matrix for global Max
- Stores H-matrix & Direction of Traversal
- Tracks back path

## Output

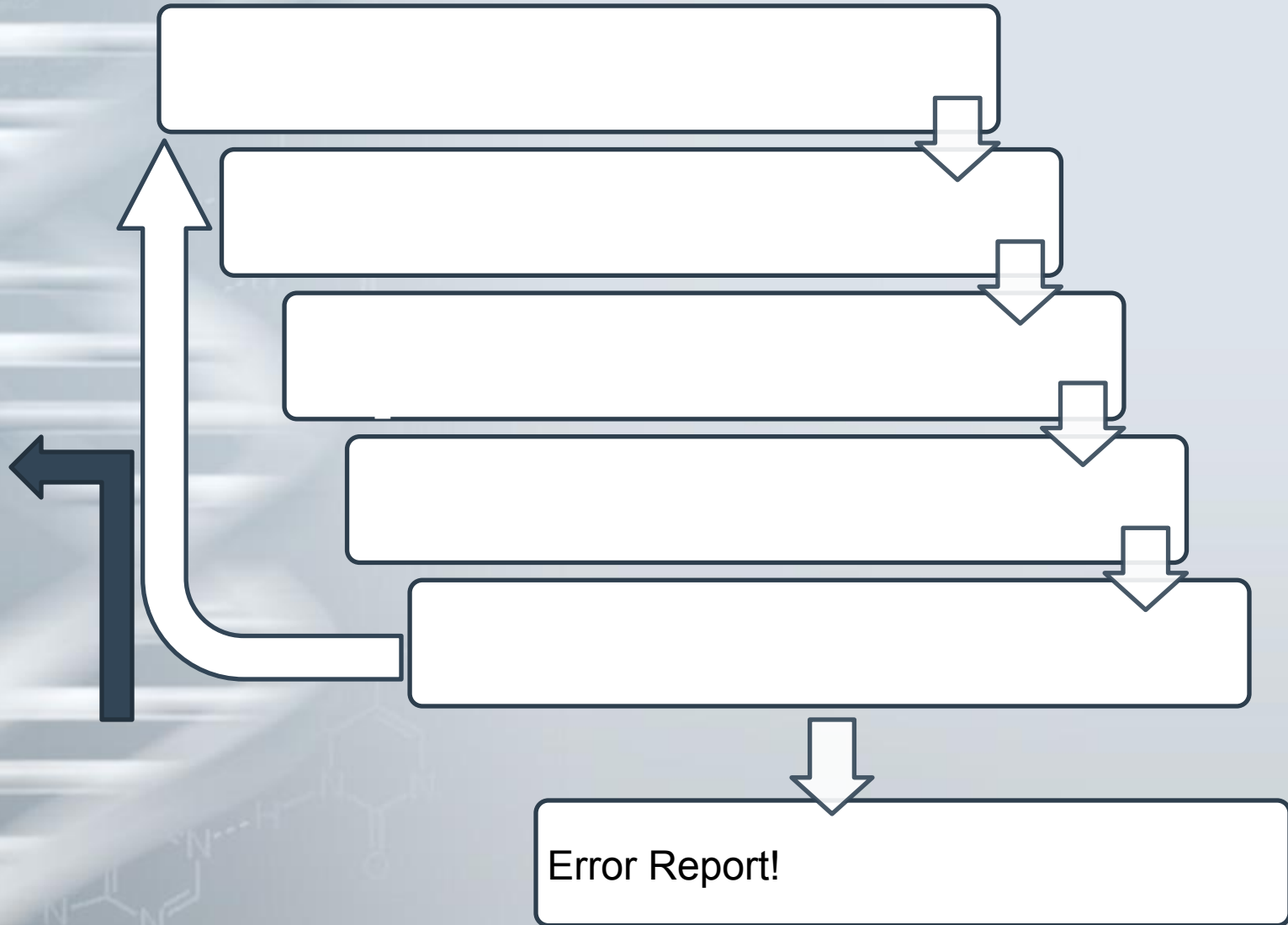
- A 192bit + 192bit mutations.
- Serialized to 8 bit output
- A done\_assert signal.



# Compute Element

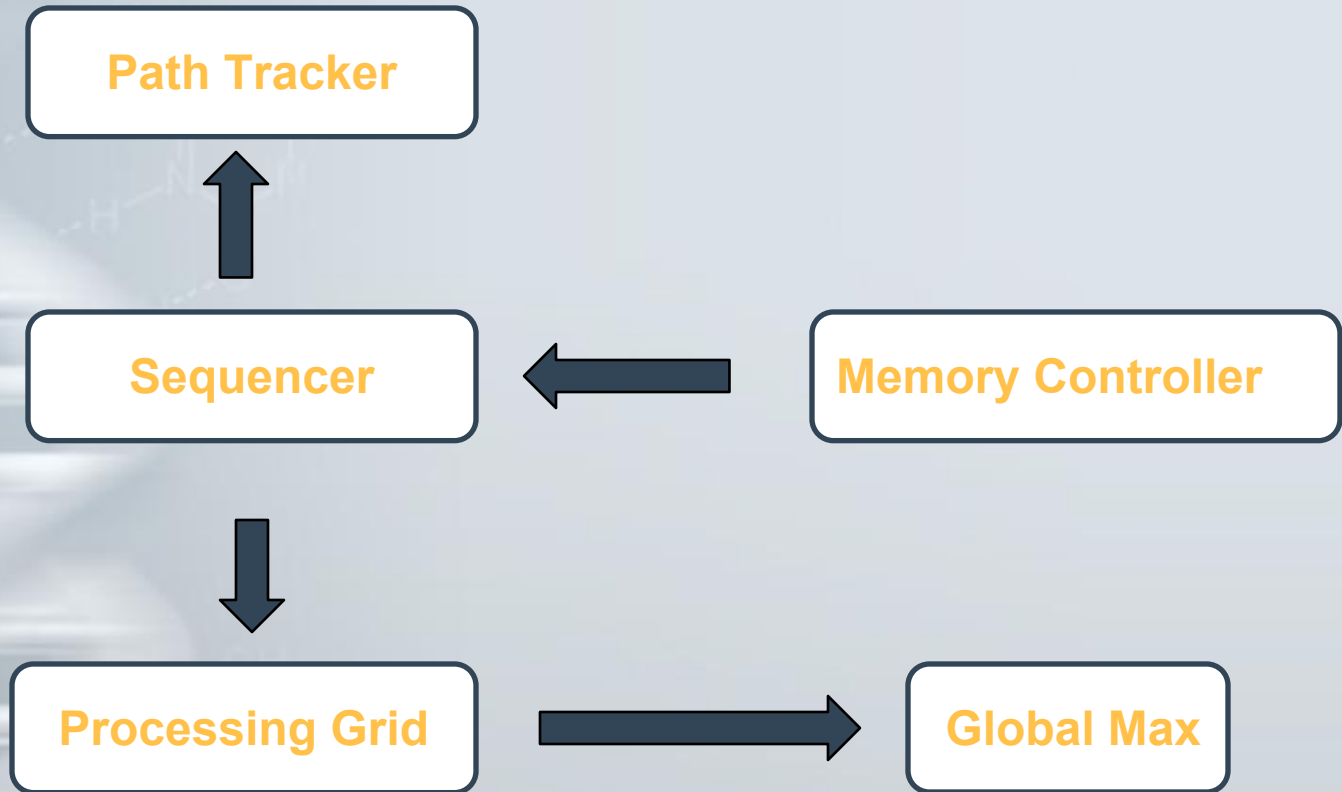


# Validation of Design

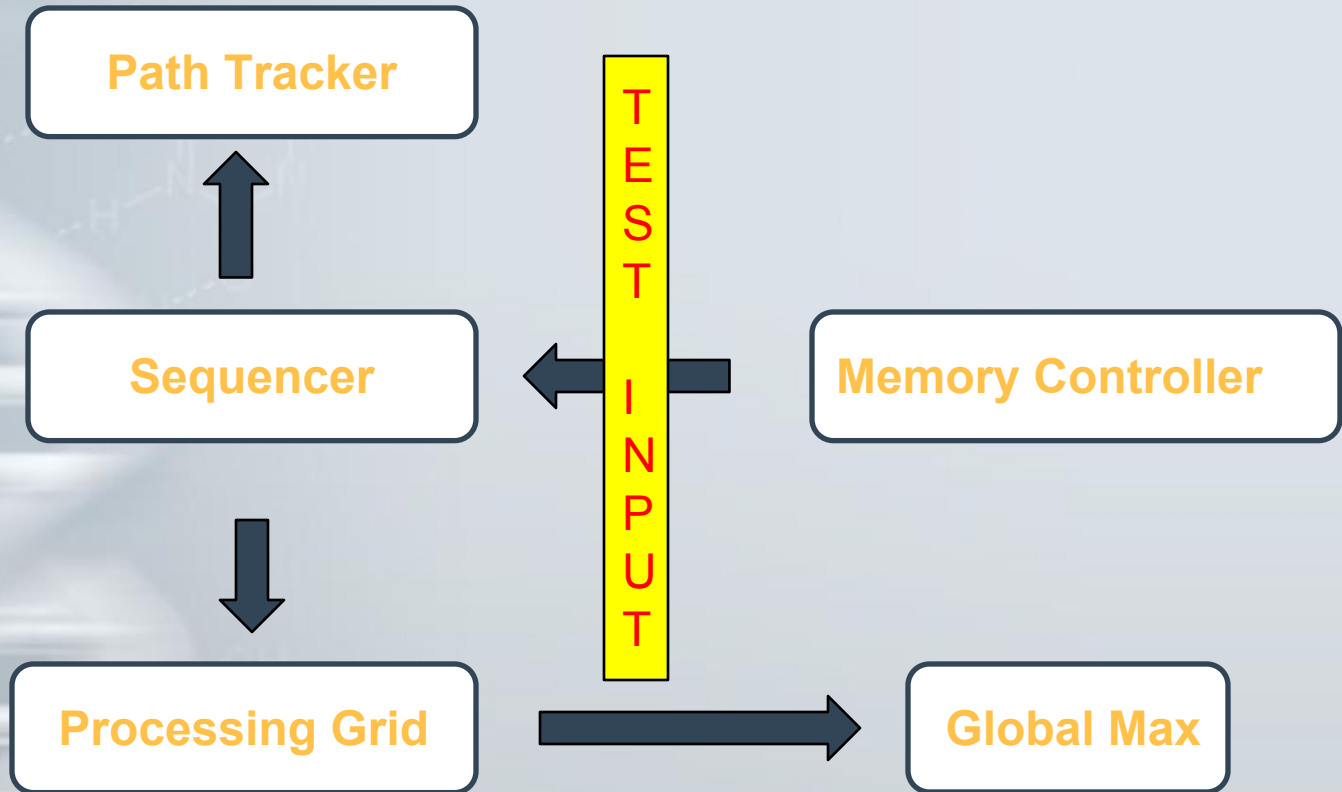




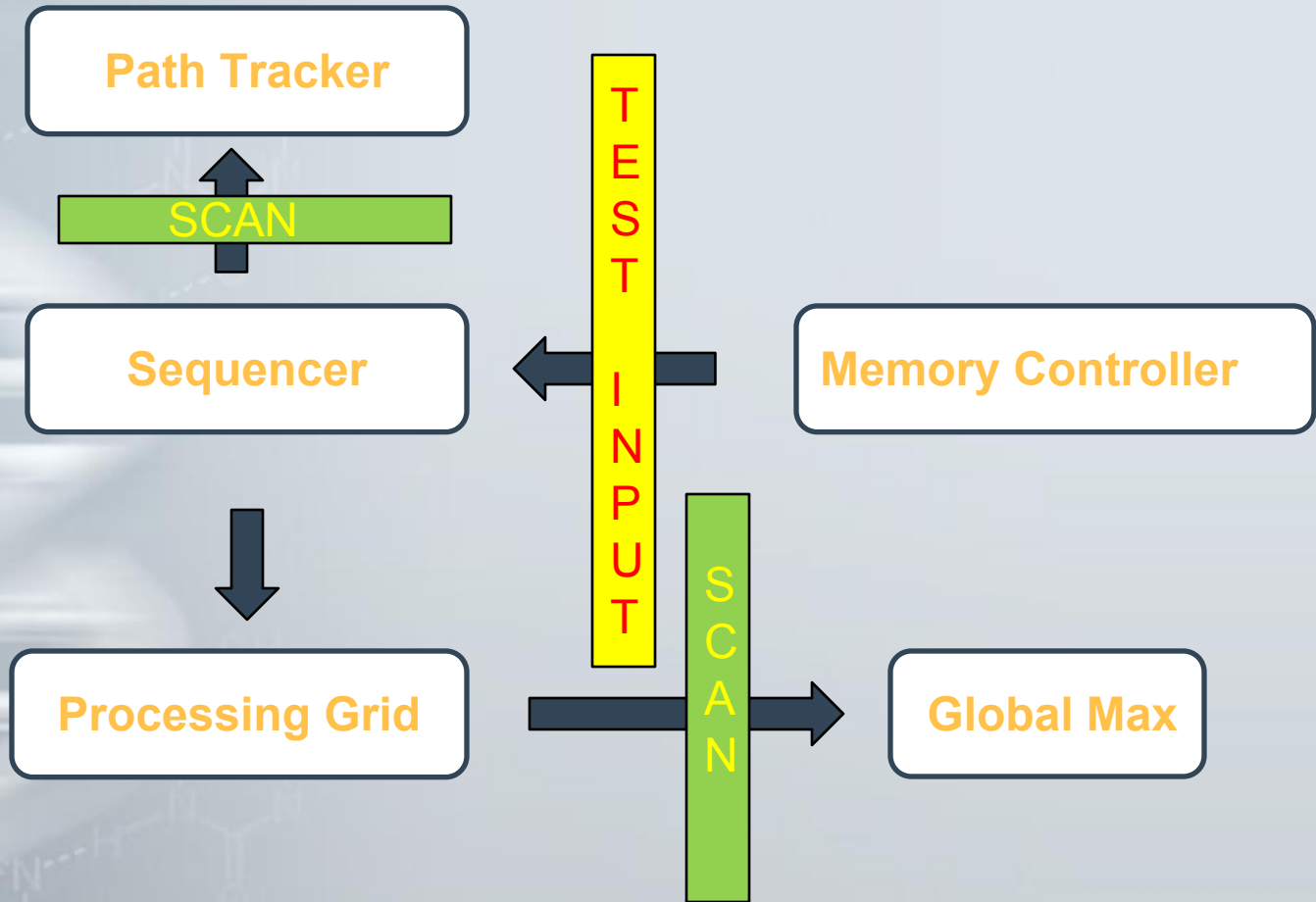
# Validation



# Validation



# Validation



# Test cases

- Random Cases Generator

- Corner cases

- Perfect match
- Perfect mismatch
- zig-zag patterns
- All zeroes

- “Grand catch”

ambiguous case-> shift by one

AAAAAAAAA ⇔ GAAAAAAAA

Results: 1) Insert:     -AAAAAAAA ⇔ GAAAAAAAA

2) Delete:     AAAAAAAAA ⇔ AAAAAA-

3) Mismatch: -AAAAAAAA ⇔ -AAAAAAAA

# Synthesis

- Synthesized phy\_top :
  - Wraps Pads, template
  - Instantiating sequencer: Top module
- Included Pad Libraries
- Synthesized for 333 MHz.
- Set\_dont\_touch on Vdd, Vss instances (for non-removal of nets)
- Minor Internal errors' debug.
- Less Clock gating due to high activity factor.

# Synthesis Summary

Clock Frequency	333 MHz
Negative Slack	None
Throughput	~9.8 Million QPS
Voltage	0.9 V
Dynamic Power	~373 mW
Leakage Power	~ 0.8 mW
I/O Pins	26

## Hardware vs. Software

Sequential version: Throughput = 0.14 Million QPS

Pthread version : Throughput = 1.8 Million QPS

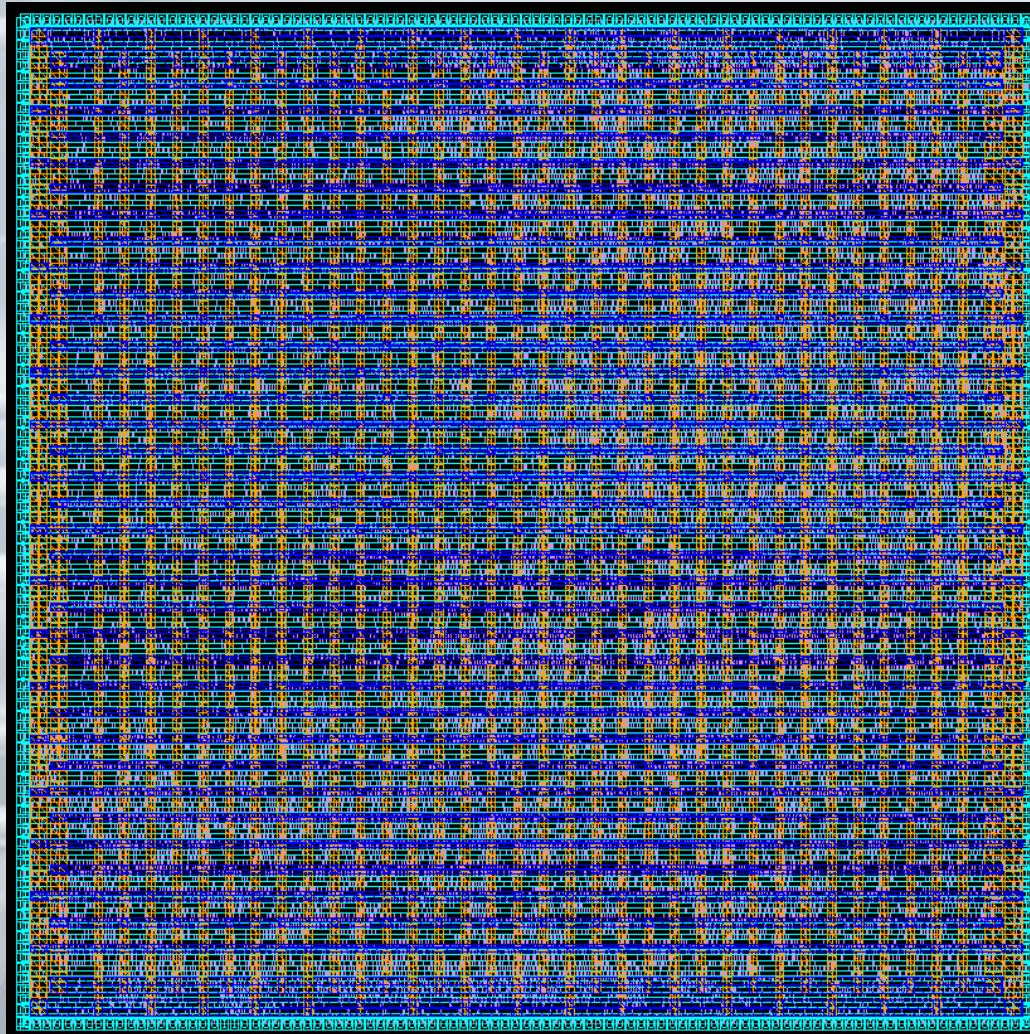
Hence, **Hardware at least 5X faster than parallelized code.**

# Place and Route

- Phy\_top netlist placed and routed.
- Tie Cells included to join Vdd and Vss nets.
- Preroute VDD, VSS to deliver power to pads.
- Set\_pad\_physical constraints and place pads
- Reduced core\_utilization to 0.5.
- Sign off
  - Filler cells
  - Antenna fixing



# P&R of Base Design (without Memory and Pads)

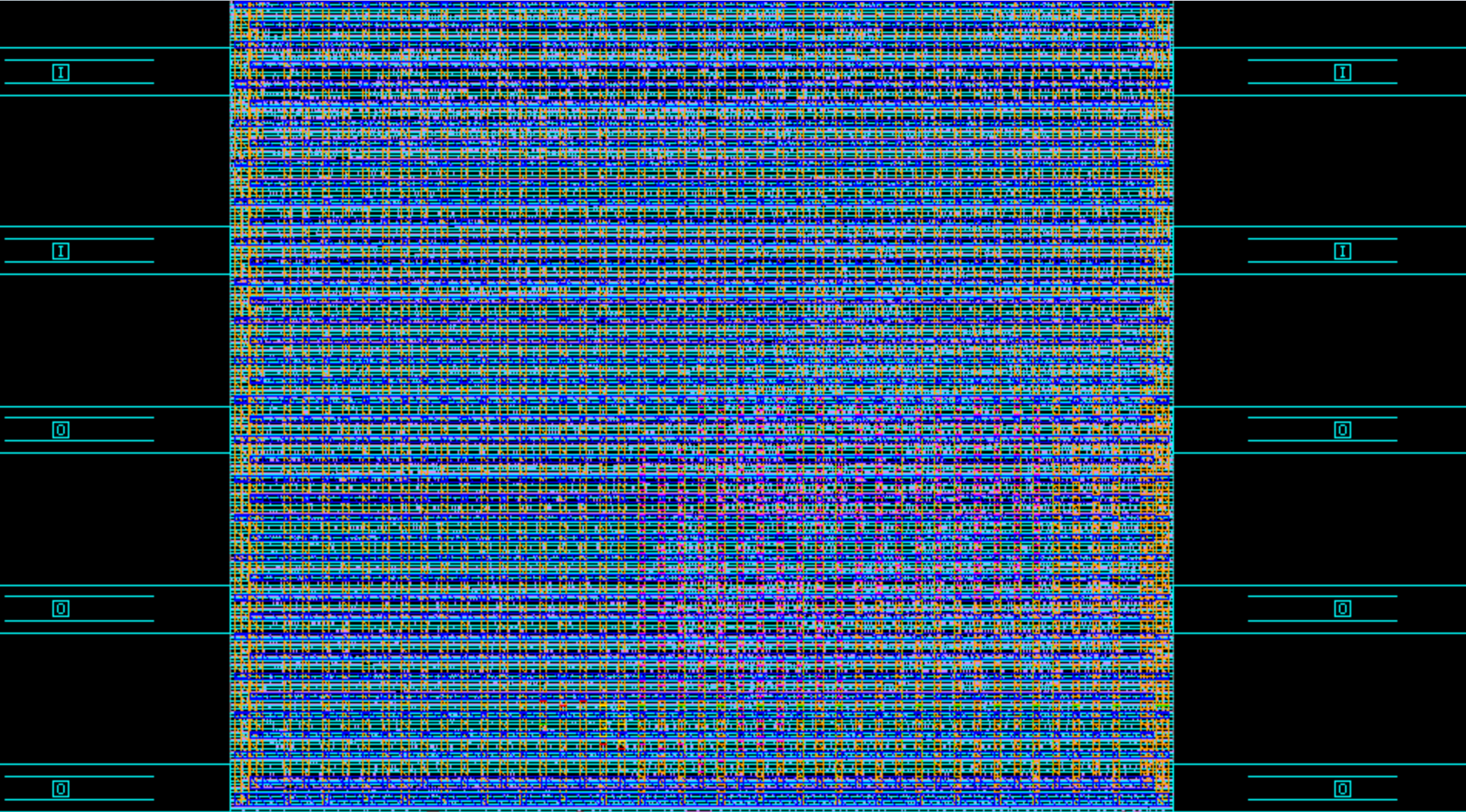




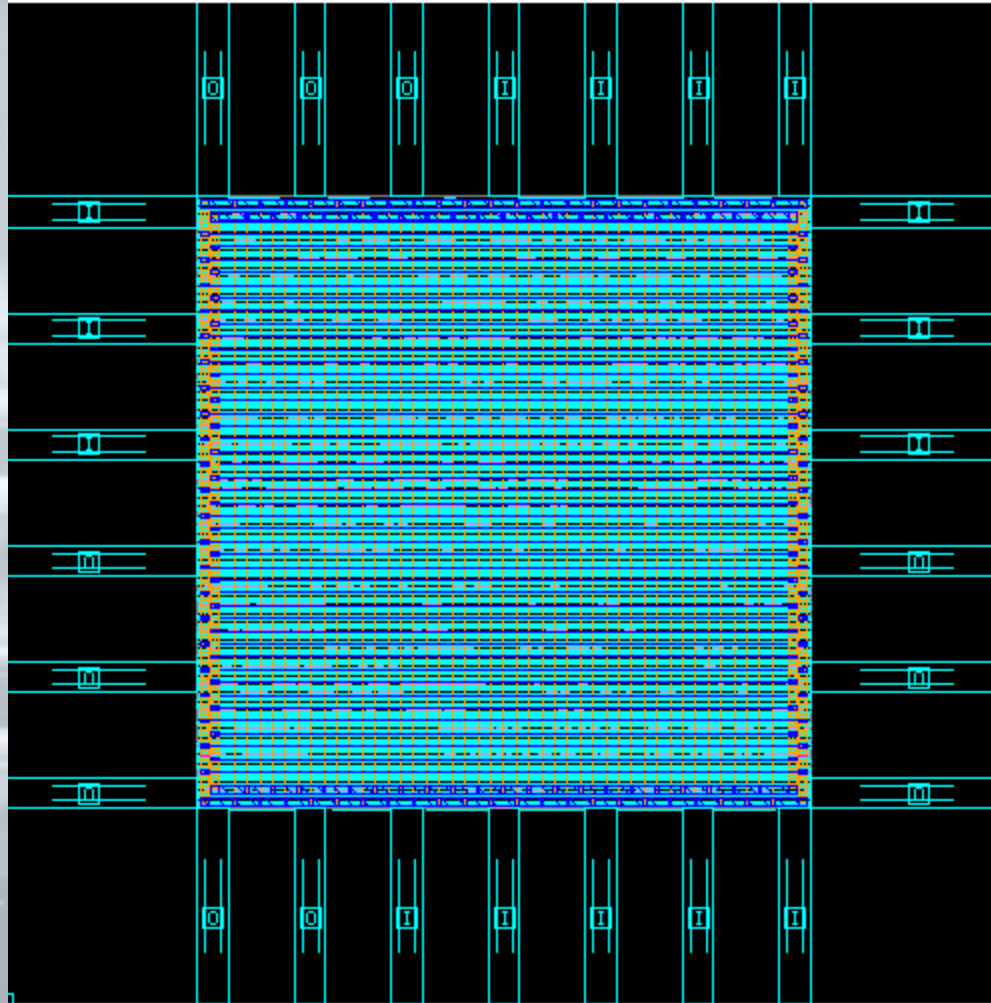
# Pads on the Inputs

pad_wrapper_pad_final_sequence_0 PDO08CDG_33.FRAME	
pad_wrapper_pad_final_sequence_7 PDO08CDG_33.FRAME	
pad_wrapper_pad_sequence_input_0 PDIDGZ_33.FRAME	
pad_wrapper_pad_trst_n_0 PDIDGZ_33.FRAME	
pad_wrapper_pad_sequence_input_7 PDIDGZ_33.FRAME	
pad_wrapper_pad_sequence_input_4	

# Overall Design



# Final Layout



# P&R Statistics

Clock Frequency	333 MHz
Timing Violations	None
Area	0.32 mm <sup>2</sup>
Cell Count	~23,000
Standard Cell Utilization	91.4%
Core Utilization	0.5

Smith and Waterman



**Thank  
You!**