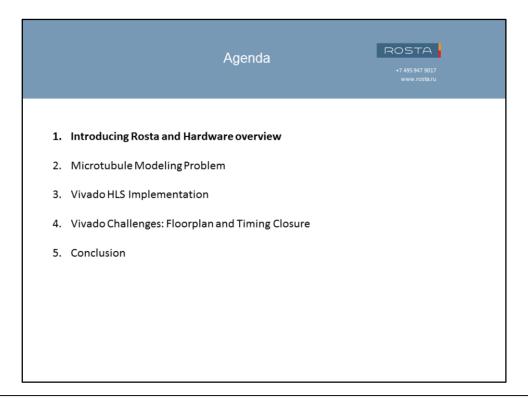


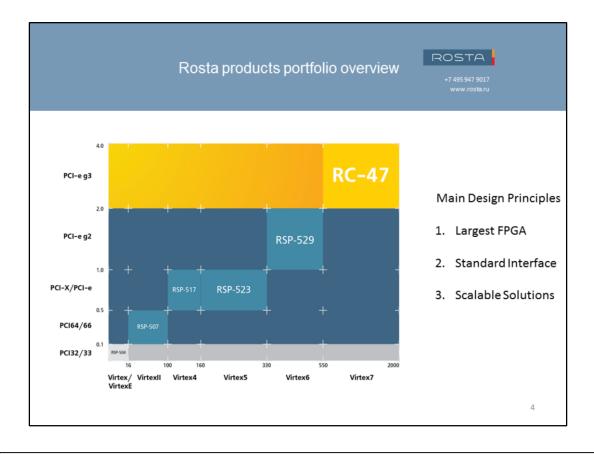
Hello my name is Yury Rumyanstev, I am FPGA and Sofware engineer at Rosta, Russian company based in Moscow. I will present details of HPC implementation of scientific computational algorithm named Microtubule modeling on FPGA using Vivado HLS tool. This algorithm belongs to molecule dynamics class and runs on multicore CPU for very long time. Using FPGA we achieved 15 times speedup.



My presentation will be as follows. First, I will briefly introduce Rosta, company I work for and describe hardware platform used for computation. Then I will generally talk about what is microtubule, why there is a need to model it and describe physical algorithm. After that, I will focus on Vivado HLS implementation of computational algorithm in C language. I will explain how we created computational pipelines and how we organized data to keep it running every cycle. Then I speak about challenges we faced during implementation in Vivado. And finally I will sum up my experience and give a hint on future work.



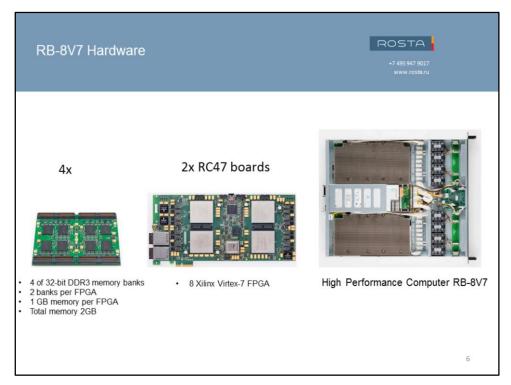
Rosta was established in 1993 and started from distribution of Transtech and Myricon technologies in Russia. Soon after that Rosta switched to design its own devices and started working with Xilinx since 2000.



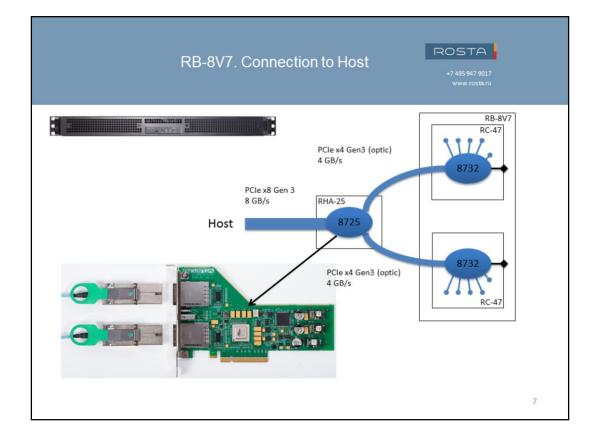
Main business was always about HPC accelerator cards. Rosta always followed Xilinx and created devices on all Virtex families also moving from PCI bus to PCI Express gen3. Our latest prototype device has Kintex UltraScale FPGA.



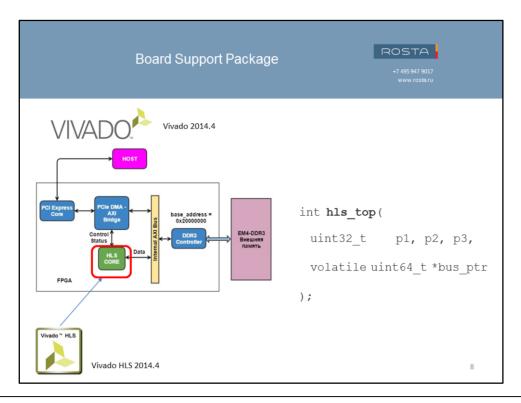
But today I'll talk about Virtex 7 computing platform. It is 1U form factor block to be installed in rack and consists of 8 Virtex-7 2000T FPGA and has PCI Express interface to host PC over optical cables.



Inside there are two identical RC47 boards with 4 FPGA. Each FPGA has PCIe gen2 x4 interface to PCI Express switch. Also 1GB of DDR3 memory are connected to each FPGA.

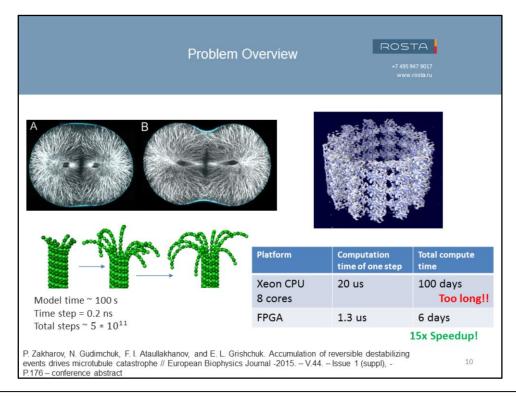


Connection to host PC is performed using two optical cables that connect two RC47 boards with PCIe adapter installed in host PC motherboard. Software running on PC sees our block as 8 independent PCIe FPGA devices.



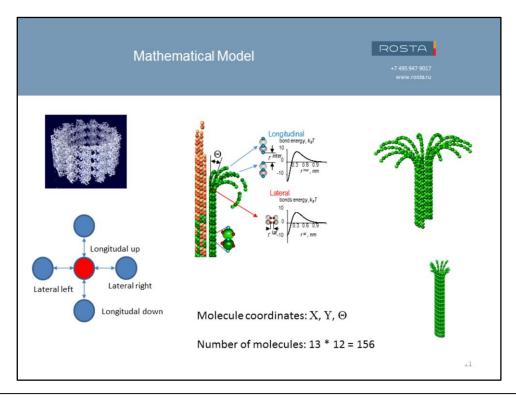
Our programming model is very close to OpenCL. We have host that is connected to FPGA Compute device. FPGA has external DDR3 memory. On FPGA side we have Board Support Package with PCIe DMA, DDR controller, Internal AXI bus and template for connecting Vivado HLS core. On top level HLS core has the following interface described in C language. Bus pointer interface is used to access DDR memory through AXI bus. Our problem size was not big so external DDR was used only for IO with host.

	Agenda	ROSTA -7 495 947 9017 www.rosta.ru
 Introducing Rosta an Microtubule Modeli Vivado HLS Impleme Vivado Challenges: F Conclusion 	ng Problem	



Microtubules are molecular structures that can be found in any biological cell during its division and are represented by long cylinders, made of tubulin heterodimers. Microtubules are dynamically unstable, that is they exhibit sudden transitions between phases of slow growth and rapid shortening and vice versa.

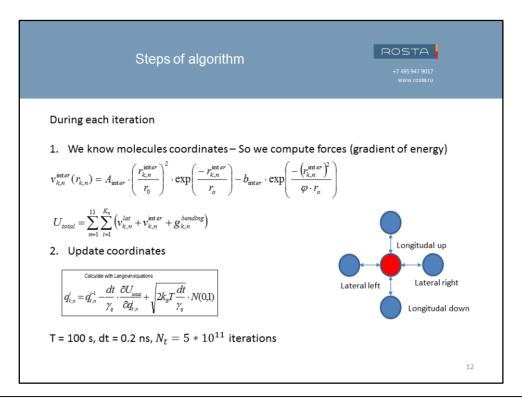
In dividing cells dynamic microtubules are responsible for search and capture of chromosomes, their delivery to cell equator and subsequent segregation between daughter cells. Inhibition of this process can prevent cell division. This fact makes microtubules one of the most successful targets of modern anti-cancer therapy. Our colleagues from Physics Department of Moscow State University have developed a molecular dynamic model of microtubule. Essential part of this model is that it takes into account heat Brownian motion and thus should be calculated with time step of 0.2 ns. They implemented this model using on multicore CPU. With this approach, it takes twenty microseconds of real time to model one time step of 0.2 ns. Problem is that to get new scientific data abound 100 sec of microtubule lifetime should be modeled which results in 100 days of computing! Using FPGA we managed to speedup computation 15 times, which makes FPGA more desirable candidate for such simulations.



So let's have a look at mathematical model. In the upper left corner, there is electronic photo of MT. You can see a cylinder consisting of 13 vertical lines of monomers organized into so called protofilaments.

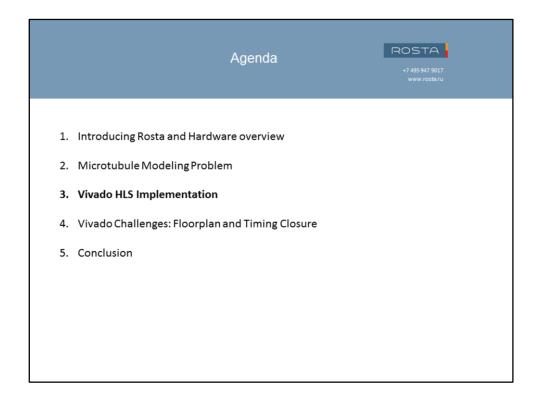
Position and orientation of each monomer is defined by three coordinates: (x_i, y_i, τ_i) , where x_i and y_i are positions of the center of the subunit and τ_i is the orientation angle. Monomers interact at four contact points with the neighboring subunits: there are two longitudal and two lateral bonds per monomer. We will address them as longitudal up and down bonds and lateral left and right bonds.

Our task was to calculate evolution of system. Have a look at animation made in MATLAB. It is built on results obtained with our final implementation. Please don't take into account flying parts. Sometimes longitudal bonds can break and upper part of PF detaches from MT. We just had no time to update software to remove them from animation.

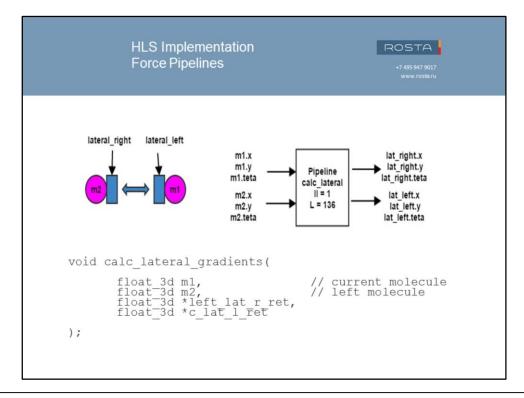


Let's move on to algorithm. We have period of time divided into time steps. On each time step first we have to compute all forces between molecules. We compute them as gradients of interaction energy which depends only on coordinates. After we know forces we can update coordinates. Physical effect can be found after modeling during hundreds of seconds with step equal to 0.2 ns. It means we have to go over 5 multiply by 10 to 11 power of iterations.

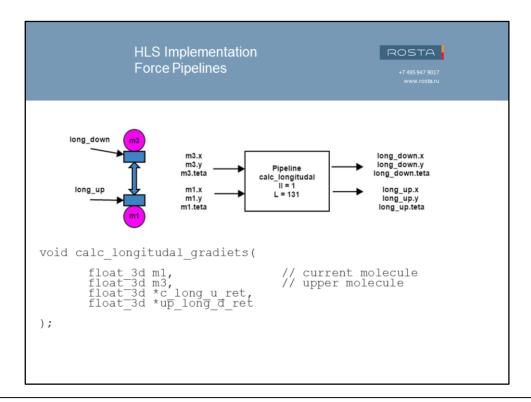
Let's take a look at coordinates update equation. This part describes deterministic part of algorithm. But our model also takes into account Brownian motion by adding normally distributed random number. We need quite a lot of random numbers. We can not afford loading them from host – in this case there will be no acceleration. Instead, we implemented pseudo random number generators inside FPGA.

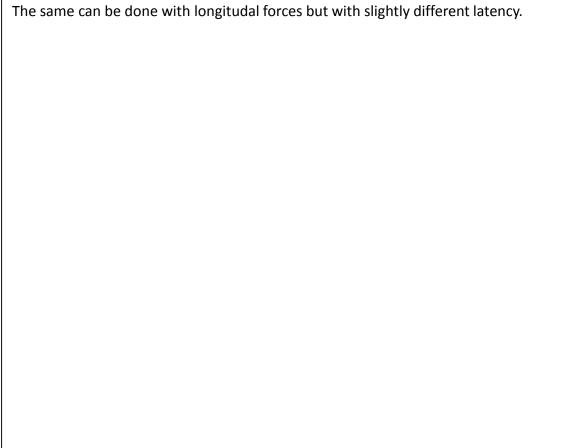


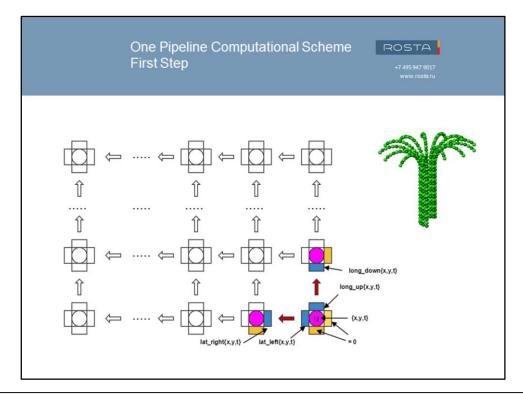
But let's talk first about deterministic part of algorithm and force computation.



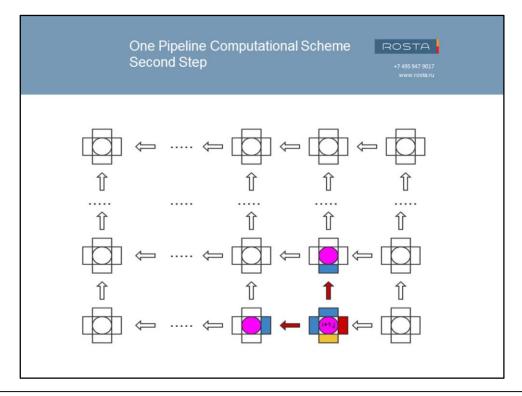
On the picture circles represent molecules and blue rectangles represent interaction forces. Force computation can be represented by C function which takes two molecules coordinates as inputs and produces two forces represented by pointer arguments as outputs. This function is synthesized as good pipeline with one cycle initiation interval and 136 cycles latency.



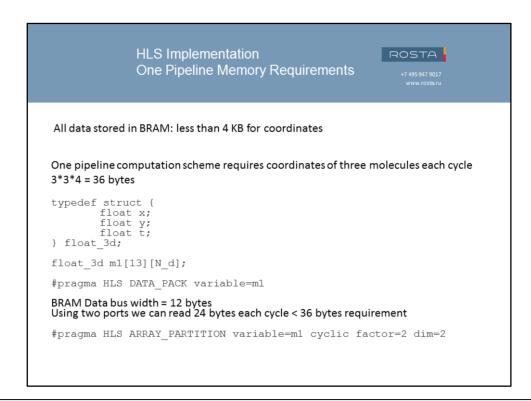




Ok now we have force computation pipelines and we start pushing molecule coordinates into them. I start from the bottom right corner of microtubule. On first step I load coordinates of 3 molecules from local memory and push them to pipeline.



On next clock cycle I load coordinates of the next 3 molecules to the left from memory and push them to pipeline. And then move on position by position from right to left. When I reach the end of the first row I switch to second row and continue. From C language point of view this is nothing but nested for loop. When after initial latency pipeline starts produce force data on its output it is used to update molecule coordinates. On bottom row I have boundary condition (represented by yellow rectangles), down force components of these molecules are zero. To update coordinates of current molecule we need four components of forces around it. Computed forces for neighboring molecules are saved and passed to next computational steps. For example this lateral right force value will be used to update coordinates of molecule on the left on next cycle. On this slide this force is red.



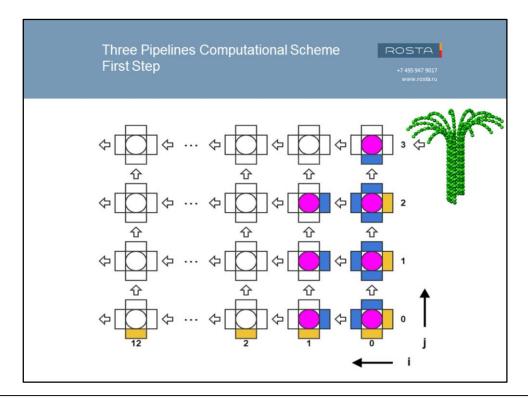
Now we have pipeline, let's see how to keep it busy. Every time iteration pipeline updates all molecule coordinates. We have relatively small number of molecules so all coordinates are stored in local BRAM. We need to load from BRAM coordinates of three molecules every cycle. Coordinates are stored in the following data type structure in two dimensional array. Using Vivado HLS DATA PACK directive I have concatenated all structure fields into one word 12 bytes wide. VHSL array is implemented as dual port BRAM so I can read 24 bytes each cycle, but my pipeline need 36 bytes. So I have used ARRAY PARTITION directive to split data into two different BRAM cores to access it in parallel.

XC7V72000T						
Frequency	II	Latency	DSP	FF	LUT	
200 MHz	1	187	208	85467	133298	Total
Period = 5 ns			2160	2443200	1221600	Available
			9%	3 %	11%	Utilization
One iteration N – number o $T_{cycles} = L + $	of mole - N	cules = 13*12	2 = 152			
$T_{it} = 343 * 5$	ns = 1,7	мкс				

After synthesis I got the following utilization. HLS core used 9% of DSP, 3% of FF and 11 % of LUT of Virtex7 2000t silicon.

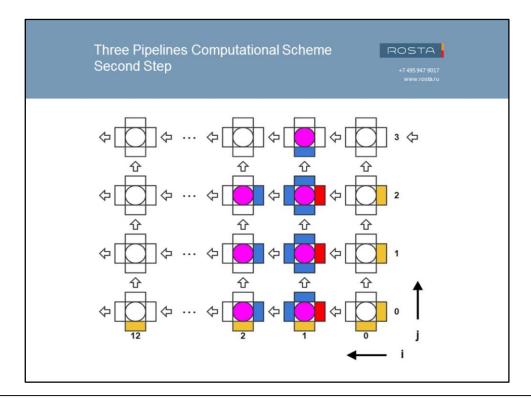
As to performance, key value here is time iteration latency. It equals to sum of pipeline latency and number of molecules. Latency was equal to 187 cycles, number of molecules was 152. The pipleline was running at 200 MHz so it took 1.7 micosecond to compute one time iteration.

We can see that there is a lot of logic left untouched in silicon so I could increase performance by adding more computational pipelines to process several molecules in parallel.



From point of view of the algorithm it is possible to compute ALL molecule coordinates in parallel. But It will require too much hardware. I chose to limit my scheme to 3 pipelines to compute 3 molecules in parallel.

Again, I start from the bottom right corner of mictotubule. I load 7 molecule coordinates from BRAM and push them to three pipelines, these 3 molecules to first pipeline, these three to second and these 3 to third.



On next clock cycle I advance one molecule to the left just as with one pipeline scheme.

HLS Implementation ROSTA Three Pipelines Utilization and Performance MWW JOSTA WWW JOSTA JU						
XC7V72000T						
Frequency	11	Latency	DSP	FF	LUT	
200 MHz	1	187	625	247349	405527	Total
Period = 5 ns			2160	2443200	1221600	Available
			28%	10 %	33 %	Utilization
Memory requir #pragma HLS One iteration la	ARRAN	Y_PARTITION	1999 (1997) - Maria Maria (1997) - Maria (1997)	· · · · · · · · · · · · · · · · · · ·	c factor	= 4 dim=2
$T_{cycles} = L + N/3 = 239 \Rightarrow 1.2$ us						

As expected, this computational scheme requires 3 times more hardware. Pipeline latency remains the same. Major difference is that now I need more bandwidth to local BRAM as compute scheme requires coordinates of 7 molecules every cycle. So I changed the parameter in ARRAY PARTITION directive and split my array into 4 different BRAM cores in cyclic fashion.

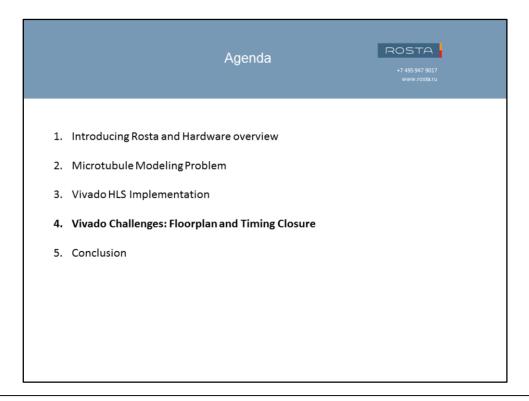
Now iteration latency is represented by this formula. There is still latency of pipeline, but now each of three pipeline should process 3 times less molecules. This leads to 1.2 microseconds per time iteration.

Theoretically I could go further and try to implement 6 or even more pipelines so long I have spare hardware. But it won't add much performance because of initial pipeline latency that will still be there. It'll be impossible to get iteration latency less then 1 microsecond, but instead there will be more timing issues during implementation in Vivado. So I decided that I was happy with 1.2 microseconds with is already 15 times faster than original implementation on muticore CPU.

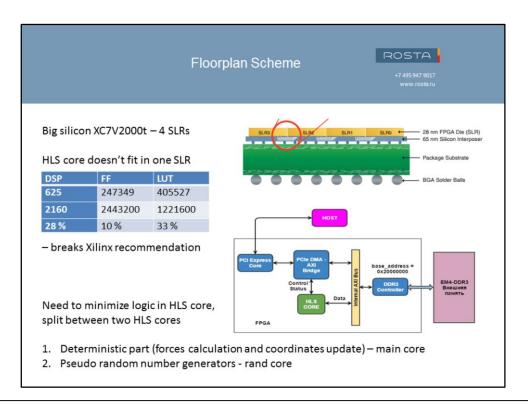
	Heat Modeling	ROSTA +7 495 947 9017 www.rosta.ru				
$\begin{aligned} & \text{Calculate with Langevinequations} \\ & q_{t,\pi}^{i} = q_{t,\pi}^{t-1} - \frac{dt}{\gamma_{q}} \cdot \frac{\partial U_{\text{tentil}}}{\partial q_{t,\pi}^{i}} + \sqrt{2k_{g}T\frac{dt}{\gamma_{q}}} \cdot \mathcal{N}(0,1) \end{aligned}$		ted pseudo random numbers				
Each cycle 3 molecules coordina	ates are updated => we need 9 r	andom numbers each cycle				
Algorithm for generating normal numbers						
1. Generate 2 uniformly distributed numbers (Mersenne Twister algorithm) 2. Apply Box-Muller transform $r_0 = cos(2\pi a)\sqrt{-2\ln r}$ DSP FE						
	$z_0 = \cos(2\pi\varphi)\sqrt{-2\ln r},$ $z_1 = \sin(2\pi\varphi)\sqrt{-2\ln r}.$	DSP FF LUT 41 9910 13166				
3. Get 2 normal numbers		2% 0.4 % 1 %				
And finally we need 5 such blocks operate in parallel						
We used Vivado HLS and achieved II = 1						

Final challenge on Vivado HLS level was to account for Brownian motion. It is modeled as small random addition to deterministic part of coordinates update. This random addition is normally distributed random number multiplied by constant. Each cycle 3 molecules coordinates are updated so we need 9 random numbers per clock cycle. We generated pseudo random numbers inside FPGA using the following algorithm. First generate two uniformly distributed numbers, second apply Box-Muller transform and get two normal numbers. We used Mersenne Twister algorithm for generating uniformly distributed numbers. It is complex and proven algorithm with huge period. It uses internal memory buffer. To get new number algorithm reads 3 words from it and writes one word back. We had hard times to make Vivado HLS fit these operations in one clock cycle but finally managed to do that. After that it was straightforward conversion using these formulas.

One such block after synthesis occupied 2% of DSP resources 0.4 % of FF, and 1 % of LUT. We needed 5 such blocks.

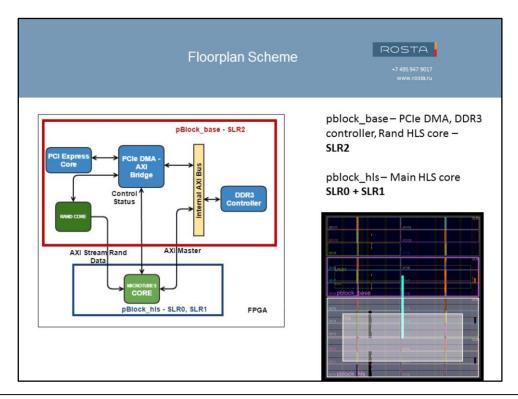


That is all I have to say about mathematical aspect of problem and implementation in Vivado HLS. At this point we had synthesized working FPGA model which was verified against golden results obtained with CPU program. Our next step was to implement this model on FPGA using our Board Support Package.

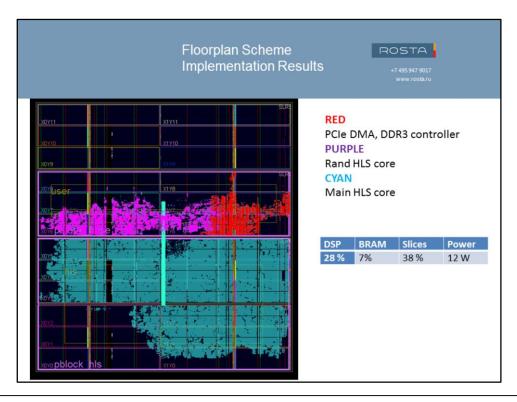


Let me remind that we have big silicon Virtex7 2000T FPGA that consists of 4 Super Logic Regions – separate silicon dies connected over interposer. Inside we have PCIe DMA, external memory controller, AXI bus and template for connecting Vivado HLS core. Pure BSP with small HLS core consumes little logic. The main problem was to implement HLS core.

Only deterministic part of algorithm without random number core utilizes lots of recourses – 28% of DSP blocks and 33% of LUTs. This core cannot fit into one SLR, which is Xilinx recommendation in fact. My first attempt was to implement only deterministic part in hardware. And it actually worked. But after I added random number generation timing score was very bad and hardware failed to operate properly. I understood that I need to separate HLS cores and floorplan my design. I come up with the idea to split deterministic and random number generation parts into separate HLS cores and put them into different logic regions.



So I chose the following scheme. I created two pBlocks: pBlock_base and pblock_hls. I put PCIe, DDR and random numbers logic into pBlock_base and constrained it to logic region two. pBlock_hls that contained main hls core was constrained to logic regions zero and one.



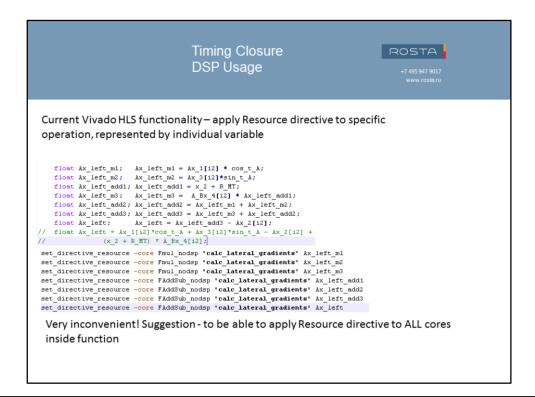
On this slide you can see implementation results. RED is PCIe DMA and DDR logic, purple is random hls core and cyan is main hls core. This approach proved to work in hardware but there was more to it than just

This approach proved to work in hardware but there was more to it than just floorplanning to get it working.

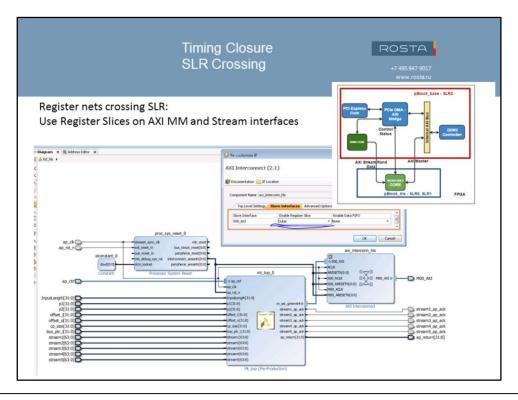
Timing Closure	ROSTA -7.495 947 9017 www.rosta.ru
n in design, require lots of D ce directive to decrease nur SLRs t FFs in address BRAM bus, t tainty. This effectively decre encies, but not dramatically	mber of DSP cores thus breaking critical paths eases clock frequency, increasing
v and John Blaine from Xilin	x!
	n in design, require lots of D ree directive to decrease nur SLRs t FFs in address BRAM bus, tainty. This effectively decre encies, but not dramatically

To get things done and obtain repetitive results we faced the following issues. On this slide I want to thank Xilinx and personally Sergei Storojev and John Blaine for helping with design timing closure.

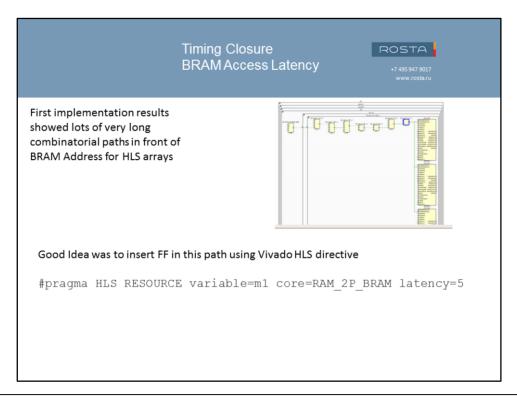
Lets discuss first three issues in more details.



DSP usage. In my code there were constructions like that. You see 4 add sub and 3 multiply operations on one line of C code. Each operation requires separate hardware block which will be implemented using Xilinx floating point IP core. This IP has parameter that controls DSP block usage for it. And Vivado HLS has resource directive that can be used to control this parameter. In my case I didn't want to use DSP recourses at all so I had to apply resource directive to specific operation represented by individual variable, so I had to rewrite my code by hand and get 7 lines instead of 1. Also I had to apply 7 different directives for different variables. Actually It is very inconvenient. My code was long and I spent a lot of time to rewrite it in one operation – one variable fashion. And here I have suggestion to be able to apply resource directive to all cores inside a function.



Another problem was to deal with SLR crossing nets. . Here you see Block Design that was used to wrap main hls core. Random generator hls core and ddr3 controller were located in different logic regions. There were nets that crossed SLR boundary. These are AXI Master bus nets that were used by hls core to access external memory and AXI Stream nets that were used to pass random numbers from one hls core to another. All nets should be registered on both sides of SLR boundary For AXI Master nets it was easy to do using Enable Register Slice option of AXI Interconnect IP. And for AXI Stream nets I had to insert different IP called AXI Stream Register Slice on RTL level – not shown here.



This is the last problem I want to mention. First implementation results showed lots of very long combinatorial nets driving BRAM address input of HLS memory arrays. HLS Resource directive can be used to increase read latency of these arrays. It is nothing that just this line. Realy nothing more. And suddenly problem disappeared. And this is magic that does Vivado HLS. It automatically adjusts control state machine and reschedules all operations to match new read latency.

	Conclusion	ROSTA +7 495 947 9017 www.rostaru
Big FPGA is capable of HPC usir	ng Vivado HLS	
My experience 1. Achieve II = 1 pipeline is a r 2. Use Array Partition directiv 3. Try to fit HLS core into one 4. Register nets crossing SLR Tips: 1. Try to increase BRAM access 2. Limit number of DSP blocks Suggestion 1. To be able to apply Resource	e to feed pipeline with d SLR. Floorplanning is a n ss latency if facing timing s using no dsp version of	nust g issues on address bus f floating point IP core
Future plan: Implement this algorithm using Ultrascale silicon	g SDAccell on Rosta new	board RC-4KU with Kintex
Thank you!		

I want to finish my presentation. Main conclusion that I can make it that Vivado HLS is capable of HPC. We took real complex scientific problem and not only made it work on FPGA but achieved 15 times speedup compared to multicore CPU implementation. We even beat GPU, but it is different story.

Another point is big FPGA. On the one hand, it gives us freedom, we have lots of hardware and can implement big algorithms. On the other hand, we need to pay attention on SLR issues.

We are on step of obtaining new scientific results using our accelerated implementation.

Our Future technical plan is to go for SDAccel. Rosta has new board with Kintex Ultrascale silicon. Right now we are working on creating SDAccel BSP for this board. We will try to implement this algorithm both on OpenCL and using regular Vivado HLS way on SDAccel BSP.