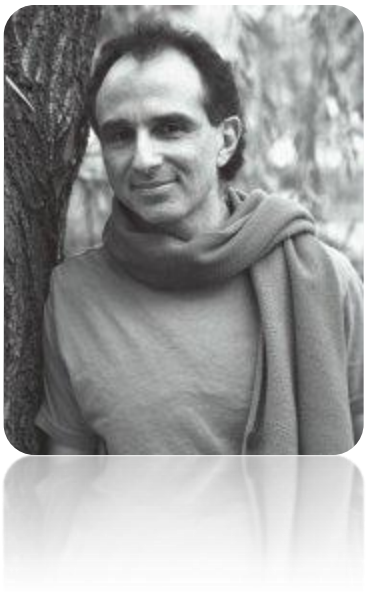
Interview with Dennis Shasha
Coauthor of
"Storing Clocked Programs Inside DNA: A Simplifying Framework for Nanocomputing"

by Peter Marino



Peter: So, Dennis, you've written this book called "Storing Clocked Programs Inside DNA: A Simplifying Framework for Nanocomputing" with Jessie Chang.
What do all these words mean?

Dennis: Well, DNA Computing has been around since my colleague Ned Seeman realized that he could built stable non-linear DNA in the early 1980s. Seeman and others have built remarkably complex geometrical structures -- millions of them at nanoscale -- since then.
They have also built nanoscale robots that can push particles around, assemble circuits and the like.

Peter: Len Adleman also did some cool work.

Dennis: Right. He showed that a simple instance of Hamiltonian Paths could be solved using DNA. After that, many people looked at the massive parallelism of DNA computing and thought they could build electronic ones. I disagreed from the beginning.

Peter: Why was that?

Dennis: Because the combinatorial explosion still bites you.
If you want to solve a 100 city Hamiltonian path problem, you have to consider a potential 100 factorial (100!) paths. That's a number that's larger than the number of particles in the known universe.

Peter: Ok, but you're not a chemist. What do you bring to the party?

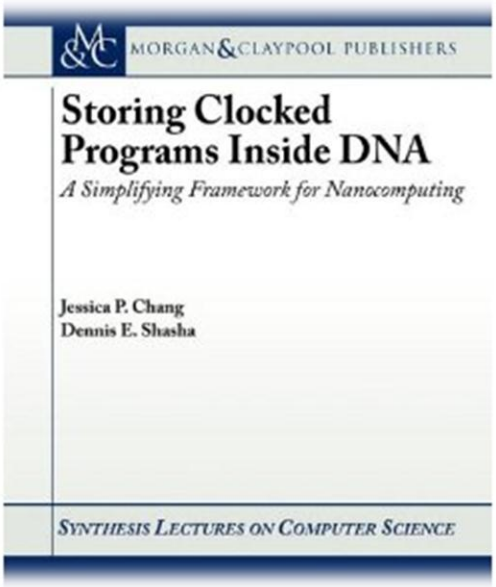
Dennis: Let's say we want DNA to do some complex task like recognize one DNA strand out of many and light up some fluorescent markers.
If you have say two marker colors and 30 possible strands, then you will want to do this in phases.
Say red in the first phase, blue in the second, then blue, then blue, then red.
That is, you want a binary readout in time.

Peter: Yeah, that's easy to do on a computer.

Dennis: Exactly, because computers have clocks.
DNA computing until now has not had clocks. Instead experimenters or robots poured appropriate strands into a DNA mix at just the right times.
We wanted to (i) store programs inside DNA and (ii) run them based on a clock.

Peter: So how could this work in practice?

Dennis: In practice, an application designer would build a DNA program that consists of a sequence of DNA strands (sequences of A, C, T, and G) perhaps with if conditions and while loops. Our method attaches this to a scaffold.
(A very clever rising sophomore Aidan Daly managed to make this work in two months last summer.) This program can be shipped around the world.



Peter: Who executes this program.

Dennis: The recipient loads the DNA into solution and then has a robot that pours in two strands that we call tick and tock.
Those strands peel instructions off of these scaffolds and the DNA computation then unfolds.

Peter: So, what new opportunities does this open up?

Dennis: Any computations that require phasing or branching or looping.
This could mean pathogen detection or nanoassembly.

Peter: What are the challenges?

Dennis: Our DNA scaffolds have few instructions but there are millions of scaffolds.
So we are talking about short fat parallelism. Compiling useful computations to that model and avoiding barrier synchronizations are just some of those challenges. So, on the computer science end, compilation; on the synthetic biology end, fast assembly of programs.

Dennis Shasha's book can be found on Amazon at: http://amzn.to/mddjb9

Interview conducted by Peter Marino, the Senior Partner and founder of reelWebDesign.com. He's also a science and technology aficionado and freelance writer on many topics. You can follow Peter @ www.facebook.com/PeterMarinoShares on Twitter @reelWebDesign and on his personal blog www.SwarmKnowledge.com.