
Getting Our Bearings In DNA Computing: A Panel Discussion

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Topics

This panel discussion will attempt to clarify the outstanding unresolved issues in DNA computing. A brief and incomplete list of concerns is given below.

1. What are the accomplishments in DNA computing to date?
2. What are the problems for which DNA based computing is the preferred solution method?
3. Can laboratory techniques be found or modified to address the need for low error rates?
4. What are the physical limits on using large quantities of DNA with existing laboratory techniques?
5. What aspects of DNA computing are most analogous to conventional computation?
6. Can Evolutionary Computations be carried out with DNA?
 - (a) Huge populations could be used. How much would this help?
 - (b) Is the effectiveness of crossover better with large populations?
 - (c) Can we predict what mutation rates might be appropriate?
7. Are new, stochastic, models of computation needed?
8. Can one encode information into strands of DNA using A-T and C-G paring in such a way the strands pair up (hybridize) *only* where they are supposed to?
9. What are the most immediate problems in DNA computing that need to be addressed?

Panelists

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- Stephen A. Karl karl@chuma.cas.usf.edu
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- Mitsunori Ogiwara ogihara@cs.rochester.edu
- Hiroshi Tanaka tanaka@nis01.tmd.ac.jp
- David Harlan Wood (Moderator)

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