

## Week Seven Response

**To Prove or Not to Prove:*****The Biological Sciences Computing Question***

As early as the 1940's, the introduction of computers revolutionized the way things were done in the world of physics. In the 1970's an attempt was made to bring about a similar revolution in the world of biology. The introduction of computing to the biological sciences has and will cause a shift towards the realm of theoretical research.

With the explosion of knowledge in the biological sciences over the last thirty years, the level of data has grown exponentially, to the point where it can no longer be handled locally by the team of researchers who produce it. Every step of the way, biology has advanced towards becoming a "data-bound science" (Lenoir, Timothy. *Shaping Biomedicine as an Information Science*). While there exist different views on the exact role of computers in the biology revolution, it is generally agreed that the major characteristic changes in the field will be brought about by the integration of computers into every aspect of biological research.

Virtually all proponents of computing in biology agree that the transformation will allow biology to become a more theoretical science in accordance with the NIH's agenda as much as forty years ago. However there is still disagreement as to how exactly the machines will accomplish this. Timothy Lenoir makes the assertion that computer models, and artificial intelligence will allow for accurate predictions of activities which were previously far too complex for human computers to tackle. The prime example sighted is the simulation of three dimensional proteins folding, which Lenoir claims can be determined explicitly if we know all the atomic forces in action and have sufficient computing power available. This view is countered by Joshua Lederberg who claims that since numerous assumedly "proven" theories have been shown to have key flaws, the same is likely true regarding the 3-D proteins. Lederberg suggests that computers can be used not to prove theories, but to accelerate the manner in which biologist identify the flaws in existing theories.

Lederberg's argument, while less detailed, is equally thorough and far more to the point than Lenoir's. History supports the claims of Lederberg, who points out thirteen individual accepted theories which were later proven to be responsible for major misconceptions and misinterpretations. It is made abundantly clear how seriously he takes this explanation when he sights his own faulty theory in example 2 (Lederberg, Joshua. *The Anti-Expert System: Hypotheses an AI Program Should Have Seen Through*). A computer with adequate artificial intelligence would be able to select the proper scenarios and a sufficient number of them to rapidly extract the singularities and abnormalities which would pin down any flaws in the theory. By accelerating this process, computers would facilitate human scientists' development of superior theories. In essence, computers would be doing all the statistical and data related grunt work, freeing biologists to focus on the driving theory of the systems.

The most effective and promising use of computers in the realm of biology is not as theorem provers, but as theorem dis-provers; in other words, computers will drive the development of new theories at an unprecedented accelerated pace. While we as humans may never be comfortable letting computers prove the theories defining world around us, they are welcome to engage us in a symbiotic relationship as our "theoretical proofreaders", pointing out our errors as we transcribe the rules of the universe.

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**Works Cited:**

Lederberg, Joshua. "Afterword: The Anti-Expert System -- Thirteen Hypotheses an AI Program Should Have Seen Through." In *Artificial Intelligence and Molecular Biology*, edited by Lawrence Hunter (Cambridge, MA: MIT Press, 1993), pp. 459-463.

Lenoir, Timothy. "Shaping Biomedicine as an Information Science." In *Proceedings of the 1998 Conference on the History and Heritage of Science Information Systems*, edited by Mary Ellen Bowden, Trudi Bellardo Hahn, and Robert V. Williams (Medford, N.J.: Information Today, Inc., 1999), pp. 27-45.