Bioinformatics lecturers enlist undergrads to tackle DNA annotation challenge

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In this week's issue of *PLoS Biology*, a team of Marseilles University lecturers led by Pascal Hingamp, describe the Annotathon – an innovative bioinformatics teaching approach that appeals to undergraduate biology students.

With an increasing interest in metagenomics – the decoding of not just a single genome, but of an entire microbial ecosystem – the amount of data produced is more than a biologist can keep up with. Because of this, Bioinformatics – the use of computer techniques to process biological data – is becoming more popular. The Annotathon teaching system aims to train a network of apprentice bioinformaticians, who can aide in the ocean of data that is generated on a daily basis.

This method asks students to randomly pick and analyze unknown metagenomic DNA fragments from a real research sequence stockpile. The student's mission, using Internet tools only, is to figure out from which organism the DNA comes from, and what biological function it might have. As well as gaining confidence and proficiency in bioinformatics, students experience the authentic research process of weighing the arguments, establishing prediction reliability, building hypotheses, and maintaining rigorous discourse.

Leaving the well trodden path of canned exercises is unnerving for instructors, but the teaching outcome is well worth the effort. "I've done both with my students: re-analyzing the prion protein year after year, and diving for these totally unpredictable pieces of DNA," says Hingamp who developed the Annotathon software. "It's hard work, but the real fun lies on the unknown side. The excitement is catching." Students, fully aware of their explorations at the edge of knowledge, and with no safety net, live up to the challenge and produce high quality work. In fact, their output proves good enough to be fed back into the public databases used daily by researchers.

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