Bioinformatics 353:
Modeling the collaborative process

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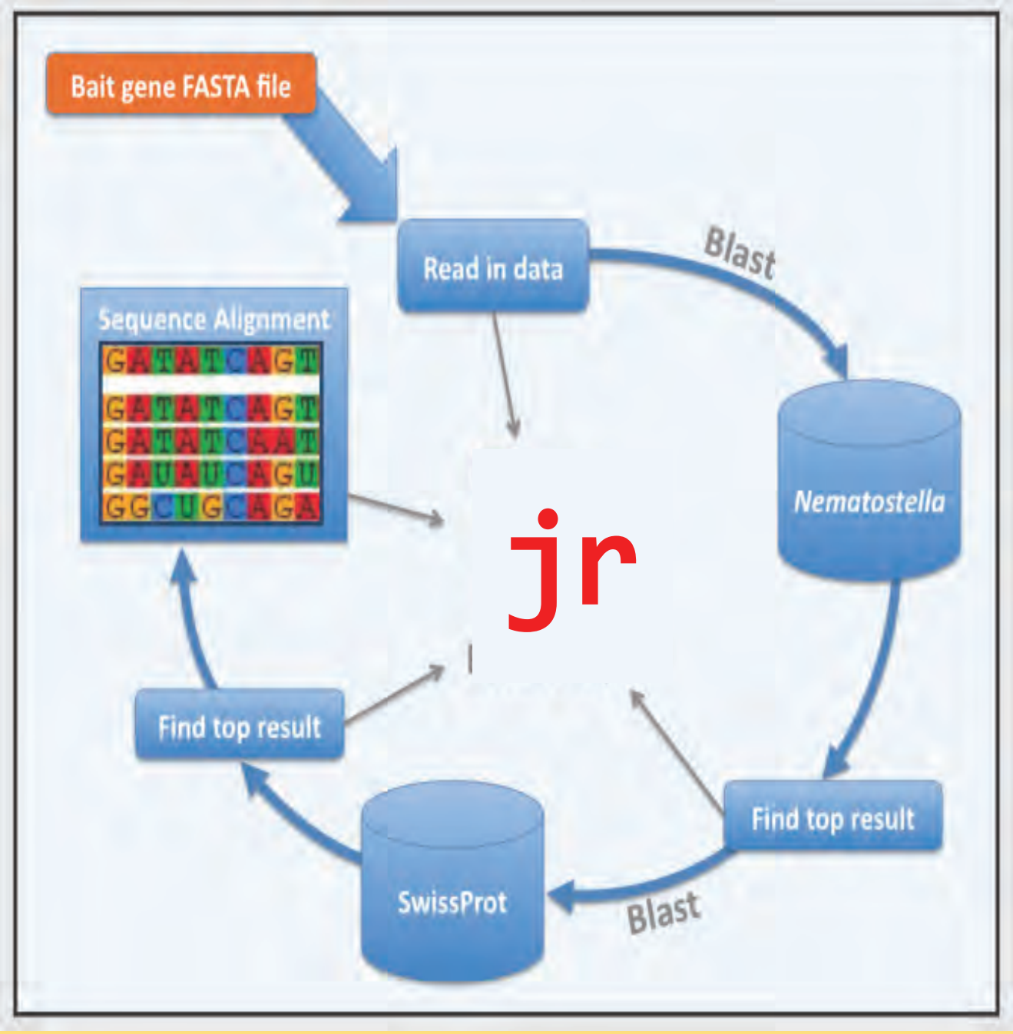
Course: BIOL/CMPU-353 Bioinformatics
Timeline: Spring '08, Fall '08, Spring '11

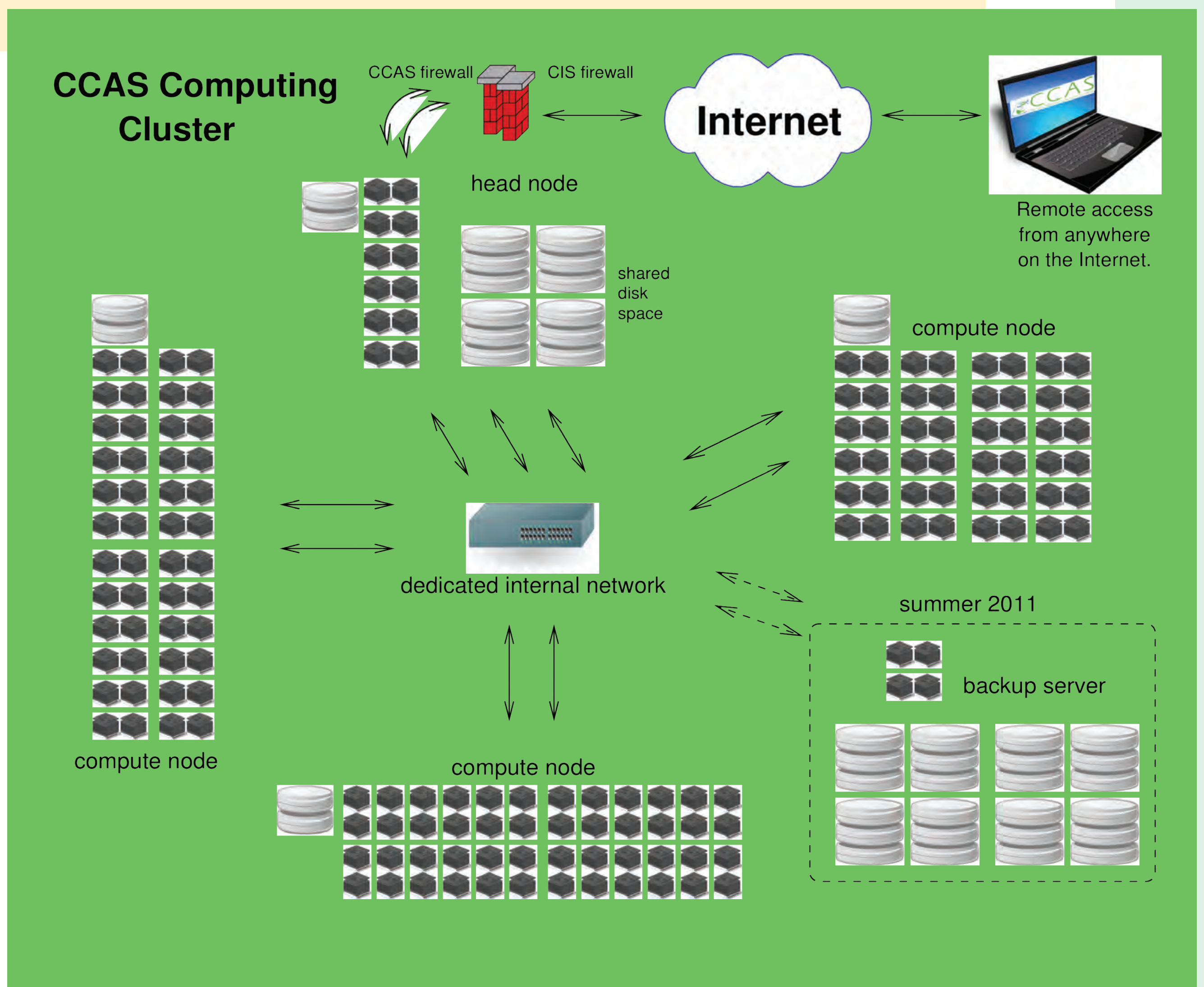
DESCRIPTION

The semester is divided roughly into three parts. The first month is concerned with cross-training, which translates into learning to speak each other's language. We cover elements of algorithm design, including data abstractions and control structures; and molecular biology, including structures, processes, and evolution. The second month is devoted to an "authentic project." This semester that project involves work funded by our Research Corporation grant with Eric Eberhardt and Teresa Garrett. The students are building a bioinformatics pipeline for mapping peptides from an expressed protein back to the anemone Aiptaisia's genome. The third month is reserved for independent research projects where the students work in interdisciplinary pairs, and formulate original research questions with a prospective bioinformatic solution. At the end of the semester, each pair presents their work to the class.



GOALS

We have major-specific goals and common goals. Goals for Biology majors are to participate in the algorithm design process, be able to read and understand code, use and compose computational tools, and one anti-goal: not to turn biologists into programmers. Goals for Computer Science majors are to be able to work with biologists to design algorithms, understand the statement of biological problems, translate biological structures into data structures, and one anti-goal: not to turn computer scientists into biologists. A common goal for all students is to realize that Bioinformatics requires interdisciplinary research: biologists are not computer scientists, computer scientists are not biologists, and we must be able to communicate to design algorithms and computational experiments.



OUTCOMES

Students learn to work collaboratively to design, implement, and perform bioinformatic computational experiments on a high performance computing cluster. The first two times the course was offered, students used the original 'bioinf' cluster, but this semester students are using Junior, a much more powerful HPC cluster with 156 processor cores, 20TB disk space, 224GB memory. Students grow in experience within their own discipline, and in confidence working collaboratively across disciplines. Popularity and interest in the course has grown since we first offered it, and this semester we had a full class (16 total students; eight registered under each prefix), and a few students on the wait list. Finally, independently founded student group BiTT (Bioinformatics Think Tank) lives on, with students helping other faculty with bioinformatic solutions to their research questions.