Comparing Bioinformatics Software Development by Computer Scientists and Biologists An Exploratory Study

Parmit K. Chilana, Andrew J. Ko The Information School University of Washington Carole L. Palmer Graduate School of Library and Information Science University of Illinois at Urbana-Champaign



The Information School

1

AATTCATTTTTTAATCCTTTAATAG TCCACAGTAATATTGTCCTAAAGA GGGTACATTGGATTTTAATTTTGC TGCCCTGATTCGTGATACCAAGTG GCTGACTTTAGAAGTCTGTAGAGA ATTTCAGAGAGGAACTTGCTCTCG AGCTGATGCAGATTGCAAGTTTGC GGAAAATGGTCGTGTGGTGGCCTG TTTTGATTCTCTAAAGGGTCGGTG TACCCGAGAGAACTGCAAGTACCT TCACCCTCCTCCACACTTAAAAAC CGCAGCCATGTTCGCCCAGCAGAT GCAGCTTATGCTCCAAAACGCTCA AATGTCATCACTTGGTTCTTTTCC TCCTCCCATGGCTTTCAATCCTTA CATACCACATCCTGGGATGGGCCT CGTTCCTGCAGAACTTGTACCAAA

Sequence\n\n"; print "ENTER THE FILENAME OF THE DNA SEQUENCE := "; \$dnafilename = <STDIN>; chomp \$dnafilename; unless (open(DNAFILE, \$dnafilename)) { print "Cannot open file \"\$dnafilename\"\n\n"; goto h; **Bioinformatics** \$DNA = join('', @DNA); print "The original DNA Sequence :=\n\n"; $DNA = ~ s/\s//q;$ print "\$DNA\n\n"; \$RNA = \$DNA;RNA = ~ s/T/U/q;RNA = ~ s/t/u/q;print "Transcribing DNA TO RNA $:= \n \";$ print "\$RNA\n"; <STDIN>;

print "This script will convert

your DNA sequence to RNA





The Information School

University of Washington AATTCATTTTTTAATCCTTTAATAG TCCACAGTAATATTGTCCTAAAGA GGGTACATTGGATTTTAATTTTGC TTTCAATATGACGGCTGTCAATGT TGCCCTGATTCGTGATACCAAGTG GCTGACTTTAGAAGTCTGTAGAGA ATTTCAGAGAGGAACTTGCTCTCG AGCTGATGCAGATTGCAAGTTTGC CCATCCACCAAGAGTTTGCCATGT GGAAAATGGTCGTGTGGTGGCCTG TTTTGATTCTCTAAAGGGTCGGTG TACCCGAGAGAACTGCAAGTACCT TCACCCTCCTCCACACTTAAAAAC GCAGCTGGAGATTAATGGGCGGAA CAATCTGATTCAACAGAAGACTGC CGCAGCCATGTTCGCCCAGCAGAT GCAGCTTATGCTCCAAAACGCTCA AATGTCATCACTTGGTTCTTTTCC TATGACTCCATCAATTCCAGCTAA TCCTCCCATGGCTTTCAATCCTTA CATACCACATCCTGGGATGGGCCT CGTTCCTGCAGAACTTGTACCAAA

University of

Washington

print "This script will convert your DNA sequence to RNA Sequence\n\n"; print "ENTER THE FILENAME OF THE DNA SEQUENCE:= "; \$dnafilename = <STDIN>; chomp \$dnafilename; unless (open(DNAFILE, \$dnafilename)) { print "Cannot open file \"\$dnafilename\"\n\n"; goto h; }

@DNA = <DNAFILE>; close DNAFILE; \$DNA = join('', @DNA); print "The original DNA Sequence :=\n\n"; \$DNA =~ s/\s//g; print "\$DNA\n\n"; \$RNA = \$DNA; \$RNA = \$DNA; \$RNA =~ s/T/U/g; \$RNA =~ s/t/u/g; print "Transcribing DNA TO RNA :=\n\n"; print "\$RNA\n"; <STDIN>;









University of Washington







information-seeking activities



Research Questions

- What type of information do bioinformatics software developers seek?
- Where do they obtain this information?
- Are there differences between the information-seeking activities of biologists vs. computer scientists?



The Study

- Semi-structured interviews
- 8 participants, 4 different labs
- Analysis: grounded, inductive approach





CS Researchers

probability theory machine learning statistical analysis

MBB Researchers

large genomic data analysis visualization of patterns

CS Practitioners

Processing raw data Supporting data transformations Database maintenance

MBB Practitioners

Processing raw data Supporting data transformations Database maintenance



Stages of development

Understanding the Problem



Translating the **Problem into Code**



Interpreting Results



print "This script will convert your DNA sequence to RNA Sequence\n\n"; print "ENTER THE FILENAME OF THE DNA SEQUENCE:= "; \$dnafilename = <STDIN>; chomp \$dnafilename; unless (open(DNAFILE, \$dnafilename)) { print "Cannot open file \"\$dnafilename\"\n\n"; goto h;

@DNA = <DNAFILE>; close DNAFILE; \$DNA = join('', @DNA); print "The original DNA Sequence :=\n\n"; \$DNA =~ s/\s//g; print "\$DNA\n\n";





The Information School

10

Working with structured vs. ill-structured problems



- practitioners appeared to work with well-structured problems
- interested in "instrumental" information how to implement a particular solution

Researchers



researchers in both categories frequently faced ill-structured problems – exploratory, complex
goal was to break down the problem into smaller, structured problems



Understanding contributing factors and interrelationships

Biologists



understood the biological relevance, but sought information to understand the technical implementation
e. which data structure to use



once they had developed their algorithms and code, they sought information to ensure the biological relevance
i.e., cut-off values in function parameters

12



Dealing with familiar vs. new problems



favor familiar programming languages and platforms, but comfortable with tackling new biological problems
looking up information about a new technology was not sufficient – needed coaching



- able to apply programming and debugging skills in different situations, but struggled with new biological contexts
- reading up on the relevant biological details was not enough – needed to talk to biologists



University of Washington

Making sense of output

Biologists



- could often determine if an output was valid based on
- inspection
- sought information to understand more complex problems or to revise their programs to do more sophisticated analyses



• could devise a technical solution or an algorithm valid from a CS perspective, but output may or may not be valid biologically



Limitations

- Small sample size
- Only perspective from North America, academic research labs
- Inherent limitation in the use of semi-structured interview techniques



Take-away points

- Biologists want to have control over their analyses but would rather not write code
- Developers need more efficient ways of learning about the domain they are working in
- Clearly a preference for informal exchange of information whether it is to solve a technical problem or to learn about the underlying biology



Software development in bioinformatics depends on collaboration

Not possible to do this type of work without mutual dependency









domain expertise and user research

- Another study looking at how user researchers work in unfamiliar domains
- Conducted 21 interviews with in-house usability experts, consultants, and managers
- Variety of domains: medical imaging, financial analysis, software development, network security, measurement instruments
- Challenges in devising and executing usability tests, and analyzing results



domain expertise and user research





Thank-you.

Questions?



Parmit K. Chilana, Carole L. Palmer, Andrew J. Ko University of Washington University of Illinois at Urbana-Champaign

