









Current Tasks





Genome Query 1.0 (deadline: 1 June)

- Info
 - SNPs
- Show
 - Protein sequence
- Find/Count
 - Common algorithms interface for KMP, SA, K-mers (Victor, Nadya)
 - Slow inexact search (wildcards M, R, N etc.) (Alexey A.)
 - Wildcards for inexact search (Alexey A.)
 - Protein search through wild-carded DNA search (Alexey A.)
- What
- Other
 - Better layout on browser window resize
 - More crosslinks in result's output (to INFO, SHOW, WHAT queries)
 - Javadoc comments to some classes (Everybody)






Genome Query 0.3 (deadline: 11 May, feature freeze: 10 May)








- Search algorithms:
 -  Fast inexact search (wildcards M, R, N etc.)
 -  WHAT command fast implementation
 -  Real-time results
 -  Inexact search (at least k mismatches)
 -  search by shift before/after gene (Alexey A.)
- Parser:
- UI:
 -  History of queries
 -  FIND/COUNT result grouping based on locations in query (extLoc)
- Annotation
 -  repeats
- Other:
 - Javadoc comments to all classes (Everybody)

Genome Query 0.2 (deadline: 20 April, feature freeze: 13 April)

- Search algorithms:
 -  K-mers for all chromosomes
 -  WHAT command slow implementation
- Annotations:
 -  locuses
- Parser:
 -  WHAT command
- Other:
 - Javadoc comments to some classes (Everybody)


Genome Query 0.1 (deadline: 23 March)

- Search algorithms:
 -  KMP
 -  Suffix arrays for all chromosomes
- Annotations are used to get more precised location:
 -  search in genes
 -  protein id
 -  exons & introns







- UI:
 -  on the fly error checking
 -  better layout for info/show/count/find results
 -  improve help layout: see current right side help
 -  show sample queries on startup page
- Other:
 -  ability to stop long running tasks
 -  sequence condensed structure
 -  preprocessing script

Backlog



Search algorithms:



- (don't need) Compressed Suffix arrays (Andrew)
-  BLAST

Parser

-  inexact search syntax (Alexey A.)
-  regular expressions (Alexey A.)
-  parsing on client side
-  find in protein-coding genes (Alexey A.)
-  find in exons, introns, genes, genome (Alexey A.)
-  alternatives for nucleotides (Alexey A.)

TODO:

- Use issue tracker!
- on the fly syntax check  client side with better error recovery 
- task estimation time based on algorithm used
- better instant input validation
- think about result layout

| Legend | |
|---|------------------------|
|  | - Must have feature |
|  | - Nice to have feature |
|  | - Under Investigation |
|  | - In Progress |
|  | - Feature Implemented |