









# 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