

Project Description

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My group's project focuses on the automated design of small interfering or silencing RNA to attack a genus of viruses. We plan on initially testing our platform with the Ebolavirus genus. The steps are as follows:

1. The genomes of the species of viruses are sent to our webserver. I'm assuming them to be in FASTA format.
2. The web server calls a sequence alignment tool.
3. The sequence alignment tool searches for shared sequences among the genomes and outputs these shared sequences.
4. These shared sequences are run through another sequence alignment, this comparing it to the human genome, since we don't want to target humans with this.
5. These sequences are passed to a siRNA generating program, which outputs siRNA in some parsable format.
6. We check the siRNA sequences against the human genome, again to make sure we aren't giving something nasty to humans.
7. Webserver goes 'ding!' and hands back the appropriate siRNA to the user.

My part in our group is to write the webserver. This essentially means I need to make a front-facing web page which accepts the input to our program and feeds it into our python scripts and prints the corresponding output.

For the sake of completeness:

input Virus genomes via a FASTA format via file or raw text.

output siRNA output to screen in FASTA format.