**Dream Version of GenSAS – Davidson Student Input**

1. All scaffolds pre-loaded for blueberry.
2. Pre-run gene and exon predictions for blueberry.
3. Pre-run BLAST results and annotations for blueberry. UNCC is working on this so we are told.
4. Pre-run SSR on all scaffolds. This would the most efficient way to run SSR – once per scaffold. Then the user would just have to recall the SSR results by inserting a scaffold number. If you can do this, some of the numbers below are moot.
5. Items 1-4 could be run on an X-grid or similar to crank through these computation intensive processes, but once done, they would not have to be repeated.
6. Built-in tBLASTn that allows you to paste in amino acid sequence or Accession Number and then BLAST. Other standard BLAST operations too, but we are using tBLASTn the most.
7. Allow E-value cutoff to be submitted by user for BLAST results listed.
8. Allow user to download BLAST alignments for the scaffolds selected (check box) by user.
9. When BLAST results appear, user can check a box next to each scaffold for subsequent analysis. Right now, SSR is the most valuable. Selected scaffolds would be sent sequentially and automatically to SSR tool. Results would be named with scaffold number in the file name as well as within the output text for verification.
10. SSR results should be just like the [www.vaccinium.org](http://www.vaccinium.org) where the output is an Excel file and contains all the same information especially primer sequences.
11. SSR primers could be selected and then visualized on scaffold relative to BLAST alignment sequences. In other words, the area where BLAST showed alignment on the scaffold would be highlighted and the primers will be illustrated as 🡪 and 🡨.
12. It would be nice to have a user-specific history list of tasks and scaffolds already analyzed.
13. It would be nice to have
14. Have strawberry, grape, blueberry, Arabidopsis, tomato genomes preloaded and allow user to do multiple sequence alignment with selected genomes.
15. Allow user to upload more than one scaffold at a time. It is not clear what the repeat masker does and when it should be used or not. What happens if repeat masker is run twice on the same sequence?
16. Video guides would be nice to walk users through the use and visualization of each tool. At this point, we do not see the value in most of the tools other than SSR.
17. Written instructions should be directed towards end-users to help them know what each tool does – what is the goal. Then show some sample output and how to visualize it.
18. Make it easier to start a task. Click check boxes and then a button says “Begin Tasks.”
19. We are not sure why feathers are icons. The color code of red and blue is not intuitive.
20. Be able to download multiple outputs at a time (check boxes to select).
21. When someone has chosen a gene for SSR marker or performed other annotation, have a mechanism to add this information to the collective knowledge. This would allow GenSAS to accumulate the collective wisdom of users. These added annotations could be tagged so other users can determine who did the annotation. The added annotations should have a mechanism to capture the supporting evidence (screen shots, text) for the new information.