|  |  |  |
| --- | --- | --- |
| Group # | Student(s) | Project Idea and Comments |
| 1 | Nick and Keegan | Newborn genetic screening, discjet, database of human diseases, combined with NCBI – healthy allele for specific disorder, how likely is your child will have/develop disease? You query and get likelihood of diseases, we have a subset you pick. Make sure you make it user friendly/laymen friendly – explain where likelihood scores come from. How does it compare to what’s already out there? |
| 2 | Chloe and Ted | Dr. Nelson’s Junior Sem – comparing wild type and mutants – looking at phenotypic differences. Lots of morphological variation in dicty…depending on mutants. Genome-wide pairwise alignment. NCBI/dicty database, web-based tools, 5 strains of dicty available. |
| 3 | Logan | Strain variation Bd – its regions of RNA – unknown how Bd is spread (endemic or humans) – compare geographical samples to try to see how it’s spread. Sequences available from specific regions but no one has done global comparisons. BLAST, global/semi-global alignments. Inter vs intra population variation. Trace the spread. Recommend MUSCLE |
| 4 | Julie, Schyler, Leah | CpG islands, methylation . Book has prediction algorithm. Tools available too. Pick a gene that’s known to have a lot of CpG. Compare different tools that predict methylation sites. What is their biological question?? Find some well-studied methylation examples, test tools, apply tools to new region and see what tools tell you. |
| ~~5~~ | ~~Alida~~ | ~~Type 1 Diabetes alleles – 18 total, focusing on 2 alleles in humans. Compare to other species to see if alleles are present. Orthologues in other species. 95% cutoff. Three or four other species. Primates, back through evolution time. Tools – Biopython to search genomes, web-based tools.~~ |
| 6 | Zach D. | Eye color gene – NCBI full gene 350,000 bp, segments, Biopython pull segments from NCBI, save as FASTA files, find where segments align, find mutations that determine eye color |
| 7 | Eric | CRSPR-CAS9 genome editing, potential alternative to antibiotics, sequence specific antimicrobial – targeted elimination of bacteria. Find resistance genes – 4 genes in 4 species – on NCBI – BLAST gene against select list of bacteria – find genes in other species….end goal – design guide RNA for CAS9 – what are minimum number of guide RNAs needed for a specific gene. Novel – no one’s looked at bacterial species. |
| 8 | Gabe | Strands of staph a. and MRSA – genetic causes – virulence causes – what will you produce? Similarity/differences within and between – what do these genes do? Consequences |
| 9 | Dillon, Nate, and Clair | Optimizing existing database for diseases alleles – making it more user friendly to use and understand results. Do statistical analysis on known disease allele…evolution/phylogeny in python |
| 10 | Chris, Hannah, Jacob | Take healthy gene, simulate random mutations – how long to create harmful mutation?  T->C mutations more common |
| 11 | Allie B | Osteosarcoma and hemangeosarcoma in dogs – comparison to humans – more common in dogs. Known genes - find if genes in each species, are there mutation patterns… |
| 12 | Allie L. | Human Hospital acquired MRSA vs human community associated MRSA – genetic relationships. Strains of MRSA from animal populations – what are you doing and why? |
| ~~13~~ | ~~Jerry~~ | ~~Evolutionary relationships – need a questions!~~ |
| 14 | Tyler and Cody | Build my forensic database to determine haplotype of new dog/cat sequence |
| 15 | Zach S and Adam | Population genomics – evolution of bacteria related to plagues, database available. Question – what makes bacteria in eursinia family similar and what makes it cause disease – possibly related to Chrons disease. Have benign species and virulent species and compare |
| 16 | Patrick | Food allergies – use bioinformatics to detect allergens. Databases available. Know human genome sequence – what are they allergic to…list of foods that might be problem. Making prick test computational. No! List of allergies and finding other foods might be allergic to |