We frequently encounter situations in bioinformatics where we need a custom solution for a particular research project. These situations can arise either because a tool doesn't exist to solve the problem or an existing tool doesn't quite do what we need*.

Problem: Someone in the lab has a VCF file they would like annotated in a specific way.

Coding Challenge: We will provide you with the VCF file from the lab member, and we would like you to create a tool to output a table annotating each variant in the file. Every variant (if multiallelic, decompose into individual mutations) should be annotated with the following information derived from the VCF and querying the ExAC database via the API (documentation can be found at: `http://exac.hms.harvard.edu`:

1. Variant type (e.g. insertion, deletion, etc.)
2. Variant effect (e.g. missense, synonymous, etc.) - Note: If multiple variant types exist in the ExAC database, annotate with the most deleterious possibility.
3. Read depth at the site of variation
4. Number of reads supporting the variant
5. Percentage of reads supporting the variant versus those supporting reference reads
6. Allele frequency of variant
7. (Optional) Any other information from ExAC that you feel might be relevant

Logistics: You will have one week to complete the challenge. You are welcome to complete the challenge in your preferred language. Upon completion, upload all relevant code and the annotated VCF file to a GitHub account and send a link to:

- kelly.foy@vai.org
- hui.shen@vai.org
- peter.laird@vai.org
- ben.johnson@vai.org
- jacob.morrison@vai.org
- toshinori.hinoue@vai.org

All relevant code, as well as the annotated VCF, will be assessed with more emphasis on code quality and documentation than the annotations.

* Please note, we are aware that there are existing packages to do this type of work - please resist the urge to use one of them, and create your own code to accomplish the task. We want to see what you can do!