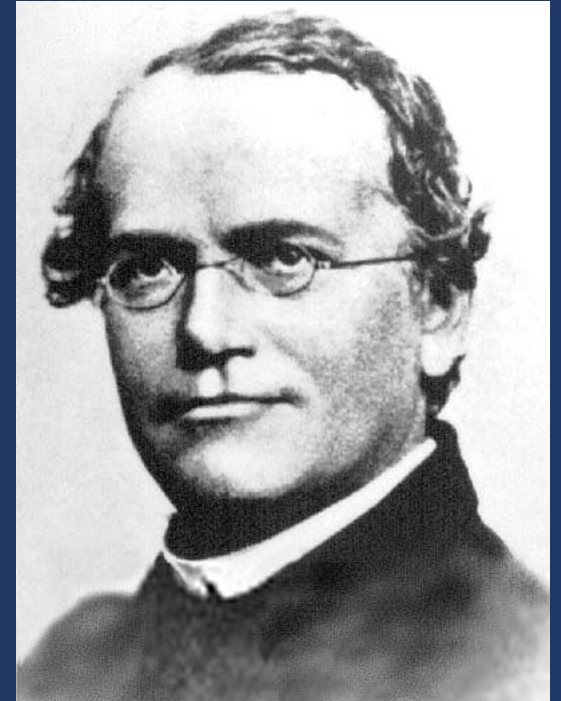


# Concluding Remarks



OpenMendel Workshop

ASHG Annual Meeting 2020

Eric Sobel, UCLA Depts of Human Genetics & Comp Medicine

# Julia: a great language for scientific programming

The Julia language was purpose-built for computational science.

This modern language is high-level (for easy coding, like R) but extremely fast and memory efficient (usually one or two orders of magnitude better than R or Matlab). Julia features include:

- completely free and open source since v1 released in 2018;
- use of an LLVM-based Just-in-Time compiler for speed;
- baked-in parallelization and distributed computing tools;
- can handle very large data sets with speed and efficiency,
- for example, Julia astronomy project in 2018 reached 1.5 petaFLOPS using ~1M threads; only C, C++, and Fortran are as fast.

# All our Julia projects are Open Source and we welcome new contributors

All OpenMendel projects are freely available on GitHub (as is common for Julia packages).

Because Julia uses a JIT compiler, once our packages are installed, all our actual software code is available on your computer to be examined and modified if you wish.

Once modified, the code will be automatically recompiled the first time it is used, and be at full speed.

If you would like your modifications to be available to all, you can then issue a standard “pull request” on GitHub and, after verification, it will be included in the standard distribution.

# Thank you!

Hopefully, this has been useful for you.

We have tried to give you a quick snapshot of how we are building a state-of-the-art system of packages for modern statistical genetics. Our existing and future OpenMendel packages:

- Are numerically accurate, computationally efficient, & statistically robust;
- Make maximal use of genetic data from relateds and unrelateds;
- Scale to big data analytics;
- Embrace parallel and distributed computing;
- Are free and open source for sustainability;
- Enable interactive and reproducible analyses.