I just want to share this with you.

https://time.com/collection/100-most-influential-people-2022/6177818/evan-eichler-karen-miga-adam-phillippy-michael-schatz/

Amazing recognition to two computer scientists. Adam Phillippy and Michael Schatz among other exceptional genomic scientists (Karen Miga and Evan Eichler).

I met Michael Schatz only once when I visited as a member of the advisory board to the Dean of Engineering at Johns Hopkins University a few years ago.

I am proud to claim Adam as one of my academic grandchildren. :)
As they say "success has many fathers and grandfathers"... :) Hopefully more and more mothers soon.

So, I will focus on his story and make a broader point. Perhaps obvious to all.

Adam was co-mentored by Steven Salzberg and Arthur Delcher. Art is a former PhD student from Johns Hopkins. Adam's outstanding PhD thesis followed up on our joint work with Steven and Art on the MUMMER system, the first open access and widely used whole genome bacterial comparison system (implemented and deployed). I was not involved in his PhD thesis.

There are numerous expansions of MUMMER in use today implemented by many other contributors doing altruistic citizen's science.

Our early MUMMER system was a brilliant effort by Art and great leadership by Steven but it was relatively easy by comparison to the "climbing Mount Everest" effort finishing the human genome by Adam, Karen Miga and their collaborators. Well, finishing is a bit ambiguous given the variation. :)

I have no involvement in this recent seminal work that led to this remarkable public recognition for two computer scientists and several other amazing genomic scientists. So the credit is all theirs, NHGRI and other centers for supporting it.

My focus in the last 30 years has been AI2BIO. As usual, thinking ahead beyond sequencing :)

But this is just great science, fundamental, ambitious and what a service to the broader community!

It also showcases an intellectual transformation manifested by computational scientists co-leading major genomic efforts - not “just” method development.

It follows decades of computational scientists such as Charles Delisi starting the human genome project, Aviv Regev co-leading the human Cell Atlas (and more) and Tarjei Mikkelsen co-leading the first draft of the Chimp Genome paper. All three are among our closest collaborators and I cannot be more proud of their accomplishments.

But there are so many others including computational scientists or engineers doing deep biology or biotechnology. Not to mention the computational work that enables transformative discovery and invention such as Koonin & Makarova et al and others.

We are seeing a real convergence of biological and computational sciences of remarkable future significance. AI will just make it converge faster and with higher impact.

20+ years ago many speculated that biology would become an "information science". Many of us felt (even then) that this is not the most ambitious or imaginative vision of the genomic revolution. We were naive but right.

These amazing efforts such as Adam, Karen et al and many others are clearly much beyond biological databases and indexed searches.

But for now, we must just celebrate this recent brave "climb" that couples genomics, robust CS, challenging data science, new biotechnology and a "simple" heroic effort. Last but not least, COLLABORATION!

In truth, there are so many heroic efforts today in deeply immersive biomedical computing and engineering, I could easily fill the entire Time 100 list with these folks.