Twitter Thread by Ewan Birney



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So - that was quite a twitter/media day for me, and welcome to my new followers; 3 threads coming up - introducing myself, explaining my background and COIs (this one); technical aspects of the new strain from my vantage; commentary on what is means for the future

(for the people who know me, skip the rest of this thread!)

A brief tweet portrait of me; I am deputy director general of @embl and co-direct (with Rolf Apweiler, not on twitter) one it's six sites, @emblebi which is based just south of Cambridge, UK.

@embl is the European Molecular Biology Laboratory, a European treaty organisation that does science, similar to CERN. EMBL does molecular biology from high end atomic structural biology to development - and in the future, bridging to Ecosystems.

EMBL is Headquartered in beautiful Heidelberg, Germany and has 5 other sites; Hamburg (Germany also), Grenoble (France), EMBL-EBI at Hinxton (UK), Rome (Italy) and Barcelona (Spain).

Like CERN, the EMBL treaty is separate from EU treaties (though we have a very productive relationship and agreement with the EU); Israel and Switzerland were both founding members of EMBL in 1973. As such Brexit does not legally effect EMBL-EBI in the UK >>

<< though it has many impacts on the operational details and general tenor of the staff at EMBL-EBI, both EU nationals @emblebi, British nationals and non-EU nationals (we are very international in our recruitment)

Overall @embl has 5 missions - Excellent Research, world class scientific services, Training (all career levels), dissemination to industry and European science coordination. @emblebi is focused on bioinformatics - data science in biology - and contributes to all of these

In particular @emblebi provides the world with public molecular biology information; most iconic is the human genome sequence and its associated annotation, but this thread goes far deeper; from the 1970s for protein structures, 1980s for DNA sequence.

In the pandemic @emblebi has provided the technical centre piece to https://t.co/N47Vc4mBnz which enabling worldwide sharing of molecular data on COVID19 - DNA, protein, structures, and impact on the human host (expression changes, human genetics, done in a responsible way)

My own personal expertise is both algorithms around DNA and more recently outbred genetics, in both humans and Japanese Medaka fish.

When life is a little slower I will hopefully regale you all on Medaka fish genetics and phenotypes (its... slow science, and all the better for it) but the main thing about this field is two fold

(a) Data science in biology - aka Bioinformatics - gets hooked into all sorts of parts of biology, and one often reuses a fundamental toolkit (processing, models, statistics) in disparate fields - it really is a wonderful "freedom to roam" and means I collaborate broadly

(b) It is very international, both in data sharing worldwide (such a good thing for humanity I can't tell you - this pandemic being one example!) and also human genetics is very much a global village - we are a small group of upright apes that have exploded quickly worldwide

The final thing to add is that I often work with companies - I have a very porous view of how academia and companies should work in terms of expertise, and then sharp discontinuities about which problems are better solved in the public sphere, and which via private money

(so - I don't find it *at all* a problem that I am for open science and also cheerlead/support companies in general and a specific set of companies; rather it is "for this problem, what is the best structure to solve it")

As such I have a list of companies I have consulted for; am consulting for now; and may well consult for. For the "past" it includes, a long time back, Compugen in Israel, more recent past being GSK (the pharma company)

For the present I am a long standing consultant to @nanopore , which makes a new COVID test (LamPORE); as such I have a clear COI on testing which I try to be squeaky clean about announcing (much to people's amusement).

The other current consultancy of note is @DTGenomics which has a variety of clever library techniques, in particular proximity ligation for assemblies, structural variation and chromatin structure. They don't have a COVID line but they might.

For the future... I can't say (obviously) but what I do aim for is transparency with everyone. As @Spikew3 from nanopore says "Better a conflict of interest than a lack of interest" and being transparent is the start to this.