Agenda

1. Introductions
2. Administrative updates
3. Collaborative projects - more focus on rigor and reproducibility?
4. Data release plans - how do we get more engagement and buy-in from all groups?
5. NIH FY20 Plans - what should HuBMAP be doing that it isn't?
6. Other NIH activities - CFDE / STRIDES, figshare
7. Any Other Business

We'll be sending out emails to ask for your progress for our APR

If you want to see what everyone is up to, you can look in Asana

You can post details from the slides what data we expect from you

Have two RFA reissues – TMC and TTD will be coming out early next year

If you know someone who's interested, let us know – not interested in funding you guys anymore, unless you have a really good reason

Want to expand out the types of tissues, different modalities

Headed to doing more lipidomic work, functional proteomics, and extracellular space

Jonathan – so another 4-5 TMCs are coming? What does that look like?

Richard – this program is structured differently – scale up over first four years, expect the HIVE to grow

Want to grow the existing groups, not add more groups to the HIVE – good to grow the experience on

Nils – so we could bring in collaborators? Yes

Collaborative projects – interested in rigor and reproducibility. Need consistent controls that have been captured

Want to try to push here as we move to the data release

Please give feedback to the projects when they present

Data Release Plans – December, March, June

Starting the process – some datasets are ready – not a huge bolus of data release, but will start us.

Maybe every six months or so – need to discuss more detail

How will be do release #2, #3, how do we grow the capabilities of the Portal?

Need a strategic plan to Release #n

Harry – so we'll release #1 and submit data for #2 the same time?

Richard – yes

Jonathan – I think the six months for the data release will shorten as time goes on

Every three months or every 6? Maybe we shouldn't try to answer, but should try to do it once first

Stephen – yes, have to learn to walk before you run. Can't get the release out without the analytics being done

Ziv – once we know how to support a certain type of data, it will be faster. If it's a new type of data it will take six months

Stephen – have to make the funder happy, have to write publications – it's an opportunity to put in the new modules, and renew the dimensionality of the data

Jason – yes, you'll be releasing data for the next 6 years.

Richard – we need to discuss this, want to move to continuous submission of data as we go on. Hard to see how we get past some kinds of data releases – want to build up boli and analysis to go with

I think it will speed up over time – don't want to make our next release back up into this release. Don't want it too long – a year before release #2 is too long, three months is too short.

Jun Hyeong – there's the process data release, and we need a governance committee

Jason – and there might be datasets that don't pass the criteria

Stephen – want to be certain your second data release is larger than the first

Yousef – so we probably won't make it for December, so we'll wait for June? Yes

Richard – Yes, I don't think six months is too long to wait.

Mike – we're going to have a big bolus of papers next year

Do we want to focus on one common tissue that everyone submits data on. More high profile publications – what can we say that we're doing that's unique to HuBMAP? Is there a target we should be aiming for?

Mike – plausible that each of the 5 centers are working on their own organ, so that's technical more bio – would look good for us.

Richard – are there common things we want across all the tissues?

Mike – you could take the five sets and see what's common across all of them. How does that play into cell identity – that would be kind of cool

That would be a substantial analysis, but that's how I see a cross paper

Zorina – should plan to be 3D – have to start planning now so we can from 2D. I think that's unique

Ziv – I like Mike's suggestion. Another thing that should be published is the CCF – that would be enough to demonstrate the utility

Mike – maybe in March we'll have a better handle on what's going on. A proper cross organ analysis is going to require to get the data out early

Richard – will need to get a common set of probes for that

NIH FY2020 –

Pondering how we're going to be spending our money next year.

Planning for a collaborative effort with HTAN, like to continue exploring working with LungMAP, KPMP, a bunch of different internal NIH things we're thinking about, the NIH/HCA meeting, thinking about a functional proteomics workshop next summer – that's what we're planning for.

Easier to ponder now instead of the end of the year. If you have ideas, tell us now publicly, or later.

Mike – HTAN is doing to the same thing of cross-platform

Stephen – 3D, and ECM are two of your stated goals for the future. I would start bringing those into the seminars now. From a technical perspective they are great, but they are going to eat you alive.

Mike – and more single-cell technology

Jason – common md platforms across the different consortia

Richard – if people are willing to coordinate with other groups, that's fine, but it can also be a distraction

Katy – does anyone have a graphic illustrator that we could borrow for our anatomical browser? If you have someone who's really good, can you let us know?

****Danielle knows someone, Tyler knows someone – they will send their names to Katy

CFDE/STRIDES – new incarnation of the Data Commons – trying to build value out of what exist – 30 different programs that aren't really connected to each other, so CFDE will try to bring it all together.

Katy's been interacting with them. Where are there areas of synergy with what we're doing? You'll hear more about it over time – it's a more meta-level thing for us right now.

Jonathan – we talked to the CFDE people a couple months ago. Questions they asked – what did you see from other CF programs that worked well and didn't work well. We don't know how to answer that without feedback.

Ananda – do you think you'll be interacting with other programs?

Jonathan – we are thinking of that, but we don't know yet – going to point back to Nick and me in a heavy way.

Mike – you're setting up an infrastructure, HMP, KPMP, HTAN, MotrPac, all setting up an infrastructure, all re-inventing the wheel

Richard – yes, there might be something that affects our data collection strategy

Mike – and at some point we'll have to make all the data comparable

STRIDES is going to get stuff up in the Cloud.

Figshare – a way to share figures – just started a month ago

Nick – PSC has a project with figshare going on, some good overlap

Richard – if we can figure out what it is, and if it's any use for us, that'd be great

Nick – making figures available to people – figures they can't usually get because they can't afford

Ajay – are we getting enough humans to say anything about biology?

Stephen – that depends on the metric you want to look at. This project is designed for a developmental aspect, which isn't a bad thing, it's a huge challenge that you aren't meant to fill. Get off the ground and start looking.

Gloria – it's not clear to me that the groups are funded well enough to do this

Zorina – and we have to pay attention to diversity

Stephen – yes, very important – what's available, and what's useful. Have to have enough data to prove you have sameness and difference.

Jun Hyong – if HuBMAP is supposed to generate data in the long term over the life span, we'll need to get a lot of people. There are degrees of variability.

Neil – need a power curve. Could try to rope in disease stuff to compare

Stephen – if you want to look over something over time, you should get the hematopoetic system

Kun – every base in the genome was sequenced 7x before it could be called a reference

Richard – and that's why we don't call it a reference. There's a huge space to explore here.

Jun Hyong – can't control the variables, so you need a lot of samples

Gloria – repositories

Richard – are interested in setting up a tissue core, but it got sidelined. I think what you're doing with IIAM will help build the groundwork.

Other Business – prizes – Voodoo dolls!