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First, and the second is I wanted to I wanted to make this my presentation as interesting as possible. I suck up latest PowerPoint slides from by students this morning and expecting that I have some time to spare before my presentation part of this call, but I was called up by the chairperson and the hunting panel discussion heated up. And I still don't understand exactly what's the you know, my slides are you know, meaning that painting so a lot of my slides will be quite messy. Let's terminate my presentation. And but I'll try my best. So Michael says how can I skip my introduction? My place is a sequencing corner but the University of Tokyo mainly for the data production. Yes, my issue and your interest of the data production for nationwide projects might know that Japan and SCADA is a vaccine center and other small projects as well. And so maybe that's why I'm here. Still and today's question, today's objective subjects topic is that they have diverse landscapes on which may not be defined by the genomic variations. So maybe kind of complementary to the Burmester. So the initial you know, the it's the pandemic is over so the topic may look my fingers all on for many of you, but they in those days we were degree did a lot of single cell analysis and we monitor a single set of profiles for the sickness if people have a severe symptoms are white moderates senior and and some people developed the enough Samia responses study. This figure shows this the how the B cells are matured and how those they are different. Between the mild case and severe critical cases. And so these are normal case, and for example, the lease maturation markers for the cell. The cells are enhanced for the city applications, but in some in some of the clinical patients. That's my first and probably not occur sampling. So that's this person's like, the hospitalization was prolonged, because he cannot cure ailments that bias. So but we are there is a study actually from a great researcher and a colleague at UQ to cut out some genetic variants are responsible for the diverse reactions and the access to locations. But I believe that that's up to minus two miles for understanding that's explained up just a part of the reasons that factors and I believe that's the My background is of transcription. So the transcript of videos that is currently in Gen profiles, collectively I will call that new landscapes are responsible and which is not always defined by the generations. And that is not true because after all, we are born with an H H and that's the death. Eventually, we are changing the consulting transcript, transcript from ice and the general problems and depending on the changes of circumstances environment performances. So we wanted to try to see how the single cell profiles are changed even among the healthy people living in a diverse environments. So and we studied this, but then the main field of the study is the suburban area. neighborhood of my mother, where we have lots of units there. And we brought in the samples lots are supposedly made from the veterans living nearby and data analysis, in a sense taking advantage of the geography. Thanks. So we did our before starting the large scale analysis. I don't know whether 50 is a big number have enough value. Before scaling it up. We conducted the pilot study and the first place the entire story of mine actually suggests a pilot study and I expecting that to be scaled to the impact scale eventually in collaboration with Minecraft, so but anyway, the single sale on there is a little more and still it's true and they're they're not single cell analysis is quite difficult symbolically. So batch effects and data control is still an issue, even though the protocol is so they but everyone is selling in that analysis. We did it that way and usual and before going into details, we checked whether about the data reproducibility, reproducibility of the data production services, and especially for some condition of the storage or frozen or fresh and we compare this is just one reason we compare the WoW which is the profiles are affected by frozen and fresh, freeze and false because it's fresh. And we found this for most of the cell types the brick and as far as this portfolio is used, we can rely on the for the previous datasets. It's true that some mitochondrial genes of someone showed up between outliners among the landlines, that's natural because some cells are developing themselves. So that is the first one and the second one is that's how we can reproduce the data from the independent sample question. So these are the first one the previous one that I showed in the previous slides fresh and frozen and differences like that range. So in this every color represents a cell, the cell population so in this case, we focus on two individuals actually with the left side, right, so So and we I submitted a plot to everything in every three days for one month, and repeated the same expense 10 times or more or 10 times and conducted single cell analysis. There is kind of there are many updated changes of the blood cell profiles, but beyond cells, innocence readings, they repeat the same experience 10 times and actually that data should not lie to us and then next from another person is the same and even beyond the data production. We are not sure what is the batch effects or the daily changes that build us daily changes. Still, there is a significant difference between individuals to individuals for example, h1 healthy one is in a sense prominent in terms of the cell immune reactions. On the other hand, that h2 is rather relies on the T cell responses. So there is a diversity between the individuals self and we are quite skeptic still. So we conducting similar analysis or using cipher is a proteome analysis focusing on the cell surface markers, and naturally to make history shows and we conduct read did we use the same drug samples to the site of analysis and found that the correlation was not so bad lots of profit will be at the Pearson's correlation, correct. He says he was on a five or so. But as far as that's an approach to that sixth sense, though, like each I showed previously in the previous slides, that they are convened for the father says Okay, so in a sense, being encouraged by the instant results with success, really an IQ test, more people have nearly from a nearby people, students or sauce, and as far as the informed consent issue is so adamant, I have to be careful not to buy so that Japanese and some students or some person is from Indonesia, try and sell everything that we did the same single cell and psychoanalysis. And so and, you know, the diverse product of the profiles on sampling from tier two, and in that sense, we intentionally included a person who is an elderly person. For experienced they're accused the cell the former of 10 years ago, having reached complete cure of the

09:00

disease, that the state still in this profile of this person is quite modest. About 50% of the cell cells are immature cells. So in other words, the empty cell is obviously a central part of the net, the initial production of the diseases, implementing pathogens and the cancer cell cell. And maybe it's tempting to statement that this person could survive because he has been able to expand this NK cells to fight against the area. So the interesting thing is this in this particular person, I'll read out if that's what's the three years ago, five years ago, when the first wave of the pandemic service colleagues came to Japan. So that was the timing for the vaccination. So we took the bullets are samples after the first and second vaccinations and monitor the changes of the province. And for many of the people, each one include the h one and h six six, which I just mentioned show for the slice and the immune reaction. seems to be quite as expected, the more size is increased the four plus helmet sizes increase and not need to sell or the sale report for is exhausted first and then recovered and repeated on the second boxnation and so on. And the strangely the person I mentioned a day of Survivor, I still have a completely different profile. So in this case, the immune responses are totally, you know, kind of unexpected, very unique. So everything was a kind of disorder and even their consequentially Consequently, the sea did not develop satisfying about of antibiotics to to the same as called Saskatoon. Okay. So in a sense, is your system a sense to you seems to be in this since you have way too much customers to eliminate the Adel row so that he doesn't have any space to left or to be to left to be left for any further preparation for the new ethics. This is so simplistic and having finished the initial analysis of initial age 10 people and we are scaled this analysis to 100 people. Actually it was started with 100 individuals healthy people, elderly people living nearby living near from my Lagasse of consumers. City. So and it's been four years and every year, we take the blood samples and from them and that's the stats and after four years survival rate is half architecture. Now, not that the survival rate is so and you know, we are having the committee so sometimes there's some half of the people stop coming up over samples of tapings sit. Still we're having a contact to 50% 50 elderly people, the biobank study is doing so we did the prep, you know, many of the analysis is like lots and a single cell analysis I told you know, lead and other things. And because three are focusing on just 50 people on 100 people, they could do as many things as possible. That is the kind of final phase and this is a holdover from swap taking or something and the other center with taking lots away distributed templates as not much to them, keep monitoring them daily, nice. And these days as many people are taking pictures of their daily foods. And so that the measure novices can tell what they're eating and what the, you know, nutritious are included in them. And so, and also we can monitor their sleep status, you know, because it's a watch, we ask them to go away or the watch owners. So, say that everything's and this is the kind of the example of single cell analysis and this is a control samples from 50s 60s. And 70s and Bs and by the way, I didn't miss this mistake, so and that's a religious survival rate is a kind of exaggeration. But anyway, the devil to be honest, we primarily said the older pupils applying it because the endpoints necess is a clear thinking about the average longevity, so which is 85 years old, so we don't have to stick to those cell phones in five minutes. Okay, so anyway, this is the one so the upper upper panels are from LEDs and the lower panel is say 50s or 40s. Okay. So there is a clear difference. They are certainly the biggest one, this is the cells or not in cells, and the red cells T cells. are in their cells. So, there seems to be a clear difference between younger people and younger in terms of cell population for us. So, we tried to condense from firstly, from the statistical point, we conducted the this kind of analysis and initially there is a maybe I didn't have time to explain in details, but there was a study on their age clock, starting from the methylation analysis. And usually we looked at we did that also the array analysis, and they that's a standard way is to do the decomposition analysis for the methylation problem and to stick to it, what is what cell types are include, even starting from the alchemists. And this is our study is also consistent with the previous papers results from the previous papers, telling best indicate cells are generally increased joy with the AC and on the other hand, car sales are decreasing with the aging introduced are consistent with previous reports. And as far as the epic Ra is concerned methylation bulk interface analysis concerned this is the limit of the resolution analysis, the cell composition and site of analysis we can go forward because there is a cell surface markers and we can do the finer and finer resolution analysis and telling this among the say NK cells, and especially let NK cells increase and even number of B cells and the memory cell memory these cells articles are more and more relevant among these cell types. So, either with the help of a single cell signal analysis this is single cell RNA seek and ataxia is the simultaneous detection of a genome and transcriptome. And with the health of the single cell analysis, we're gonna go farther. So these are NK cells and some of these cells and the naive cells and then not C not at sales, and the idle conduct at this point in time, the cells cell types that are associated with the plastic responses of the new cells seems to be real less relevant in the era of aging. So, and even with the gene expression with the clustering gene expression information, we can kill father and even among NK cells, and based on the clustering analysis within NK cell populations, depending on the every cell marker of the MSL ranges of the details into cells, and we found that even though generally the NK cells are increased with the AC on but not eve the TAs NK cell which are represented as a series of 56 Bright NK cells decrease with age. So generally, the cell population analysis assesses deaths for dementia about the same, there is no significant change this this officer for the monocyte leads except for I excluded those cases from this analysis entirely. The case really detecting the cases for criminal drug clonal hematopoiesis, which is the chairpersons research and legal status is triggered by degenerative mutations beyond the scope of the salary, which is focusing on drastic changes. So and except for this chip cases, and there was no changes more in more size. And the aura indicates our cells, T cells and B cells and T cells are very new, which I will explain later. And so the along with age, certainly not eve the plasticity that cell types are decreased. So it's may suggest that solidstate as the with aging, some plastic responses are gradually deteriorating with the elderly.

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So after looking at the cell level, you know, the challenges with aging, we try to go farther into the age related genes, individual terms. So we were able to detect some genes which are associated with aging in terms of the chromatin openness and the gene expression levels. We found off the synergies and the replacement of the ones are like this, these days, CD 240 A King is shown the red related to decrease like this, and so so is the cross promoting openness. So the dream is having close chromatin with aging and so then, on the other hand, the consistently, the gene expression levels reduced so that the patient voices to these numbers and these are shown here. So the chromatin is closed and the gene expression is worse are we really detected? That's 145 genes with HIV AIDS related in terms of the oral expression levels, and the only other has a chromatic openness level 50 gs en us age related, but somewhat unexpected. Those G's rarely open. So in other words, there is not all this consistency between the chromosomal change and epigenome changes and the gene expression changes, only three genes have or even though these genes are key genes for controlling the cell, you know, not even as and the cell proliferations to maintain the cell operation. And one genes are totally remain unknown. So maybe the Chapter Two The targets are from our analysis, but it's a kind of like, the genes are not always there for the gene regulations. The Chroma chromosome chromatic chromatic openness and the gene expressions are not always strictly speaking. So that says that I forgot to mention that this is the bulk level analysis see the bulk analysis all the cell types taken together. And we were tempted to go further into details and this is an airport all cell types meet together to identify the genes associated with Asian and we try to identify genes associated with meetings with every cell type separate monocytes and T cell and B cell and emphasis so and we were able to identify a larger number of genes associated with the aging and in terms of RNA expression and chromosomes. And we found that Si, RNA expression and exchanges are not always normal, each other but still we were able to identify by these numbers of chains having the agent Association in terms of the trusted domain and the open chromatin outcropping, openness respectively. So and we found that the chance of the most relevant invoices like this, and therefore by you in your cells, and the home period to those offices depends on the type of individuals and that's obvious. But this for the other cell types like the acquired type in essence, the invoice acquired immune responses in these cell types, T cells B cells, the changes in terms of the level of gene expressions are received less. So, okay, so the G firstly on the monocytes here after my presentation will be like discount for sale and the team experimenting and each meta analysis shows let's say the model for these things the model size, the age rating, which is depicted in the model size some days, the mostly those days are inducible genes. So, the like the self IR reform is one of the most remember representative checks and different responsible party is the chain which can be induced Okay, by the set infections or the new stimuli because reactions, so, and this is all under the same ATS and these are the overstaffing T's So, the induction level if others notice the healthy stage that changes may not be relevant always. So that's is the reason why the changes in the legislation levels and will promote the openness levels are not are not always consistent, okay. But when it comes to the industry, by the consulting, say infections and so on the the degree of the induction sensitivity is relevant in over 80s rather than on the status and that is represented by the gene expression enrichment. The gene enrichment analysis library is shown here. So, and other datasets are alike that's monocytes T Sam B cells and these are kind of in between. So, different sets of genes are detected us is lated from T cells and B cells showing that the acquired immunity and innate immunity is they have different influences five is okay. So, and that instinct inside of say, the diverse gene sets depending on so between the innate immune responses as your cell types and acquiring cell response types, and we looked at we look examined, more than any of the T's are calling for changes, regardless of the net and apply them. So we found that Steve are really QGIS like 36, which is the system demethylation of SDK 27. Okay, which is a key player of the genome replacing gene is demethylases depressed, that's honestly okay. So, and the monocyte and NK cells are all are in the RNA level of the use. For all the cell types. But this for the reduction is the gene expression or reduction is the most relevant for monocytes and NK cells. And men seems to be in theory, that repression of this gene, so stabilizing the gene expert chromatic chromosomal repression, so, and to eventually make the cells less reactive to the any infectious, the responder responses. So, and the sub conclusion here is the the types are quite different between the myeloid cell cell types and lymphoid neoload and lymphoid cell types, okay. So, the seller population changes are more relevant in lymphoid cell lineages lineage, okay. Like this, right? And on the other hand, the gene expression level changes are more revenue in monocytes RedEdge NK cell, which is having both of both of cells, number of the cells are changing and also inside of the cells I change that because that is probably because the NK cell is the junction point collecting the India cell response to the acquired cell response. So, yeah, please, others. Before going forward, please understand my I'm talking but this is just a preliminary No, anyway, sickness in that number. Yes. And yes, that the results are now fully validated. So, they are all wants to listen to my talk with us. So, can that's is enough. Currently we have this we are thinking that that will do we will be doing the validation analysis to ensure those participations are taking place in Davao in annual sets. So, that's the thing and we I talked from the statistical viewpoints but the reality is that's the status we are during looking at the daily stuff statistical analysis and looking at the genes by genes, the cells types by cell types, okay? We know this deaths. The Profiles are so diverse between the individuals and so depending on cell types, so there I was quite doubtful suspicious. Whether we can do this statistical analysis might outweigh and we can say that it's as you get to do or is something more realistic thing is the profile sometimes depending on the individuals. So with that mistake, this is an exaggerated exaggerated example, extreme example. In this case, this is our elderly person, and having this is a different person from the previous one. Somebody from the AML this is this person shows up in say in 21 in 2001 15, not so rare, but not so. Not so frequent, but not so very rare sale, and NK cells are here. Maybe you can see how these cells in profiles of box are kind of new twist from the usual. This is the average of 7070s 70s. So it's more than doubled the NK cell population was so we looked okay, there is a bit there we looked at the genomic mutations and ensure that the you know, chromosome accumulate from our

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clonal hematopoiesis. And that mutations were found in that similar property in the cancer population and left us there is chips to patients and individuals on a chip profiles, like this way, but that is not that's another story. So, even though those individuals are how they are very standard in their cell professions, no genomic mutations, more of these from these two individuals. And that those are two with less than 30 persons here and if you're 75 years old and 80 to five years old and had a very standard and good populations, and we follow that these two individuals and one is therefore the second block sampling, and one individual showed the decrease of the empty cells. So maybe this person was suffered from infectious diseases or from maybe possibly information artifacts when the test was taken. So and this is the expression profiles for the donor one time at the time point one and 10.2. They especially this molecule, it's like a cycle, it came all times and granzymes decrease in time for us. And in this case, on the other hand, in the donor tube, the expansion of the MK sustain for more than two years. So there's a kind of clonal expansion of medical cells. And the interesting thing is that as compared to the say, the MK or the MSL profiles of the this information time point in donor one, so this they don't have to throughout the time course they expression profiles on this from sales since CBT, as these patients into cells are kind of losing the immune reactivity in terms of information reactions, okay? So it's almost at a similar level with the recovered time points of the donor one. So we looked at actually apps are found there is a set of serum proteins profiles are using all income analysis and and found that's really the best take the best individual are showing the clonal expansion of the NK cells. The patient, the same focus on this inflammatory than say, the other person. So taking those things together, we have a game desk, there are several people in which the US thus landscapes are having the condition of this untidy format, even though they indicate cells are expanding to some extent, and showing that it's you know, so and without looking at the gene expression of individual genes, we will now be able to tell the difference between those two cases. And that that's that changes are firstly become relevant when those individuals are infected. And may or may develop diseases and cancer. These are the immune responses are why. So and similar stories are we have had a discussion with the human Cell Atlas people. The similar you know, the four or five things are starting throughout the Asia South East Asia and Southeast Asian countries because every country has a different in yourself probably have the compare the landscapes depending on different ethnic backgrounds and countries. And please note that in some of the Asian developing countries, infectious diseases are still relevant the main cause of the diseases in their infancy arrangements. So the shape of them in other states may be quite different from those in Japan, or developing countries developed countries like here, so it's important to understand inflate our previous medical workers are to shape the credit union logistics. So and this is how many minutes left for me. May I have things Okay, so, so this is not currently we are matching the best molecular profile data with their life so much that they're smart, also considered matching the smartwatch data. So and on the other hands and we are quite excited. The results are simply simply quite interesting in the sense of single cell analysis, but the obvious issue is this. The single cell analysis is very costly. Okay. Big money is going to 10 XX cells and only have their hands and the way you want it to scale. That's analysis to say 10 times larger number of people that you know, no funding we I cannot find any time agency to separate us from other money. We, we only have that has as a sequencing core, digital core. We are doing lots of special things these days, using Xin okay often accent AmEx, mainly focusing on cancers and other those kinds of diseases. And we tried when we can make use of the zendium analysis from a single cell analysis even though we're looking at the PBMC which is of liquid, but we can prepare the smear in a sample, putting the cells scatter over the Xenium slice. And so it's possible actually, and the good thing is that we can organize mediums of cells on the sides at the same time, which is 100 200 times larger higher number than usual Chroma. So then the clustering can be finer and the cost can be reduced because we can put till the separate but separate that multiple samples by looking at the office. I'm not part of actually, we can separate the areas of the smear samples, physically sales, sales, and we can separate and I'm very tempted to say 22 September 20 Depending on how many how many cells you want to on us, assuming that the two menial cells can be analyzed on a single size. We can use we can use it for the analysis of 20 images so that it's 20 times less costly than the current a chromium analysis. And so the data shows up like that's why the whole cell profiling and I provided the protocol will connect someday. Format protocol using the five case any images recently, not yet launched, or it will be launched very shortly, and actually does that perform worse and we compare the results with these singles cell analysis across goal setting and flex single cell sequencing. Starting from the FFP fixed blood samples, the results are mostly consistent with each other, each other some T cell types on the same form single cell RNA class help single cell previous symbols are all there or SeaPlex. But we have a new test is a new analysis is more real, because it's known as the newer in the course of the PBMC purification and the analysis some help cell types are most likely so you don't feel is is not enough to share. Your significant Yes, that's the one I was looking for. And these are clearly presented things in a usual single cell. He said the same thing that can be done on the immunostaining as well. And we're forgot to mention but we are using this point of Biosciences on the phenol cycle of fusion. And recently we are you know we did have kind of a design that does normal things. And the good now we can use exactly the same size. Firstly for shading and them that in using does the same slide to the following psilocybin analysis. So we can detect simultaneously the RNA and proteins. So the results are shown this way. So this is the screenshot from the last tutorial. I don't remember set number but anyway, that immediately makes sense. And this is a CD for posterity reg and CDA is the place as the cells are normally interacting with each other in their cell anyway, so that's, I'm sorry. So anyway, we can we may be able to reduce the cost. So and with that perspective, we're, it's we now I think, on this I believe it's time to see or to think about, we can integrate a single cell analysis to the part of the biotech, a cohort analysis, which started with the genome sequencing. So this is the conclusion and single cell data, I believe, should provide a very important information in addition to the genomic diverse diversity and alive data insight. I did not mention levels of isolation in the market, but that's coming in so and the international collaboration is of course, very important because different people are having different lifestyles and different ethnic backgrounds and that's the benefits should be diverse

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people, so and this anyway,

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please contact me at YSZ UK I have a CCT and LJP and I'd be happy to share the information because most of the data is collected on the hybridization based protest. So there is this restriction from the informed consent issue is less strict, because it doesn't present any sequence information. So we are coming to a free view we can feel free to share in terms of data sharing as well. So this is a very last slide and I like to thank all the participants who are sticking to my kind of crazy, you know, that single field analysis the other people didn't see that area, and as some might poke here and thank you for your kind attention. I'm happy to take any business thank you

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I was really interested to see the survivors

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answer that's fine. But I was just wondering, were they actually less able to fight off like a virus infection or bacterial infection? Because you said that from the from the vaccine data, we're not able to just avoid it actually worse of ourselves.

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Yeah, yeah. Yeah. And everything is still really messy. So that's a nice collection of labor pieces of information. So that this is a molecule of data and maybe taking the life of data taken together. Presenting the body temperature and vibration great and so maybe we can tell whether the person is belt is not yet

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an interesting path. I have a question about this study design. So far, the correlation cell type correlation with age. So why not just do a large scale samples and then do computational income motion to examine the correlation between cell types and age. In that case, we'll have larger samples.

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Of this is the 50 samples mixed together and the statistical analyses coming to the plateau even though these things so it does the answer to your question.

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Like you mentioned that it's always Yeah, so let's take the samples, right. So if you want to have maybe a larger sample size and if you do a bulk I RNA sequencing,

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I don't think so, because the you know, the on the other hand stream diversity is an issue from the outside from the other hands, okay. So, and actually at the bulk level, all the all the subtasks linked together, the statistical analysis lady, probably, in the usual sense but when we went to deeper into the cell type specific model, we have a T employer yet different statistics, this is still statistical level. For example, in this case, I omitted dispersion and that they this every not because it's the top from the individual. So in this case, there is there may be a statistical correlation between the expression and individual Asians. But then we have to employ this, I don't know locally estimated stepped up for

42:10

smoothing analysis,

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which is quite tricky. I have to admit, and they're overseas. Yes. And so they're you know, increasing the level of samples will make things more even more messy, and most messy is not a bit more self the more challenging. Okay. So, there we have to develop yet different new methods to deal with this. Kind of originally diverse profiles to throw high stress, some statistically live updates, the statistical reverses can take the worst because the everything every event is taking place on the individuals cell, an individual person is living happily on his or her own cell.

42:55

At right, so let's study does anyone know I mean, if you're new crazy sample size, you can come from more covariance, right. So that was a sample. My second question is you want to examine the correlation between cell type proportion and age, but then there are different covariates like maybe the location, the individual live, sex, yeah. Are habits. So they're all relevant? Maybe it's not relevant to age but naturally, according to some type, of course.

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Even in those cases,

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I said, that's easy. Even though in that case, that's profile is that that's presence. We call this of age or gender, sex lifestyles, and the marriage we cannot generalize. That's the weekend of Islam. It's mainly beauty. As I said, those features we have the gene expression in their molecular profiles, but still I can say it's true for that.

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There's a conclusion about you know, because you have some flour to the patient as aging cell types, decrease some type of force and decrease. So that was one of the conclusion that it was

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an issue. We are now thinking that the history is large enough number to say anything statistical, per se from each individual. I'm almost confident that these are even these things. So that's a way of thinking how you think about make use of these data sets. If you think I will make use of that data for the personal size for us in the ServiceNow responses. For example.

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I had a question to remind you to ETech analysis that he performed so how did you define openness? That's a very

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tentatively you know, I cannot edit

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harmony right now, sir. And we try several cut offs. And it's a it's kind of tight now of tasks. And number of enlistment, the degree of enrichment of the given function, and we found that the target is spent on this promoter in reasons so we didn't come the enrichment of the enhancers because we are all in the share rarely across all of it. So there are lots of things in terms of detecting the complex so is the case of our next film.

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There might be like more enhancer gene regulatory, yeah. Could be more specific, which might not be seen at the promoter level. So so it will be interesting. Yeah.

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Based on the Sanders the new model the beginning of the story, see most of things Sonia said Yeah, I know that we I'm, you know others in I'm presenting more questions more customers is

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that a separate question from an immunology perspective also, sorry, exports, you have extent UCEDD extension and NK cells and your one patient who as a co variable of cancer, and then you see a decrease of natural killer cells. What can you say that these are? What are your thoughts on saying that these are expansions based on site off and single cell RNA seek data we're just proportions. And

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because they for years has passed since the initial start of the analysis and MSA strict as analysis taking some individuals are starting to develop diseases including cancers, and I did not mention about that because it says it's a somewhat different story. So,

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this specific base like are they actually extending or other cells contracting your your NK cells, express proliferating genes? Case like C seven

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publice. I can Yeah, it's nothing is annoying, but clearly Vani did, but looking back the data once we saw the actual development of the diseases, we're it's also first thing, but we are thinking that some you know the sign is still relevant even said before the actual event that the onset of the diseases so yeah, it maybe it's a different way to answer a question. Thanks.

47:23

Thank you very much for your beautiful talk. I have a simple question. I do understand there is big difference between among the individuals and also the even the time for sample collection like daytime and nighttime. So my question is, and also you analyze, so you analyze the single Samsung data and also the proteome data as a validation. I just wondering as a match data, I mean for each sample to get is multi omics data like transcriptome or some new things are already being discussed. Thank you. So in that case, I have another question. So the messy mission for us the new money can Is it possible to get the bank met Dina also

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can you repeat your question against the

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masa you mentioned for saving money amid a single cell sequencing technique is very expensive. So the method you mentioned there's a method to save money yes

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or no as far as the cell population is proportional, the seller population is concerned. I think it's high office enough, which is cheaper than the single cell analysis. But the you know, if you want to go to the gene level, individual gene levels and sell the single cell analysis is needed. And maybe we can reduce the costs are once the targets or the separation, separating and practice on the solid does that set up a Surface Book is most wherever and we can focus on set pallial type analysis. And that's the same in our based analysis is maybe one of them and we can it's in between, and we're looking at the number of genes, selected novelties, and together with the same projects. So there are many ways to think to scale the smallest the initial reference surface. Thank you.

49:33

Okay, thank you so much. Chuck Christian from behind. closed session. Thank you so much.