Okay, hello everyone.

Today, we are very fortunate to have Dr. Codruta Chiuzan as our speaker.

Dr. Chiuzan is Associated Professor, Institute of Health System Science at Northwell Health New York. Before that, she was an Assistant Professor in the Department of Biostatistics at Mailman School of Public Health Columbia University.

In her research area focus on earning phase clinical trial designs and an average aging real-world evidence to prove all the cons and increased diversity.

Now, she is in receipt of Junior Faculty Research Award and the Columbia Public Health Innovation Award from the Mailman School of Public Health. So, Dr. Chiuzan, has a very strong record of mentoring, both master’s students, PhD students and clinical fatal.

She is an active committee member of JSM, Diversity Mentoring Program and she had held leadership positions as the President of the American Statistical Association and New York City Metropolitan Area. and she as the Chair over the Student Scholars Committee.

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So, welcome Dr. Chiuzan and time is yours.

Thank you so much Wei, for the invitation, it’s a pleasure, I’m going to share my...
Is anybody (indistinct).
The host, can you disable the screen sharing
so I can share the slides?
Oh, perfect.
Okay, can everybody see the screen, the full screen?
Okay.
All right, so it’s a pleasure to be with you
even virtually and I’m glad to see so many people in
person with academic semester ongoing.
Today I’m going to talk about one area of my research
and that is early phase designs for immunotherapies
or cancer immunotherapies and I will take you
through a journey, through a story by giving some
eamples
and explanation of what are these cancer immunotherapies,
what are the promises, what are the challenges
and how do they actually reflect in the early phase
designs?
Then I will talk about current models
and a model that we developed on has been implemented
in an R package and the Shiny app
and will conclude with a practical demonstration.
Please, if anybody has any questions at any point,
please feel free to raise a hand or just ask,
I like us to have an interactive session
to have a continuous dialogue if you’re able please.
So what is immunotherapy?
The New York times called it a long awaited reality
because immunotherapy has been developed
since the early 1900s, actually by a New York surgeon
that saw that in cancer patients that develop flu, had a better anti-cancer response. So immunotherapy works on a different paradigm compared to cytotoxic agents and by cytotoxic agents, I mean, chemotherapy or radiations. So immunotherapy boosts or leverages the body’s own immune system to fight cancer, to recognize it, to attack it and ultimately to kill the cancer cells. The three Rs of cancer immunotherapies are reverse tolerance, rejuvenate the immune system and restore the internal environment homeostasis. So, you’ll probably hear more and more updates and FDA approvals for cancer immunotherapies. Between 2017 and 2020, over 65% increase has been seen in the number of immunotherapies and these immunotherapies, most of them have been approved for immune checkpoint inhibitors, Ipilimumab, Nivolumab and Pembrolizumab that works by incubator thing, the relationship, the association between the PD-1 and the PD-L1 receptors, but the largest growth has been seen for cell therapies. And what are these cell therapies? The most frequent and the most study one is called T-cells, so far, which will be approvals. So that these old therapies use the T-cells in the body to fight cancer and then you do that by first, taking blood from the patient, isolating the T-cells in the lab in the Petri dish and genetically modify...
these T-cells to display a specific receptor that then is introduced and after that when the cells are being introduced into the body, this T-cell receptor will bind to specific antigen present on the cancer cells and trigger an anti-tumor reaction.

So these are the T-cells, these are the cell therapies that are being studied and they’re very promising in terms of prolonging overall survival and also in lowering the toxicity, killing cancer without killing the patient. Last year update from the Cancer Research Institute has shown that, as I said, that the most promising field in cancer therapies are, has been seen in this T-cell therapies, most of them for a solid cancer, nonsmall, renal cancer, colorectal cancer, but it’s moving into the non-solid cancer as well.

So, Hype versus Hope, I entitled this slide, immunotherapy, is it the holy grail is the answer to all cancer therapies, yes or no, because of course it comes with some challenges. Some of the challenges are immunotherapy sometimes can trigger delayed responses, meaning that the treatment has to continue even if initial response has not been seen, there’s been cases of hyper-progression where the cancer tumor seen this rapid growth in the early stages and that can be the problematic on diminished overall survival.

And most importantly, we’re not really sure exactly what to measure and how to incorporate end points
into all phases of drug development from early phase, phase one and two, where we’re looking at identifying the optimal dose to later phases. So, because it’s still under development, there is a lack of biomarkers to predict the responders versus not the responders and the difficult to correlate these immunological biomarkers with outcomes, clinical outcomes, overall survival response progression, free survival compared to cytotoxic agents, chemotherapy, immunotherapies have different toxicity profiles, meaning they can have lower toxicity and also different grades and different profiles, is called by, also called as immune-related adverse event. So if you’re familiar with drug development phases, as you know that usually it will start with early phase. Phase one, identifying the maximum tolerated dose to be carried forward then for establishing efficacy and in later phases. In the old paradigm, so the objective was to find the MTD and the MTD was mainly based on toxicity as binary, yes or no DLT, the patient has after receiving treatment, we quantify the number of those limiting toxicities, unacceptable toxicity within a certain interval. However, the new immunotherapies have, as I mentioned before, they have different toxicity profiles, this old paradigm of finding the MTD, does longer stint, there are a lot of trials where the dose escalation moved quickly to the maximum dose level and MTD.
There were no DLTs, the MTD was not identified and most importantly, toxicity and efficacy might not necessarily be those dependents. So you might be able to find a safe dose, but that might not necessarily be the most promising one in terms of efficacy.

In many cases, we actually see this plateau trend where after a certain level, the efficacy levels out plateaus and we don’t see any effect. Another challenge, so in this context of different toxicity, is different levels of toxicity incorporation of efficacy into the dose finding process, we need to reconsider the definition and think of more in terms of identifying the optimal biological dose versus the MTD, a dose that is acceptable in terms of toxicity, but also this place, a good efficacy profile.

So in terms of methodology, again in early-phase, research has been dominated in the past decades by algorithmic designs by algorithmic, I mean the three plus three, which is definitely not preferred by, and actually strongly disapproved by statisticians and even until 2014, when we did the last review of early-phase methodology, we saw that over 90% of this trials have implemented a rule-based design. Rule-based working only on toxicity with absolutely no statistical background.

From 2012, we saw more than 60% of the trials that the tested targeted or immunotherapies
and only 7.6 actually used a model-based design.

So what do I mean by model-based design?

Well, we criticize in three plus three, but are there alternatives actually several.

One alternative that addresses the matter of late onset toxicities that is usually seen in immunotherapies, meaning you see DLTs on toxicity outside of DLT window, that is usually 28 days so longer toxicities, for that we have the time to event continual reassessment method that was proposed by Jenga Chapelle in 2000.

The problem with multiple toxicities across different varying grades and moving away from the binary DLT has been tackled by Ezzalfani and others by using, by incorporating these types, different toxicity types and different grades into the total toxicity score, which is a quasi continuous measure.

As I mentioned for immunotherapies, it makes more sense to incorporate both toxicity and efficacy and for that we have models that look at, that incorporate both toxicity and efficacy and these are the F-stocks designs method or the bivariate continual reassessment method. And more recently, other measures have been looked at in immunotherapies and these are the PK, the pharmacokinetics or the pharmacodynamics and these have been incorporated by, for example, Ursino, in a patient design proposed in 2017.

So this is to present the status quo
of what’s being proposed out there, what we are suggesting is also a design that is specific or for immunotherapy trials and this was published in 2018 and since then we have added a different measure of toxicity, we have implemented it into an R package that is on a available on cram, iAdapt and also can be tried using charmia. So this design for immunotherapies uses both toxicity and efficacy to identify the optimal dose. Optimal dose meaning unacceptable dose with promising efficacy profile. The design is unique in the sense it can incorporate both binary or quasi continuous toxicity scores, and it’s looking at the continuous efficacy outcomes. Most of the designs that I mentioned before are using either binary or ordinal efficacy. In this one we’re looking at continuous outcomes, such as T-cell persistence at followup compared to baseline why the cell persistence, as I mentioned before, well, about this engineered T-cells when they are being put into the body, they maintain the steer soul store, then the genetic information and the trigger and tumor response and it’s been shown, there’s some studies shown that the number of T-cells that are still present, still survive in the blood at one or two months after being reinfused tends to predict response on the overall survival on the long-term.
The design has, does not impose any monotonicity assumption in terms of those efficacy relationship and does not account for dependence between toxicity and efficacy. So now let’s take a look at the two, the difference between incorporating toxicity only and looking at efficacy also. So the cartoon on the left shows the dose toxicity relationship or five dose level. So in this graph, let’s say we have five dose levels and we have a threshold of unacceptable toxicity set at 40%. So based on this graph, we have about four dose levels that are below the threshold, one dose level that is above. So if we have 40% toxicity threshold, dose number four would be identified as the MTD, the maximum tolerated dose. However, if we are to look also at efficacy, and in this case, the dose efficacy has this umbrella, this non-monitoring trend. We will see that by looking at the MTD, we would totally miss the optimal dose because dose number four has actually a lower efficacy as compared to dose number three. So this is to pretty much justify the need to incorporate both toxicity and efficacy into the dose finding process. So the design has two stages. In stage one, we’re establishing the safety profile at each dose, after we establish the safety profile, the acceptable doses are carried to stage number two, where we using efficacy driven randomization.
to allocate patients to acceptable doses that emphasis towards more promising efficacious ones. 

So, now let’s take a look at stage one, establishing the safety profile.

We have a number of pre-specified dose levels and we start by defining the set of hypothesis,

where hypothesis one represents the unacceptable DLT rate and hypothesis two, represent unacceptable DLT rate.

DLT, meaning the Dose Limiting Toxicity.

So the quantification of this evidence in favor of hypothesis one or hypothesis two, is done by the likelihood ratio V, the evidential paradigm.

So to give you a little bit of a background, in statistics there pretty much three school of thoughts, we have the frequencies approach based on Pearson, you’ll have the patient school of thought, and then you have the evidential paradigm.

The evidential paradigm and the frequent tests are somehow similar, but the difference between the two is the evidential paradigm based on the law of likelihood the couples, the strength of evidence from uncertainty.

So the strength of the evidence is quantified by the likelihood ratio and our certainty is quantified by the probability of misleading evidence and the probability of observing weak or strong evidence in favor of the other two.

Yeah, in comparison the frequent is the approach, that’s not the couple, the strength of evidence and from uncertainty.
So evidential paradigm used to establish acceptability in stage number one. And how do we do that? Let’s say we have a certain number of levels, each show, and we treat cohorts of size M patients to each of these dose levels based on toxicity information, we calculate the likelihood ratio and evaluate evidence as one of the three, either we have strong evidence in favor of hypothesis two, declaring that the dose is acceptable. Either we have strong evidence in favor of H1, it’s unacceptable or we conclude the weak evidence that doesn’t support either of the hypothesis, the likelihood ratio is compared to a threshold, okay? So how do we, let’s take a look at an example to see how we set the hypothesis and how we started this threshold, okay? So let’s say that we have hypothesis one 40%, this is unacceptable, the DLT rate toxic and hypothesis two 15%, that is an acceptable DLT rate and we want, we evaluate each dose based on these two hypothesis. And for that one, in this case, we use a k threshold equal to two, so there’s been a lot of literature written on this evidential paradigm and the k thresholds can vary, we can take values from two, four, eight all the way to 32, depending on the sample size, the bigger the sample size, the bigger the k thresholds. Because in phase one, we tend to deal with limited
sample sizes, 30 maybe all the way to 50 number of patients,

of k threshold or two or four seems to be sufficient
to be able to quantify the strength of evidence.

So I teach dose levels based on cohorts of three patients,

we compare the likelihood ratio and if the likelihood ratio

is greater than one over k in this case two,

we decide that the dose is acceptable and safe

and it will be carried forward to station number two.

Otherwise, the dose is considered unacceptably toxic

and it’s being discarded and will not be considered

for further evaluation.

So in this case, let’s say that we have two or more

the maximum doses in stage one, we continue to stage two

to employ an adaptive randomization.

So in stage two, we use a linear model

to calculate the randomization probabilities

based on efficacy and in this case we use indicator variable

for each dose level and Y represents the continuous

immunological response and as I mentioned before

in our application, that response is a T-cell persistence

at one month after infusion.

So based on the estimated Ys,

we calculate the randomization probability for each dose

and allocate patients sequentially based on this path.

So how does this look, let’s say again,

that we have for dose levels and three patients treated

at each dose level, we measure the T-cell persistence

for all patients within the cohort
and we feed the linear model to generate the estimated efficiencies. Based on the estimated efficiencies, we calculate the randomization probabilities. So for each dose, in this case, the randomization probability for dose one is 5%, the highest is for dose number 49. So the next patient that will be allocated, will probably be randomized to dose number four, because this one has the highest randomization probability, and the process continues in stage two and feel you have reached the maximum sample size that you’ve specified for the trial.

So how did we evaluate the model behavior? Well, we looked at two different sample sizes, 25 and 50 patients in total for the trial. The number of levels varied from three to five, we don’t recommend using this design for less than three of dose levels is just not enough. The design that you don’t gain anything by using it if you have less than three.

We use the 5,000 simulations for each scenario and in terms of establishing the operating characteristics, we quantified two things. One, we looked at present those allocation and we looked at estimation of efficacy outcomes, because that is the main goal actually, after implementing, you’re looking at both toxicity and efficacy in determining the optimal dose.
with the goal of allocating more patients, skewing the allocation to a dose that is acceptably safe and has promising efficacy, in this case has a higher percentage of these helper system. So this is our combination of efficacy and toxicity scenario in panel A you see that we have five dose level on the x-axis and on the y we have the T-cell persistence increasing to non-monotonic and also to plateau, which is scenario number three. As I mentioned, this is a pretty frequent scenario at a certain dose level, the efficacy, that’s not, we don’t see any big increases in the efficacy. In terms of toxicity, again, different flat trends on the steeper dose toxicities scenario. In terms of beta stimulation, toxicity was stimulated from a Bernoulli distribution, persistence was simulated from a beta-binomial and for variance, the variance was assumed to be a constant, but we then read the values of small and large, and to give you an idea of what means a large variance at 1%, that is equivalent to about 20% deviation from the mean T-cell persistence. toxicity and efficacy are modeled independently. Some results, the paper on had the has several scenarios, but just to illustrate, this is for a total sample size of 25 patients both in stage one and in stage two and the design was compared to MTPI,
which is the Modified Toxicity Probability Interval.

And we wanted to compare and this is one of the operating correctors, 6% patient allocation.

How does the design allocate patients based on toxicity and efficacy?

So in this case, that toxicity we see is toxicity three, we have five, dose levels, the three dose levels have toxicities lower than 15%.

Dose number four has a toxicity between 15 and 40%, and dose number five pretty much is at the maximum DLT threshold.

’cause remember that we had two hypothesis, 15% acceptable toxicity and 40%, so dose one, two, three are considered acceptable.

Dose four is within the interval, 15, 40% as shown in red is considered a toxic dose.

So this is the same toxicity for different efficacy scenarios increasing, this non-monotonic this umbrella plateau.

this umbrella trend.

Dose four is constant efficacy across all doses. So what we noticed that the design does a good job allocating most of the patients to a dose that is considered safe and also has the optimal efficacy.

So this would be dose number three in panel A, again, dose number three in panel B and similar for C and so ultimately we allocate most of the patients.
to this optimal level.

Now let me, I would like to show you an illustration of how can we use this design, its implementation in the R package and in the Shiny app, because the package has two purposes. One, is to run simulation, to observe to quantify the operating correctly sticks for different dose, its toxicity dose efficacy scenarios and another benefit is that you can implement it to actually allocate, to run the trial, to allocate the next patient to the optimal dose.

So simulation and implementation and the scenario that I will discuss next is inspired from a real study that we worked on when I was at the Cancer Center at Columbia and this was a phase-one trial evaluating modified autologous T-cells this genetically modified T-cells in patients where the recurrent solid tumors.

So if you think that all these designs are usually theoretical or just great statistical proposals, actually this one had an implementation and had a real setting. So the initial design that was proposed was of course, an role-based design derivation, this was a two-by-two with up to five dose levels, and I wanna bring your attention to the dose levels. So in immunotherapy, especially in this T-cell therapies, the dose levels are not quantities of dose age of the medication are not milligrams, but they are actually the number of T-cells.
that are being infused back into the body. So in this case the dose levels vary from 50 to 10
to the six to 500 and 10 the six viable T-cells, so millions of cells.
And we wanted to explore what is the optimal dose
for this regimen.
So, this is a snapshot of the Shiny app, we redesigned the trial to incorporate both toxicity
and continuous efficacy and in this case continue, this T-cell persistence was a reasonable biomarker,
we looked at five dose levels, we had in simulations,
you have to specify what are the toxicity to toxicity
rates and what are the T-cell persistence levels.
The true toxicity rates varied from five to 40%,
the T-cell persistence varied from 15 to 40%.
We didn’t see that we’re going to see more than 40%
persistence followup and we looked at the total sample size
of 30 patients for the trial, this was feasible
and practical.
So the setup it’s very simple,
you just put the number of dose levels,
you specify the toxicities, you specify the mean efficacy,
the variance for the efficacy, we chose 1%,
but this can take different values,
then of course, this is a dialogue that you have with your clinical investigator,
Hopefully with data supported from previous studies
and what is considered to be to very these parameters.
Then for stage one, you have to specify the two hypothes-
acceptable and unacceptable DLT.

For this one, we set it at 15 and 40%,

the likelihood ratio was set at two

due to the sample size of 30 with k equals to two

is reasonable and three cohorts, three patients per cohort,

meaning each of the five dose levels we have three patients

allocated each.

Total sample size of 30 on the stopping rule,

stopping rule meaning if none of the doses

are considered acceptable in stage one,

we’re going to allocate up to nine patients

at the first dose to further establish toxicity,

and this can be changed to six or other number.

So these are, how did the scenario looks?

This is the graphs actually generated by the app

toxicity and efficacy as a function of dose level,

and now I’d like to ask you, ask for your participation,

looking at these two scenarios,

what do you think would be an optimal dose level,

the recommended to be studied in phase-two or later?

Okay, maybe we need some hint,

so we want an acceptable dose.

Dose number three, dose number three,

due to dose number three is way outside

of the acceptability range and also dose number three

tends to have a good efficacy after dose number three

don’t see any improvement in terms of efficacy.

Dose number four is between the 15 and 40%

then dose number five was probably toxic.
So, dose number three is the optimal dose and what we would like to see, is most patients being allocated at this level. So in simulations, this is simulations for stage one, where based on observed the DLTs, we calculate the likelihood ratio and mark the doses as being acceptable or unacceptable. So in this case, based on the simulations, we see dose one, two, three and four are considered acceptably safe and they will be carried forward to stage number two, to be considered for that different organization, dose number five will be discarded and will not be used in stage two. And why is that? Because the likelihood ratio is less than 0.05. Now these are the simulations for a stage number two, so in the first part, we had five dose levels, three patients each, so that’s a total of 15 patients starting with patient number 16, we moved to stage two and we do this adaptive randomization until we reach the maximum sample size of 30. So the app actually gives you simulations and allocations for all the patients from 16 to 30 dose assignments and efficacy outcome and this gives you a graph of the estimated efficacy and the medians and inter quartile ranges. So we repeated this a hundred times, you can repeat it more in terms of allocation based on the setting.
Based on the parameters, the hypothesis, the k threshold, the toxicity and efficacy scenarios scenario, we see that dose three tends to be favored in terms of allocation, where the highest media allocation, 26.7 and going all the way to 33.3 for the 75th percentile. In terms of efficacy estimation, dose number three or if you remember when we specify the true mean efficacy was 40, the median estimated efficacy in this case is 39.75, the 75 percentile goes all the way to 45, but of course that will be improved with as the sample size increases. So in conclusion, what does iAdapt proposals? It’s an option, it’s a viable option for incorporating toxicity and efficacy outcomes, especially for immunotherapy trials. The novelty is in the designing allows to model toxicity, both of binary and also as quasi-continuous measures and this was actually updated this year in the package to use the several types of toxicities and several grades, that continuous efficacy outcome is very relevant for immunotherapies and I really showed the example from the trial with T-cell persistence, it is a relevant biomarker, but you can use for example absolute counts, you can use a full changes, so design is flexible in incorporating other continuous outcomes. As far as I know, this is the only design at this point that uses continuous efficacy outcomes.
So in terms of operating characteristics, the design as well and allocating, skewing the allocation to optimal doses, estimation is marginally improved depends of course, on the level of various and the sample size and if anybody wants to try, you can use the R package, you can use the Shiny app to simulate to look at the behavior of different scenarios to put that in trial and of course, to use it to run the trial. I’d like to thank two former students, Alyssa and Laura, that helped in uploading the R package and Laura has created the Shiny app. And I do have some references in case you’re interested, but I can also share the slides later on. So I think that is it and I wanted to allow some time for questions and comments and feedback from you. Thank you very much professor. Do you ave any questions in the room here? Does anyone from Zoom have any questions? Cody, thank you for the presentation, I think it’s very useful to talk her way, as well as my future like your possible designs of the trials related to immunotherapy, I have one question. So you mentioned toxicity and... Does anywhere in the design actually dependent on the independence of toxicity and efficacy profile? It’s a great point to talking
0:45:18.4 -> 0:45:22.82 if we actually modeled jointly toxicity and efficacy.
0:45:22.82 -> 0:45:26.205 So I'm actually looking at the slide
0:45:26.205 -> 0:45:31.205 that you have the toxicity and like also efficacy profile,
0:45:32.935 -> 0:45:35.713 I think like say if we have an ordinal categorical,
0:45:36.72 -> 0:45:41.72 lets say for example, like say we pick a number three
0:45:42.29 -> 0:45:46.04 because it's intolerable toxicity
0:45:47.1 -> 0:45:49.94 and maximize the efficacy, right?
0:45:49.94 -> 0:45:52.24 And anything above that will be too much
0:45:52.24 -> 0:45:54.97 and anything below that will be like,
0:45:54.97 -> 0:45:58.803 say not like effective enough.
0:45:59.956 -> 0:46:03.89 So if they are actually,
0:46:03.89 -> 0:46:07.053 how about certain joint distribution,
0:46:08.79 -> 0:46:13.29 is there any thing we can do in order to like,
0:46:13.29 -> 0:46:16.953 'cause that actually affect the simulation much?
0:46:17.86 -> 0:46:21.55 So the current model does not account
0:46:21.55 -> 0:46:23.71 for the joint distribution,
0:46:23.71 -> 0:46:27.22 it models toxicity and efficacy separately.
0:46:27.22 -> 0:46:32.22 But as a next step we can look under to try to model
0:46:34.87 -> 0:46:37.95 that dependency between toxicity and efficacy,
0:46:37.95 -> 0:46:41.38 and especially for this novel agents,
0:46:41.38 -> 0:46:46.38 we've seen that most of the times toxicity as is related
0:46:47.64 -> 0:46:52.57 to efficacy, a stronger ethical, a stronger response
0:46:53.5 -> 0:46:58.5 does come with some higher levels of toxicity,
0:47:00.1 -> 0:47:01.81 but the current model does not look,
0:47:01.81 -> 0:47:03.873 they twist them independent.
0:47:05.79 -> 0:47:10.74 So do we, so is there, do you consider any,
0:47:10.74 -> 0:47:12.43 like penalty for example,
0:47:12.43 -> 0:47:16.01 like say when there isn't such a good, like a compromise
0:47:16.01 -> 0:47:20.386 between like minimizing toxicity
0:47:20.386 -> 0:47:22.7 while maximizing efficacy, right?
0:47:22.7 -> 0:47:25.5 So in the demonstration we have a compromise,
which is dose level number three,
if there’s, for example, if there is like a conflict
between dose two and we can, like we don’t really have,
like the obvious optimal, like say optimized solution.
Do we constantly there, like, for example, penalties
do we always pay for like toxicity,
like say minimizing toxicity over like,
say maximizing efficacy?
And then think it’s always, I think so for example,
in that situation, so you could actually take both
dose three and dose number four,
you could consider both to be considered for future trials.
so it’s not the definite that the dose selected,
that you’re always gonna reach a minimum of toxicity
and maximum efficacy, but you can look at different options
with as long as toxicity is acceptable,
you can consider maybe in phase-two
to look at randomized trial, look at dose level combo one
dose levels combo-two based on efficacy
and we’ve actually seen this in a lot of trials,
the immune check point inhibitors review that I talked,
it’s now in progress, we looked at phase-one and two
and the rate of success and the design that are being used
and the doses that are being carried forward from phase-one
and phase-two, and surprisingly only 30%,
in 30% of phase-two trials the MTD was used from phase-one,
the rest either they use a lower dose or they use a higher dose, but not the MTD. So absolutely we can have like a range, because if you think about it, we have a limited sample size, right? We need more information for efficacy, so to complete the clear, the winner based on efficacy might not be sufficient at this level. Okay, great, thank you. So the answer is before phase-three and as long as it’s below the MTD, the efficacy is important, is more important to prove, like, say to move on to next stage. Thank you.

Just connection. Sorry, we’re still having a little weird audio issues obviously, but does anybody in the room have any other questions for the professor? Or even we end the Zoom. Hello, we have a question there. Hold on.

Hi professor, I know we probably mentioned this already, but I probably didn’t typed that, can you repeat, maybe repeat what it was, what do you consider would be like an advantage of having a continuous efficacy compares non-continuous efficacy in your model? Yes, lots of information, so a lot of the lines
are looking at the efficacy as a binary or ordinal, there is actually one, I don’t know if you’ve heard of the Boyne, that’s also was published for immunotherapies and that’s using you take the efficacy levels and you either dichotomized to represent what is a successful or promising efficacy versus not, and you pretty much modeled the probability of a response, right one versus zero or at an ordinal level. Number one, I think we were losing some information when we do this categorization, number two might be difficult to actually establish this cutoffs and what represents a success or how do we partition this efficacy range for this novel agents. So by looking at the continuous values, we make the most out that information and we let it on, we modeled it as such, plus in the last couple of years, this T-cell persistence has been shown to be a promising biomarker. So it’s right on par with our proposal. I know this might be a tough topic to digest for students with early finding it’s not such a... It’s a (chuckles) framework on its own. So maybe not that everybody’s familiar with the whole terminology on the landscape. During that stimulation, you specifically... So the toxicity was stimulated from a continuity distributions,
0:53:57.98 → 0:53:59.34 is there any specific reason
0:53:59.34 → 0:54:02.6 why you choose these distribution versus there's,
0:54:02.6 → 0:54:06.383 and if we similarly from a different distribution,
0:54:08.28 → 0:54:10.54 well, how about different conclusion like,
0:54:10.54 → 0:54:13.07 well, there would be any dependence
0:54:13.07 → 0:54:15.433 between efficacy and toxicity.
0:54:17.14 → 0:54:21.026 Yes, so that’s, and so in this case,
0:54:21.026 → 0:54:25 the results that I showed you were for toxicity,
0:54:25 → 0:54:27.38 for binary toxicity, yes or no.
0:54:27.38 → 0:54:31.47 So in a cohort of three patients for each patient,
0:54:31.47 → 0:54:35.64 you observed either a zero or a one response,
0:54:35.64 → 0:54:39.1 given the binary structure, it makes sense to use
0:54:39.1 → 0:54:41.86 this Bernoulli right distribution
0:54:41.86 → 0:54:44.743 and that sums up to binomial zero or one.
0:54:46.22 → 0:54:50.43 In terms of dependency is with what Dr. Cheng
0:54:50.43 → 0:54:55.06 was mentioning, we did not specify any correlation
0:54:55.06 → 0:54:57.06 between toxicity and efficacy
0:54:57.06 → 0:55:00.18 and did not look at the joint distribution between the two,
0:55:00.18 → 0:55:04.09 we modeled them separate and probably
0:55:08.625 → 0:55:11.72 that would be a good point moving forward.
0:55:11.72 → 0:55:15.97 What’s difficult is how do we, what would be interesting
0:55:17 → 0:55:20.99 is looking at different levels of correlation
0:55:20.99 → 0:55:24.89 and see how in this joint distribution,
0:55:24.89 → 0:55:29.87 how the results with change, if we would capture that.
0:55:38.43 → 0:55:40.647 Okay, so any more questions?
0:55:50.318 → 0:55:53.158 Okay, so thank you Dr. Chuizan,
0:55:58.789 → 0:56:01.52 Thank you, and if you have any questions,
0:56:01.52 → 0:56:03.462 please email me anytime.
0:56:03.462 –> 0:56:04.48 (chuckles)
0:56:04.48 –> 0:56:06.28 And I’m sorry that you (indistinct).
0:56:10.4 –> 0:56:13.41 Okay, I’ll see you shortly, bye.
0:56:13.41 –> 0:56:14.31 Thank you.