0:00:01.11 –> 0:00:04.98 Hey everybody, I’ve got noon,
0:00:04.98 –> 0:00:06.12 so let’s get started.
0:00:06.12 –> 0:00:09.627 So today I’m pleased to introduce Professor Yiwen Liu.
0:00:10.5 –> 0:00:13.26 Professor Liu earned her BS and MS in Statistics
0:00:13.26 –> 0:00:16.32 from the Central University of Finance and Economics
0:00:16.32 –> 0:00:19.11 in China and her PhD in Statistics
0:00:19.11 –> 0:00:20.94 from the University of Georgia.
0:00:20.94 –> 0:00:22.92 Today, she’s an Assistant Professor of Practice
0:00:22.92 –> 0:00:25.89 in the Department of Epidemiology and Biostatistics
0:00:25.89 –> 0:00:29.04 at the Mel and Enid Zuckerberg, Zuckerman, sorry,
0:00:29.04 –> 0:00:32.243 College of Public Health at the University of Arizona.
0:00:32.243 –> 0:00:34.95 Her research primarily focuses on developing
0:00:34.95 –> 0:00:36.54 statistical methods and theory
0:00:36.54 –> 0:00:39.15 to harness a variety of issues in analyzing
0:00:39.15 –> 0:00:43.26 the high dimensional data or the complex data set.
0:00:43.26 –> 0:00:45.54 More specifically, her research interests
0:00:45.54 –> 0:00:48.3 include developing model-free dimension reduction methods,
0:00:48.3 –> 0:00:50.28 which are high dimensional data regression
0:00:50.28 –> 0:00:53.1 and integration methods for multiple source data.
0:00:53.1 –> 0:00:54.48 Today, she’s gonna talk to us
0:00:54.48 –> 0:00:56.94 about a model-free variable screening method
0:00:56.94 –> 0:00:58.59 based on leverage score.
0:00:58.59 –> 0:00:59.99 Let’s welcome Professor Liu.
0:01:03.96 –> 0:01:04.793 Thank you, Robert
0:01:04.793 –> 0:01:07.8 for your nice introduction and it’s my great honor
0:01:07.8 –> 0:01:12.06 to be invited and present my work here.
0:01:12.06 –> 0:01:16.02 So in today’s talk, I will introduce a model-free
0:01:16.02 –> 0:01:18.72 variable screening method based on leverage score,
0:01:18.72 –> 0:01:22.29 and we named the method as the weighted leverage score.
So as we know, this is a joint work with Dr. Wenxuan Zhong from the University of Georgia and Dr. Peng Zeng from Auburn University.

So as we know, as we’ve heard there’s big data error, there are numerous data produced almost in every field of science including biology.

So we are facing data extremely with high dimensionality and also data with really complex structures.

Thank you.

And we are facing data of extremely high dimensionality and really complex structures and how do we effectively extract information from such large and complex data pose new statistical challenge.

So to motivate my research, let us see an example first. Currently cancer has graduated from the primary cause of death across the world. Nowadays cancer is diagnosed by an expert who has to look at the tissue samples under the microscope. You can imagine that there are millions of new cancer cases each year and this often means that those doctors will find themselves looking at hundreds of images each day. And this is really tedious work.

And because of, you may find that, because of the shortage of qualified doctors, there could be a huge lag time.
0:02:56.58 –> 0:02:59.1 before those doctors can even figure out
0:02:59.1 –> 0:03:00.8 what is going on with the patient.
0:03:02.13 –> 0:03:05.13 So detect cancer using only manpower,
0:03:05.13 –> 0:03:07.821 looking at images is not enough.
0:03:07.821 –> 0:03:11.52 And we intend to build a statistical
0:03:11.52 –> 0:03:15.963 and mathematical model to identify, detect cancer
0:03:15.963 –> 0:03:19.357 in a more accurate, less expensive way.
0:03:22.104 –> 0:03:25.17 Okay, so the the second generation sequencing
0:03:25.17 –> 0:03:28.68 makes this becomes possible and promising.
0:03:28.68 –> 0:03:32.73 And so a typical research,
0:03:32.73 –> 0:03:35.79 critical inference is to find the markers
0:03:35.79 –> 0:03:37.59 that related to cancer.
0:03:37.59 –> 0:03:39.42 Right now there’s new sequencing technology
0:03:39.42 –> 0:03:41.797 called spatial transcriptomics.
0:03:41.797 –> 0:03:45.6 You know that for bulk I sequencing data,
0:03:45.6 –> 0:03:47.49 it just sequence the whole tissue
0:03:47.49 –> 0:03:51 and it generate a average the gene expression data.
0:03:51 –> 0:03:54.78 But with this new technology called spatial transcriptomic,
0:03:54.78 –> 0:03:57.42 this kind of cancer tissue will be sliced
0:03:57.42 –> 0:04:00.213 into several thin sections.
0:04:01.32 –> 0:04:05.94 And within each section, the grid point in the section
0:04:05.94 –> 0:04:08.25 will be sequenced simultaneously.
0:04:08.25 –> 0:04:11.43 So you can see that here we have two areas
0:04:11.43 –> 0:04:13.5 of invasive cancers, okay,
0:04:13.5 –> 0:04:16.53 all the dot points within these two sections
0:04:16.53 –> 0:04:21.42 will be invasive cancer areas for invasive cancer pa-
tients.
0:04:21.42 –> 0:04:25.32 The other six areas, they are noninvasive cancer areas.
0:04:25.32 –> 0:04:29.1 The grid points in these locations
0:04:29.1 –> 0:04:32.071 will be noninvasive cancer areas,
but for other parts, they’re normal part, okay?
And the data that we will have is because this new technology will sequence the whole tissue, all those grid points simultaneously. This data matrix that we will have, each row corresponds to a location within the section and the other columns, each column corresponding to the expressions for certain genes. The Y’s are labels for those patients, the normal noninvasive or invasive. And we will get a gene expressions for all those P genes for each location, okay?
So this is the data that we have and our goal then comes to identify marker genes for those noninvasive and invasive cancer areas. As showed in this figure, this is the tissue sections. There are points, color dots here with the color of the dots showing the expression levels. Okay?
So the the dots with a yellow color shows a higher expression. We intended to build the models to identify such genes. These genes are show remarkable differential express the levels across issue sections, okay? These two genes have higher expression.
Okay, we intended to build a status quo model to identify such genes but there exist several challenges here. Usually the data that we have, the samples or take the locations here is only our label the data is only around hundreds, but the number of genes could be tens of thousands. This is so-called a large piece modern problem. Usually for any traditional methods, there’s no way to utilize those traditional methods to solve this problem.

And the talk mentioned that there is a further layer of complication between the gene expression levels and the cancer or normal types, okay? Usually how the gene expression levels would influence, could affect different types of cancer, this mechanism is largely unknown and the association between them is beyond linear. So these are the two challenges.

That means that we’re going to, what we need is a statistical methods that can do variable screening in a more general model set up. So we, to achieve this goal, we choose to build our efforts under this so called general index model. In a general index model it describes a scenario that which is the response will have relation to pay linear combinations of X-i.
So that’s beta one transpose X-I

0:07:51.33 to beta K transpose X-I

through some anomaly function F.

So this is the general index model

and we know that here, X-i is a P directional vector

if K is a value that is much smaller than P,

then we actually achieved the goal of vanishing reduction

because the original P directional vector

is projected onto a space of a pay dimensional,

pay beta one X, beta one transpose X-i

to beta eight transpose X-i.

And we choose this general index model

because it actually is a very general model framework.

If we map this general index model to our problem here,

the Y-i could be the label for location i.

And, for example, the non-invasive location.

And then X-i is a key dimensional vector

and could be the gene expression levels

for location i of those P genes

and then beta one transposed X-i

to beta k transpose X-i

could be those K coregulated gene K groups

coregulated genes.

And those K groups of coregulated genes

will affect the response through some anomaly function F.

Okay so this is our general model setup.

We utilize the general index model

because it’s a general model framework

that encompasses many different model types.
There is three special cases, for example, the linear model is one special case. Here, $K = 1$ and $F$ anomaly function acquires an identity form. Okay so this is the linear model and the error term is additive. So linear model is one special case for it. The number per match model is another special case for the general index model. That is where $K = P$ and $\beta_1$ to $\beta_P$, it forms an identity matrix. Thank you. And then the third one, the single index model is another special case for the general index model that is when $K = 1$ and that error term is additive. So the reason that I show these three special cases, just to let everyone know that general index model is a very general model framework. In this case, using this model framework to do a variable screening or variable selection, we can say for those, this is determined by the whether we should screen or whether we should remove certain variables is determined by the coefficients here. Say, for a specific variable, if the coefficient $\beta_1$ is zero if it’s coefficient across those $K$, that $K$ different factors are all zero, then we say this value, this variable, is redundant. Okay so this is how we utilize the model.
0:11:15.633 –> 0:11:18.36 in a estimated coefficient
0:11:18.36 –> 0:11:21.183 to do a variable screening or, say, variable selection.
0:11:26.76 –> 0:11:30 So the question becomes how can we estimate data
0:11:30 –> 0:11:31.89 under this model framework, right?
0:11:31.89 –> 0:11:34.17 Just like made estimating beta
0:11:34.17 –> 0:11:36.66 in a simple linear refreshing model.
0:11:36.66 –> 0:11:38.64 So let’s see a simple case.
0:11:38.64 –> 0:11:43.64 That is when F function can is invertible.
0:11:43.98 –> 0:11:45.09 So that is to say,
0:11:45.09 –> 0:11:48.99 we have the model becomes F inverse of Y-i
0:11:53.337 –> 0:11:57.36 Okay and this is very similar, looks similar model, right?
0:11:57.36 –> 0:11:59.13 And if we want to estimate beta,
0:11:59.13 –> 0:12:02.85 we can just simply maximize the correlation
0:12:02.85 –> 0:12:07.44 between inverse of Y-i and the equal transpose X-I.
0:12:07.44 –> 0:12:12.44 Using this optimization problem we can recover beta, okay,
0:12:12.57 –> 0:12:16.533 given that F is invertible and F function is known.
0:12:18.69 –> 0:12:21.19 But we know in real case, F function is unknown
0:12:23.7 –> 0:12:26.13 and sometimes it is unconvertible.
0:12:26.13 –> 0:12:30.54 And then what can we do to estimate beta
0:12:30.54 –> 0:12:31.983 when F function is unknown?
0:12:34.47 –> 0:12:36.6 So when F function is unknown,
0:12:36.6 –> 0:12:39.6 we can consider all the transformations of Y-i
0:12:39.6 –> 0:12:41.278 and we can solve beta
0:12:41.278 –> 0:12:45.21 through the following optimization problem.
0:12:45.21 –> 0:12:47.94 We consider all transformations of Y-i
0:12:47.94 –> 0:12:50.85 we know as E of Y-i
0:12:50.85 –> 0:12:54.15 and we define our square of eta
0:12:54.15 –> 0:12:58.95 which is a function of eta as the maximized correlation
between NA tran E of Y-i and eta transposed X-i.
And this maximization is taken over or any transformations E, okay?
So using this function, beta basically is the solution for this maximization problem and with certain conditions satisfied, we can simplify this objective function with respect to eta, we can say R transform this, R square of eta into a this really nice quadratic form. Okay, in the numerator, it’s eta transposed times this conditional variance times eta and in the denominator, it’s either transposed the variance of X-i, eta.
This is a very nice projected form. Basically, the solution of this, the solution beta, is just taking factors, okay, corresponding to the pay largest taken values of this matrix in the middle. That’s how we solve beta in this case. But as we know, as I mentioned, that there is a really like big challenges here. One is that we have really large P here in the sigma X is a P value matrix. Sigma X given Y is also P value matrix. And we know that we are dealing with a case of P is larger than N, in this scenario, it would be really difficult to generate a consistent estimate based on a scenario when P is larger than N. And we also have this inverse here for a very large matrix,
it would be really time consuming to produce an inverse of the matrix. That alone, this matrix is not a consistent estimate, okay?

So this matrix in the middle, if we want to estimate that in the P brought up in this scenario, it would be really problematic, right?

And in the following, I will show how we gonna use the weighted leverage score, the method that we proposed to bypass the estimation of these two matrix and then perform the variable selection once again if the reduction under the general index model.

So we call our method the weighted leverage score. Let us first take a look at what is leverage score and what is weighted leverage score, okay? So let’s consider a simple case that is the linear regression model and then the rhet D single value competition of X as X equal to U log to T-transpose. This is the singular value competition X. And then, so in statistics, the leverage score basically is defined as the diagonal element of the hat matrix. And then the hat matrix, we use the further least the singular value competition. It can be simplified to UU transpose. And then which means that the diagonal element or the hat matrix basically is the real norm of the U matrix, okay?
And then actually this leverage score has a very good interpretation. It is the partial directive of Y-i hat with respect to Y-i. Okay, which means that if the leverage score is larger and closer to one, it would be more influential in predicting Y-i hat. So there is a recent work of Dr. Pima who’s using this leverage score to do a sub-sampling in big data. As you can see that again, that message here is that if the U-i norm is larger, if the leverage score is larger than we say this point is more influential. Think the motivating example is like this, in the first figure, this black dots, they are original data and the solid black is the actual model. And if we want to do a linear regression, usually sometimes if the really big data is really large, so it is hardly possible to utilize all the data points to generate the line here. So a typical strategy is just to do sub-sampling from the such big data and then performing a linear regression model. Right now, you can see that the regression line produced by a random sub sample from the population, those data is represented by the screen crosses. So we’ll generate a linear regression line that largely deviates from the true model.
So that is when the random sampling does not work in this case.

However, if we do a sub-sampling according to its leverage score, okay, you will see that, in the second graph, these red crosses on the data sub sample we’re using utilize the so-called leverage score and the red dashed line is the model attempt value in those sub samples, okay?

So we can see that using the leverage score to the sub sample can help us to generate a line that is very good, can approximate the true model.

So what I want to say using these graph is that the leverage score, the UI norm, can be used, say, as an indicator of how you fully ensure the data point is to the prediction.

Okay so UI is the role norm of the left single matrix but we are talking about variable selection. So UI norm can be used to select the roles. Intuitively, to select the columns of X, we can just do a transpose of X.

So X transpose equal to the V AU transpose. To select the columns of X basically is to select the roles of X transpose.

Intuitively we can just use the rule map of V matrix, which is the right single matrix to do a selection, to select the influential columns effects, okay, right? And then, so we call the rho nu of U, we call the U as the left singular matrix V as the right singular matrix.
And we call the rho mu of U as the left leverage score, rho of B as the right leverage score. So I want to say, use the previous two slides is that basically, the raw information, intuitively, the raw information is contained in the U, the column information of X is contained in the V matrix and we know that there is a fertile complication between X and Y, which is unknown link function F. So how do we utilize the information from the column and also the anomaly function to generate a same method that can help us to the variable selection that is to select influential columns for X.

Okay, let us get back to the matrix we derived in the previous slides. We have the conditional variance in the denominator and we have variance X in the numerator and the variance of X in the denominator. And with simple statistics, this can be simplified to variants of expectation of Z given Y where Z is a standardized X.

Okay, further we used a singular variety competition, Z can be simplified to UV transpose and then it’s IJ element basically is in the product of Ui and Vj, so Vi basically contains both raw information and column information.

And then we proposed the weighted leverage score, which is defined in this equation. And the interpretation of the Wj,
which is the weight leverage score for J’s predictor

So first of all you can see it contains

both the column information and the raw information of X.

And we know and thus, in the second fold,
you can see in the middle, basically contains

the information from the unknown function F

because we have the conditional expectation here,

expectation of Ui given Y,

basically it’s a kind of a reflection

of the anomaly function F.

And third, this method is viewed

under the general index model

and it is model three,
in the case that the general index model

encompasses many different model types.

Okay so this is kind of a population version

of the weighted leverage score.

In terms of estimation,
you will see we only need to estimate

in the matrix in the middle,

which is the variance of the expectation of Ui given Y.

To estimate this matrix,

we can see that Ui is actually three dimensional

because this is a directly single value composition.

Ui is a three dimensional vector.

Y is only one dimensional.

This is a function of one dimensional variable.

So it can be easily approximated by dividing, okay,
the range of \( Y \) into \( h \) slices as much as \( h \) and within each slice, okay?

Within each slice we calculate the slice mean for all roles of \( U \).

Lastly, illustrated in this graph, we can first the slice into \( Y \) into edge slices and then within each slice, if those \( Y_i \) fall into the same slice, we find out their corresponding use and then do, calculate its mean for each \( U \).

And in that way, we can simplify, we can simply estimate expectation of \( U_i \) given \( Y \). And then further we can estimate the variance of those averages.

Basically just taking that the variance of \( U \) one bar to \( U \) edge bar.

So this is the way how we estimate the variance of the expectation of \( U_i \) given \( Y \).

Okay so in that way we actually generate our estimate weighted leverage score.

we define as the right leverage score weighted by the matrix in the middle.

Okay so first of all, this weighted leverage score is built, say, upon the general index model, it is considered as model free because \( Y_i \), the response is connected with hitting combination of \( X \) through anomaly function \( F \).

And this model is general to encompass many different model types.

So we can consider it as model free.
And second, this to generate this weighted leverage score where there is no need to estimate the covariance matrix and there is no need to estimate anomaly function F. So we can bypass all those procedures to calculate this weighted leverage score.

So this weighted leverage score actually encompass a very good feature that is it is an indicator of how influential of the columns are and we can basically run our predictors according to the weighted leverage score. The higher the score is, the more influential the predictor will be. And later I will show why this ranking properties would help or even with the leverage score. So this is a basic procedures for giving weighted leverage score to a variable selection or variable screening. So given that we have this matrix, which is an impart matrix and we have the responses, the labels, for each of the location, we only need one time singular value composition, okay? This is a rank D singular value composition of X. And then we can just calculate the weighted leverage score according to the equations, rank those weighted leverage score from the highest to the lowest. Select the predictor that we use, the highest weighted leverage scores.
This is the basic screening procedure using the weighted average score and there is still implementation issue that we will later address. First one, how can we determine the number of D? So given the data which is an IP, how can we determine, say, how many, say, spiked or how many singular values to be included in the model? And then the second implementation issue is determine the number of variables to be selected in the model. So you can see that the weight leverage score procedure is screening procedure only include one type of singularity, competition is quite efficient. Okay so, in the next, let us using two slides to discuss a little but, basically just one slides to discuss the ranking properties of the weighted leverage score. So as I mentioned, the weighted leverage score has a very nice property. So it is guaranteed by the theorem here. We show that, given certain conditions are satisfied, we have the minimum value of the weighted leverage score from the true predictors will always rank higher than the maximum value, maximum weighted leverage score of those redundant predictors. And this holds for the population with leverage score.
we utilize the two step procedure. So first of all, we show that the estimate weighted leverage score is very close to the population version of the weighted leverage. Okay and then the estimated weighted leverage score will also have the ranking property that is the estimated weighted leverage score of the active predictors or important predictors ranks higher than the estimated weighted leverage score of the down predictors with probability turning to one. Okay so this, the ranking properties basically is guaranteed by these two properties. And then further, we also know that there are two implementation issue. The first one is determine the number of spiked singular values d. So how many single values we need to include in our model? This is a question and it’s quite crucial because we need to know how many of the signals contain the data and we need to remove all those redundant or noise information. Okay so here I develop a criterion based on the properties of those aken values. DR is a function of, R is the number of values to be included in a model. DR is a function of R and the theta I hat is the ratio between the highest aken value.
and the largest aken, value, number one hat.

And then, you can see that as we include more, say,

single values in the model,

this, the first term will decrease

and then tier to some point.

The first, the decreasing of the first term

is smaller than the increasing of the second term.

And then we can use the criterion to find D hat,

we show that we had is very close to a true D.

Okay, you meet this criterion,

we can select the true number of signals in the model.

And the second implementation issue

is about how many predictors, how many true predictors

we need to include in our model.

Okay again, we’re ranking our weighted leverage scores

and here we utilize the criterion here

based on the properties of the weighted leverage score.

Okay, as we include more predictors into the active set,

the first term will decrease, okay?

The summation of the weighted leverage score will increase,

but the increment will decrease

and then the second term will increase, okay?

So, as we include more predictors in the model,

there’s some changing point

when the increment is smaller than the increment

of the second penalty term.

We show that, using this criteria,

the set we selected using this criteria,
which is A, will always we’ll say can include all the true predictors with probability pending to one.

Okay so that’s how we using this criterion to determine the number of predictors to be selected in the model.

Okay in the next step, let me show some empirical study results of using the weighted leverage score to do the variable selection in the model.

In the example one, as I mentioned, we are utilizing, we are proposing our method under the general index model framework. So the first model is the general index model.

Well why there’s two directions? The first one is in the numerator, so this is so called a beta one transpose X. The second direction beta two transpose X is in the variable system, the term within the variant, this is beta two transpose X.

So in this way, we generate both X and Y, let’s see how the performance of variable selection
give you the weighted leverage score.

In our scenarios, we let N equal to 1000 and the rho equal 0.5.

In example one, there are four different scenarios.

For scenario one, we let P as 200 and then we increase P to 200, sorry 22,000 and 2,500.

We also increase the variance of the error turn.

as 1.5 this now to 1.3.

Okay, there are three criteria we used. The first one is the false positive.

So it means how many of the variables are falsely selected?

False negative which shows how many variables falsely excluded, how many true predictors are falsely excluded.

The last one, the last criterion is because, is basically is our model size.

because we have this ranking properties.

All those methods have ranking properties.

So I want to know how many variables I need to include.

in the model so that all true predictors are included because we have this ranking property, okay?

You will see that weighted leverage score basically have a better performance.

in terms of the false positive and the false negative.

and also the model size.

I want to say a bit more about model size.

We can see that when N is 1000, P is 200,
the minimum model size is 6.14, meaning that we, in total,
we only have six true predictors, okay? We only need to include the six variables
to encompass all true predictors. Basically all those six variables are rank higher
than all our other novel variables, right? In a second model, when P increases to 2,200,
we only need seven predictors in order to, on average, in order to include
all the true predictors. Meaning that overall, all the true predictors
ranks higher than those redundant predictors. And then when sigma increases and when P increases,
we still need only the minimum number of variables just to include all true predictors.
Okay so this is for the first example of the model index model.
The second is more challenging, it’s called a heteroscedastic model.
You will find that, in the first model, the X, those active predictors only influence
the main response, okay? Only influence Y in its means.
But here, you can see four different types
for those variables, the average of Y, the mean of Y is zero
because error term is in the numerator
and those X, those active predictors will influence Y
in its variance. So it’s a much challenging case.
In this case, we also assume that \( X \) follows a very normal distribution, given mean is zero and a covariant structure like this. In our scenarios, we let \( N \) equal to 1,000.

So let’s see, in a heteroscedastic model, what are the behaviors of our methods?

Okay, sorry, I forget to introduce the method we are compare these with true independence ranking

And both of these methods can be utilized to measure, say, the association between the response and the predictors.

So we can compare the minimum model size for all the methods.

Regards the false positive of these two methods, there’s no criteria proposed to select the number of predictors.

And in all those methods, I just use a harder stretch holding in order to be included in the model.

Okay let’s see, in a heteroscedastic model, what are the behaviors of those three methods?

Okay, when we have \( N \) greater the number of predictors, you will find that there are slightly larger, with false negative for the weighted leverage score.

This is because both the methods within the our threshold, they select around 140, more than 140,
true predictors out of 200 from the model. So that’s why they have very small false negative, but if you look at the minimum model size, you will find that our weighted leverage score still maintains a very good performance. Okay, it has a smaller value of the minimum model size. Okay in general, we only need 46 variables in order to include our two predictors in the model. And then as P diverges, as CSP increased to 2,500, basically the weighted leverage score will measure 1.3 variable true predictors from the model. And every method have a really hard time to identify all the true predictors. They have really large minimum model size. So this is basic a performance of the using with the leverage score to perform a variable screening under general index model. So I only present two examples here for interest in odd scenarios. We can talk about that at the top. Okay so let’s get back to our real data example. So in a motivating example, as I mentioned, we utilize this spatial transcriptomics data. We are sequencing the grid point within each section, okay? Basically these locations are invasive cancer areas, the other areas are the noninvasive cancer areas, and then these are the normal areas. So how to determine the invasive, non-invasive areas?
These are determined by qualified doctors and they’re utilizing some logical information of these locations. Okay in general, for these two sections, we have identified 518 locations, 64 invasive areas and 73 are noninvasive areas. And there are rest of the areas, 381, they are normal. And we have our gene, about 3,572 expressions, gene expressions across the section. Okay so in general, basically we have our data matrix it is about 518 times 3,572. So we trying to identify biomarkers, okay, within those three genes that can help us discriminate between invasive cancer, non-invasive cancer and normal areas. So we utilize the weighted leverage score, we apply the weight leverage score screening procedure for this data set. And we identified around 225 genes among all those P genes. In the plot, a heat map here show the results because just for the ease of presentation, I only printed around 20 genes here. And with the top, say, weighted leverage scores, you can see that there are certain patterns here. This group of genes are more highly expressed for the non-invasive cancer area. There are certain group of genes right here. They are more highly expressed in the invasive cancer areas. Okay so this is the gene expression patterns
of those top 20 genes. And then we also plot the expressions of those genes in these sections. Again, these are invasive areas, noninvasive and the normal areas. So we plot a group of genes, I can’t remember exactly what our genes are, but these genes have, you can see, have a higher expression on those noninvasive cancer areas. And we plug another group of genes, basically are these three genes, in the section, the expression shows a higher, this means that these three genes have higher expression, okay, in the invasive cancer areas, okay? Basically this means that the genes that we selected show a remarkable spatially differential expressed patterns across the tissue sections. And later we do a, say, pathway analysis and see that there are 47 functional classes for those all those gene 225 gene that we have identified. And there are several cancer hallmarks, for example, of the genes that we identified enriched in the regulation of apoptotic process. This is a kind of cancer hallmark. And then another 41 gene that we have identified are involved in the regulation of cell death. More specifically, because we are really interested in the invasive cancer, so we identified these three,
there are like three genes for example, in the regulation of brain process, they have many relations with the breast cancer, okay?

And later we can investigate or, say, even adaptation of those, those genes that are enriched in the revelation of apoptotic process.

So, in summary, that weighted leverage score that we have developed is a variable screening method and it is developed under the general index model. And this a very general model framework. It can be used the two address the curse of dimensionality in regression and also, because we utilize both the leverage score, the left leverage score and the right leverage score to evaluate a predictor’s importance in the general index model, we provide a theoretical underpinning to that objectify that you need both the leverage scores of both the left and right leverage scores, we can evaluate the predicts importance. Okay so this is kind of a new framework for analyzing those numerical properties, especially for the single matrixes under the general index model. Okay so, this is basically a summary of the weighted leverage score and I wanna stop here and to see if anyone has any questions.
or comments about weighted leverage score.
 Questions?
 Anybody on Zoom have questions?
 Can I ask a quick question regarding this weighted leverage score?
 So when we look at results, this weighted leverage score has much better performance with less inverse regression regional one, right?
 So I wonder, is this correct that the reason why improves so much is because it utilize the information on the line, maybe, total make sense in a lot of applications that those important features, they may be like more contributing to like also leading to like variation of other features and as a result, maybe could show up in the top as vectors in the design matrix.
 Is this correct?
 Yeah, thank you very much for your question, it’s a very good question.
 So first of all, I want to clarify, maybe I’m not very clear about SIRS.
 Basically this is representing the true independence ranking and screening.
 So it’s also a method that is based on the slicing versus regression. So yeah, and the other one that why with the leverage score has a much better performance comparing these two methods is basically
because, one of the reason is because the true independent screening and the distance correlation, they all just utilize the partial and partial correlation. So between X and Y. Okay so it does not utilize any of the information within X. It's kind of a marginal correlation between each variable X and then one, okay? However, the weighted leverage score will utilize both the raw information and also the variance information, the correlation structure within the model, which is the V matrix, as I mentioned, is derived from the covariance structure of X. The V matrix basically is the vector of the covariance structure, covariance of X. So it utilize the, say, kind of a correlation between all the X variables and a variable screening. So I'm not sure if this answers your question. Yeah, thank you.

0:48:17.88 -> 0:48:18.947 Yeah, thank you.

0:48:19.907 -> 0:48:21.69 I think it is, you answered my question. Essentially, I’m thinking like if those important features, they are actually not the top contributors to the top other lectures, then we wouldn’t expect the weighted leverage score to aim true way. Thank you.

0:48:42.24 -> 0:48:43.32 Any other questions anyone wants to bring up right now?

0:48:50.8 -> 0:48:53.8 (students mumbling)
Can I ask naive question?
Yes, Vince.
So I’m wondering kind of, you know,
when I think about doing SVP on data,
the first thing that I think of is easier
and I keep coming back to that,
and I can’t tell if there’s a relationship?
Yeah, basically, right,
we can generate U and V in many ways, right?
We can using regression model,
we can generate the U and V as well, right?
We can generate, we can do a,
so it’s basically, I think a lot of inhibition
is that the right score can generate the left and right
singular vectors, so we can use many different ways
to generate that.
Yeah, it’s not really.
Thank you for that.
All right, well then, if there’s nothing further,
let’s thank the teacher again.
Thank you everyone for having me on.
(students overlapping chatter)