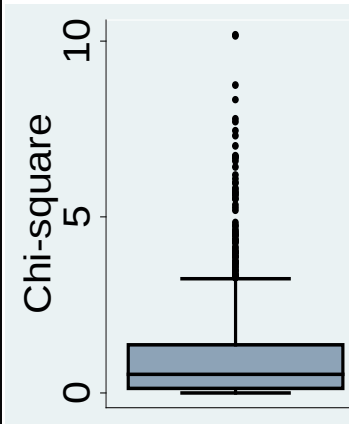
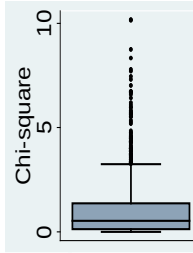


Repeated Measures, Lecture 2, Part 1

*Charles E. McCulloch,
Division of Biostatistics,
Dept of Epidemiology and Biostatistics,
UCSF*



Outline

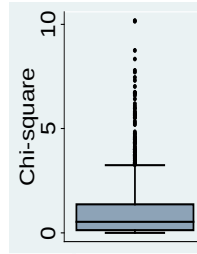


1. Two overarching analysis approaches to accommodating correlation: Generalized estimating equations (GEE) and mixed models.
2. Longitudinal designs
3. Lecture 2 covers numerical outcomes, so the analogs of linear regression.
4. Part 1: GEE (xtgee) methods
5. Summary



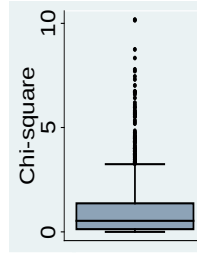
Analyses for correlated data

- Generalized estimating equations (GEEs)
 - Stata `xtgee`
- Mixed effects (ME) models
 - Stata `meglm`
 - Or specialized routines for different outcome types
 - Numeric (`mixed`)
 - Binary (`meologit`, `meprobit`)
 - Count (`mepoisson`)
 - Ordered categorical (`meologit`, `meoprobit`)
- *Interpretations are virtually the same for corresponding correlated and non-correlated analyses (linear/linear, logit/logit)*





Analyses for correlated data

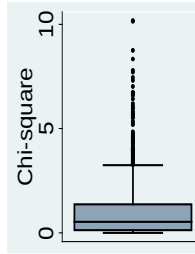


- Generalized estimating equations (GEEs)
 - Only works for one level of clustering (e.g., patients).
 - Requires largish number of clusters (ideally > 50) and works best when the number of clusters $\gg$ number of observations per cluster.
 - Does not require modeling of the correlation when using “robust” standard errors.
 - No overall measure of model fit like likelihood or R^2 .
 - Less robust than mixed effects models to possible bias due to missing data or dropout.



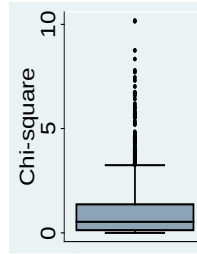
Analyses for correlated data

● Mixed models



- Can handle a wider variety of data structures. For example times within patients within doctors or compartments within knees within time within subjects.
- Requires modeling the correlation.
- Gives additional information about the correlation.
- Based on likelihood fits, so can conduct likelihood ratio tests to compare two model fits.
- More robust to potential bias due to missing data and dropout.

Consider first longitudinal data



Longitudinal design: Individuals (interpreted broadly) are measured repeatedly over time.

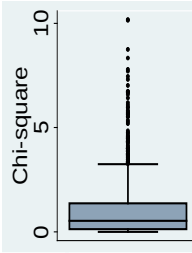
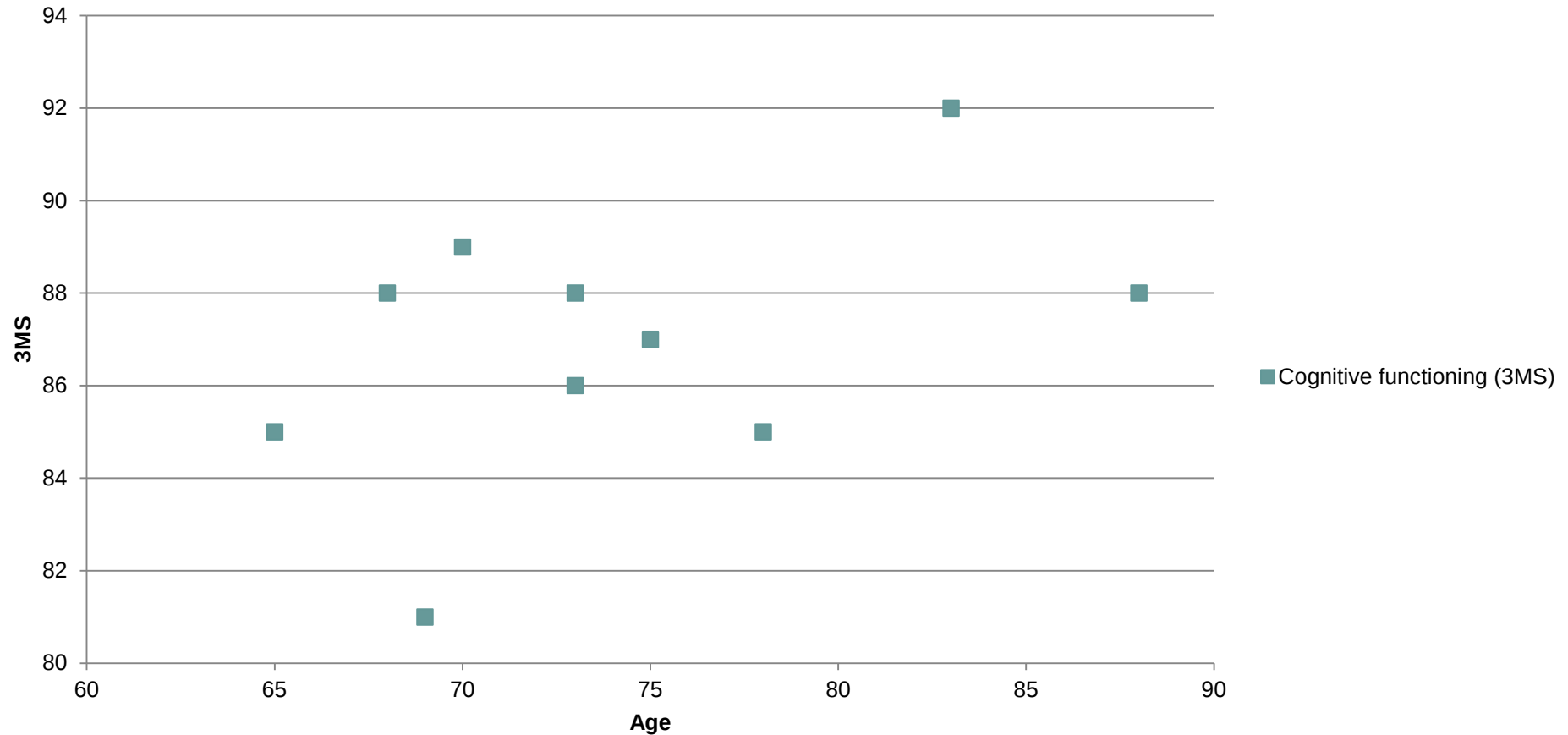
Key features: Can analyze change over time within an individual.

GEE methods are a very common approach for longitudinal data when there are large numbers of individuals and not so many repeated measurements.

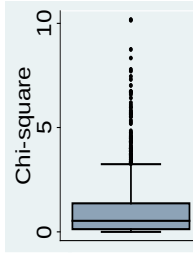


Measuring change

Cognitive functioning (3MS)



Modified Mini-mental State Exam



Numerical score from 0 to 100

Tell patient “I'd like to test your memory; say these words: boat, cucumber, wire” (up to 3 points for 3 correct answers)

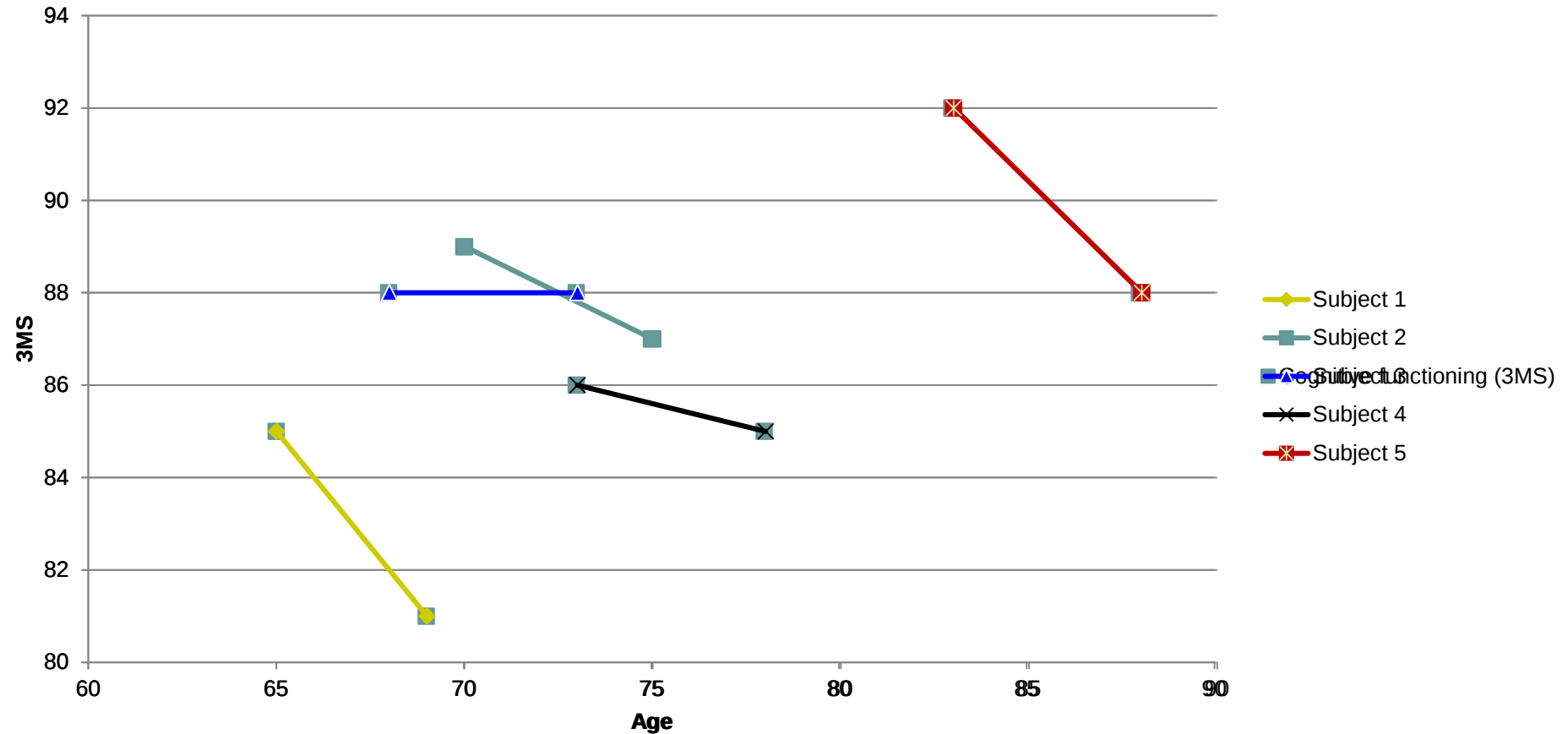
Tell patient “Begin with 100 and count backwards by 7” (up to 5 points for five correct answers)

Tell patient “Can you name the three objects I named before?” (up to 3 points for 3 correct answers)

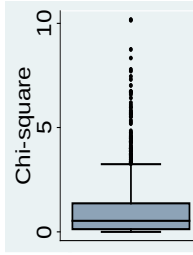


Measuring change

Cognitive functioning (3MS)



Analyzing change with longitudinal data

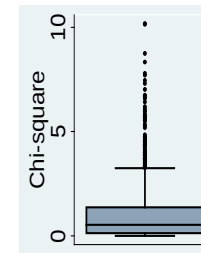


Example (SOF): It is well known that women who are overweight and obese have higher bone density. However, is the *change* in bone mineral density related to whether a woman is obese at baseline? We will define obese as $\text{BMI} > 30$.

How should we get started?



Example: SOF basics

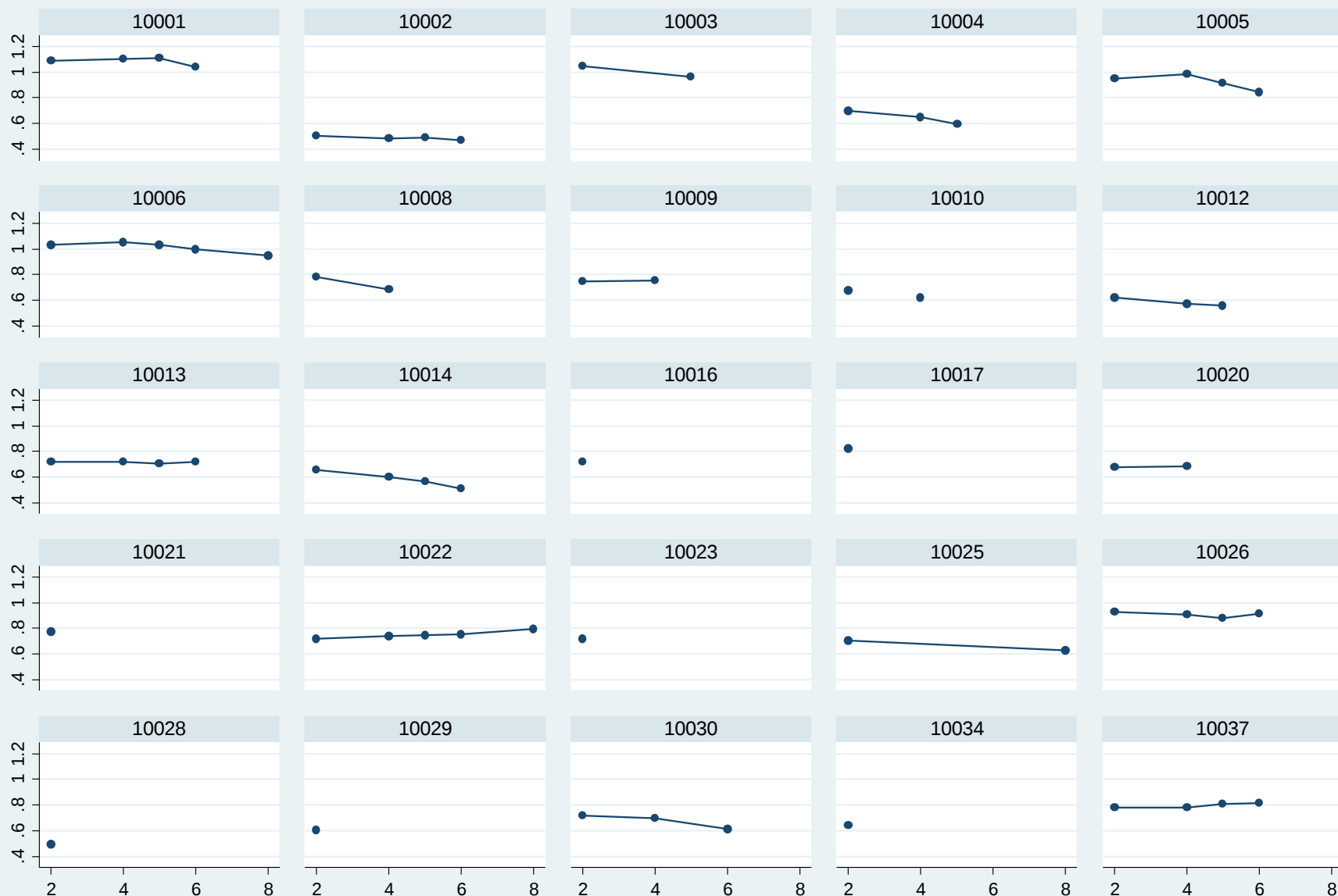


```
. xtset id visit
      panel variable:   id (unbalanced)
      time variable:   visit, 2 to 8, but with gaps
                  delta: 1 unit

. xtides
      id:  10001, 10002, ..., 42486          n =          8590
      visit:  2, 4, ..., 8                  T =              5
      Delta(visit) = 1 unit      Span(visit) = 7 periods
      (id*visit uniquely identifies each observation)
```

Distribution of T_i:			min	5%	25%	50%	75%	95%	max
			1	1	2	3	5	5	5
Freq.	Percent	Cum.		Pattern					
-----+-----									
2275	26.48	26.48		1.111.1					
1734	20.19	46.67		1.111..					
1696	19.74	66.41		1.....					
926	10.78	77.19		1.11...					
... .									
99	1.15	90.94		1.1.1..					
89	1.04	91.98		1..11.1					
689	8.02	100.00		(other patterns)					
-----+-----									
8590	100.00			X.XXX.X					

BMD

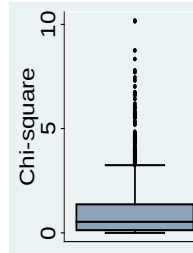
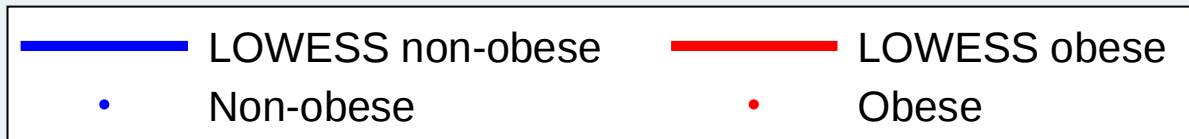
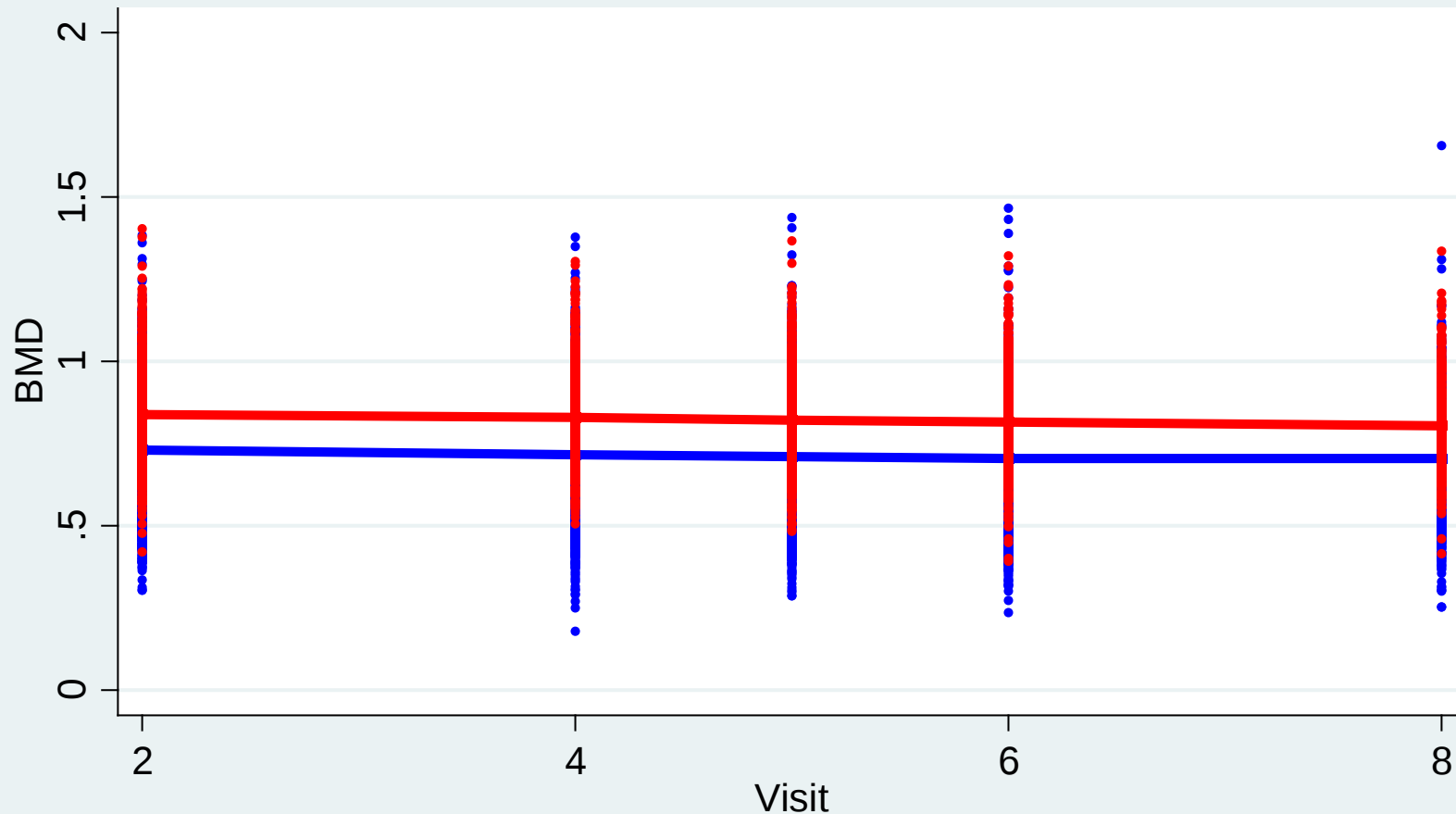


Graphs by ID



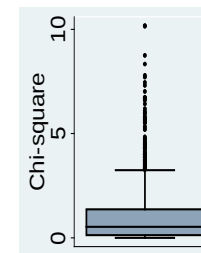
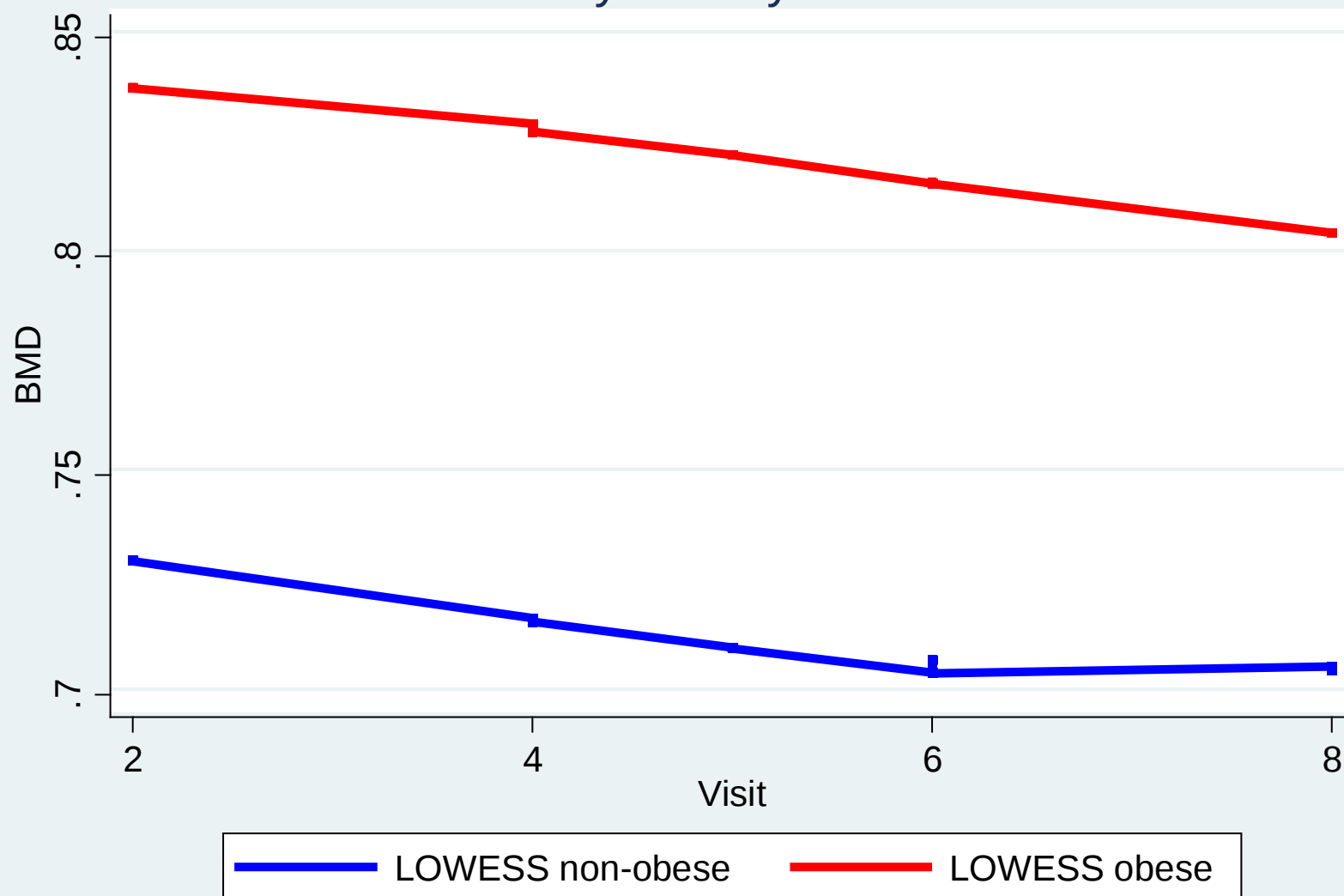
Example: BMD/Obesity

BMD vs visit by obesity status at baseline



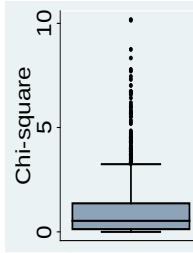
Example: BMD/Obesity

BMD vs visit by obesity status at baseline



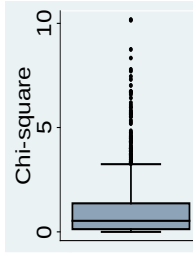


Analyzing change with longitudinal data



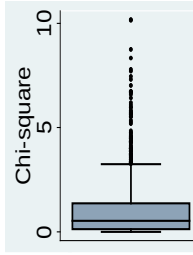
- Including a variable for *time* (or *visit*) describes the change over time.
- Inclusion of *time* (or *visit*) interactions with baseline predictors allows analysis of whether baseline predictors are associated with change over time.
- Inclusion of a time-varying predictor (e.g., BMI at sequential visits) allows analysis of whether change in that predictor is associated with change in the outcome.

How to handle “time” in a longitudinal analysis



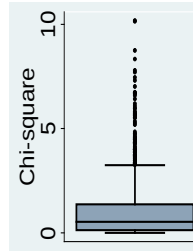
- We often try to model the shape of the change in the outcome over time.
- There is a natural “ladder” of handling a time predictor like visit, moving from simpler (to model *and* interpret) and more restrictive to more flexible: linear, quadratic, spline (flexible smooth fit), categorical.
- Moving up the “ladder” is a simple way to test adequacy of the simpler model.

Example: BMD/Obesity



- Want to characterize the change over time and see if it is the same or different between the obese and non-obese.
- Plot suggests that the trend might not be linear over time.
- So we need to check.

Example: BMD/Obesity



```
. xtgee totbmd visit##obese, i(id) robust
```

Summary information about hierarchy

GEE population-averaged model

Group variable: id

Link: identity

Family: Gaussian

Correlation: exchangeable

Scale parameter: .0169246

Number of obs = 26829

Number of groups = 8468

Obs per group: min = 1

avg = 3.2

max = 5

Wald chi2(9) = 3733.60

Prob > chi2 = 0.0000

(Std. Err. adjusted for clustering on id)

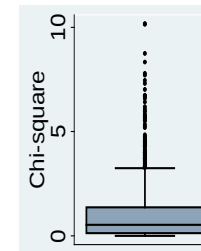
		Robust				
totbmd		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]

visit						
4		-.0164933	.0004961	-33.25	0.000	-.0174655 -.015521
5		-.0270842	.0006331	-42.78	0.000	-.028325 -.0258434

etc.



If there are interactions between two variables in the model, the “main effect” of each of those variables is the effect when the other is at its reference value.



		Robust				
totbmd		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
visit						
4		- .0164933	.0004961	-33.25	0.000	- .0174655 - .015521
5		- .0270842	.0006331	-42.78	0.000	- .028325 - .0258434
6		- .0383912	.0007898	-48.		
8		- .0513558	.001284	-40.		
1.obese		.033644	.0018641	18.		
visit#obese						
4 1		.0064715	.0014952	4.		
5 1		.0044571	.0017778	2.		
6 1		.0057885	.0021825	2.		
8 1		.0008468	.0032882	0.2		
_cons		.7410788	.0013913	532.6		

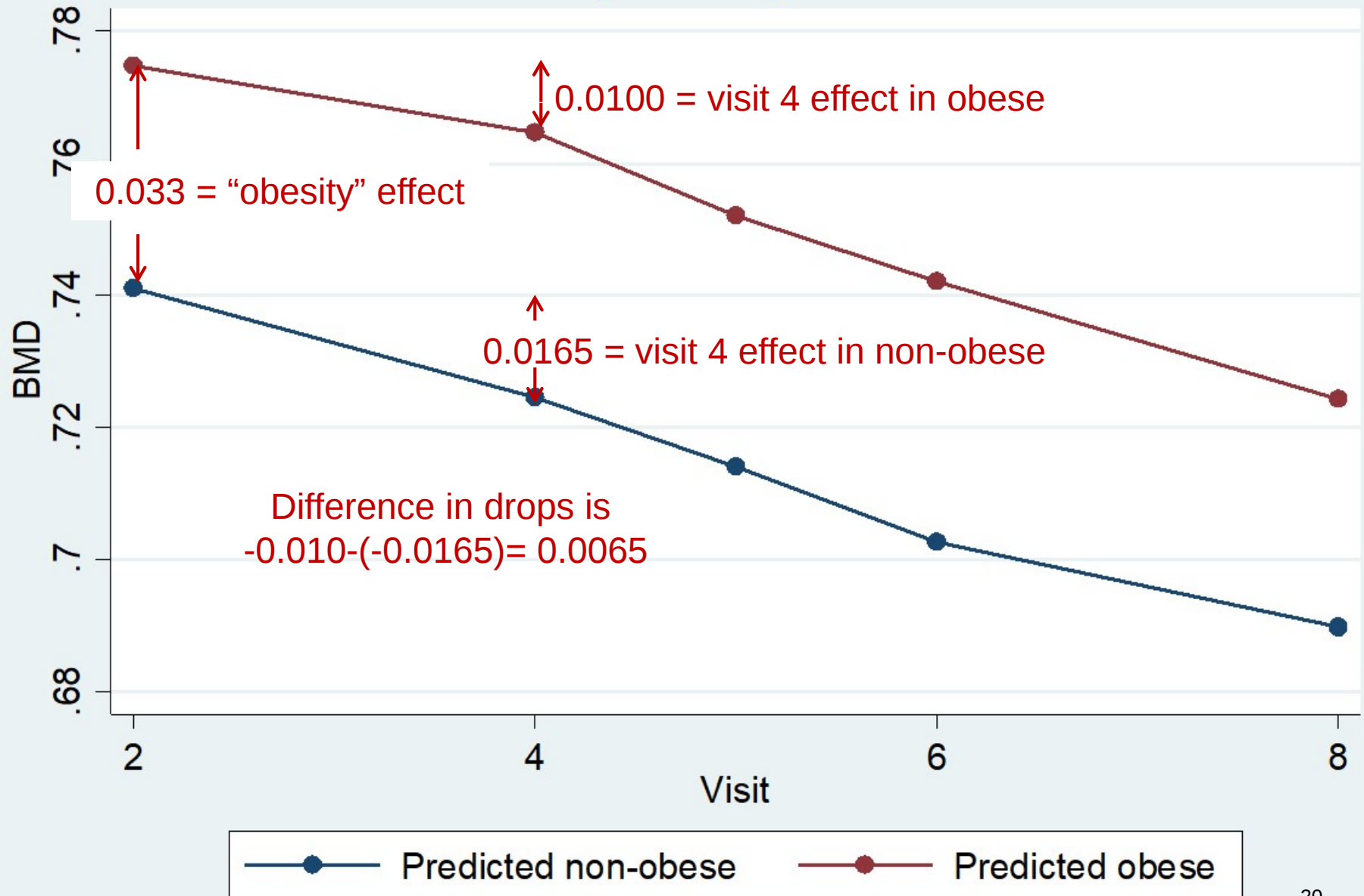
On average, BMD drops by .0165 from

On average, BMD

On average, BMD is higher by 0.033 for the

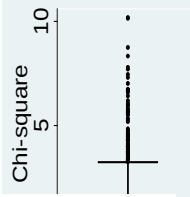
The difference in the drop for obese v. non-obese between visits 2 and 4 is 0.0064

BMD vs visit by obesity status at baseline





Example: If you prefer tables



```
. margins visit#obese
```

```
Adjusted predictions      Number of obs      =      26,829
Model VCE      : Robust
```

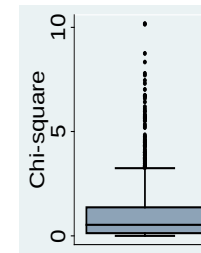
```
Expression      : Linear prediction, predict()
```

		Delta-method				
		Margin	Std. Err.	z	P> z	[95% Conf. Interval]

visit#obese						
2 0		.7410788	.0013913	532.65	0.000	.7383519 .7438057
2 1		.7747228	.0021152	366.27	0.000	.7705771 .7788684
4 0		.7245855	.0014573	497.22	0.000	.7217293 .7274418
4 1		.764701	.0019559	390.97	0.000	.7608676 .7685345
5 0		.7139946	.0015048	474.47	0.000	.7110452 .7169441
5 1		.7520958	.0019877	378.37	0.000	.7481999 .7559916
6 0		.7026876	.0015825	444.04	0.000	.699586 .7057892
6 1		.7421201	.0021336	347.82	0.000	.7379382 .7463019
8 0		.689723	.0018483	373.17	0.000	.6861005 .6933456
8 1		.7242138	.0030273	239.22	0.000	.7182803 .7301473

```
-----
. *Drop in obese group from visit 2 to 4 is from .7747228 to .764701
. di .764701-.7747228
-.0100218
```

Back to the science: BMD/Obesity



```
. testparm visit#obese
```

```
( 1)  4.visit#1.obese = 0
```

```
( 2)  5.visit#1.obese = 0
```

```
( 3)  6.visit#1.obese = 0
```

```
( 4)  8.visit#1.obese = 0
```

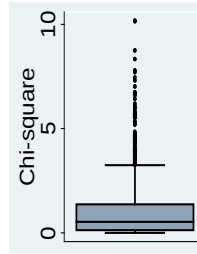
```
      chi2(  4) =    22.20  
Prob > chi2 =    0.0002
```

The rate of change in BMD during the study is different for the obese and non-obese. The obese change less (since all the interaction coefficients are > 0).



Back to the science:

Checking the linearity assumption

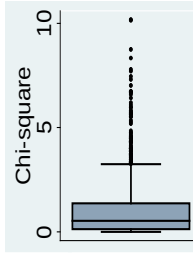


```
. xtgee totbmd c.visit##obese visit##obese, i(id) robust

. testparm visit#obese
( 1)  4.visit#1.obese = 0
( 2)  5.visit#1.obese = 0
( 3)  6.visit#1.obese = 0
      chi2(  3) =    19.02
      Prob > chi2 =    0.0003
```

The categorical interaction is statistically significant after fitting linear, therefore linear inadequate. Stick with categorical visit variable.

Example: BMD/BMI (time varying predictor)



- Including a time-varying predictor automatically models a change over time

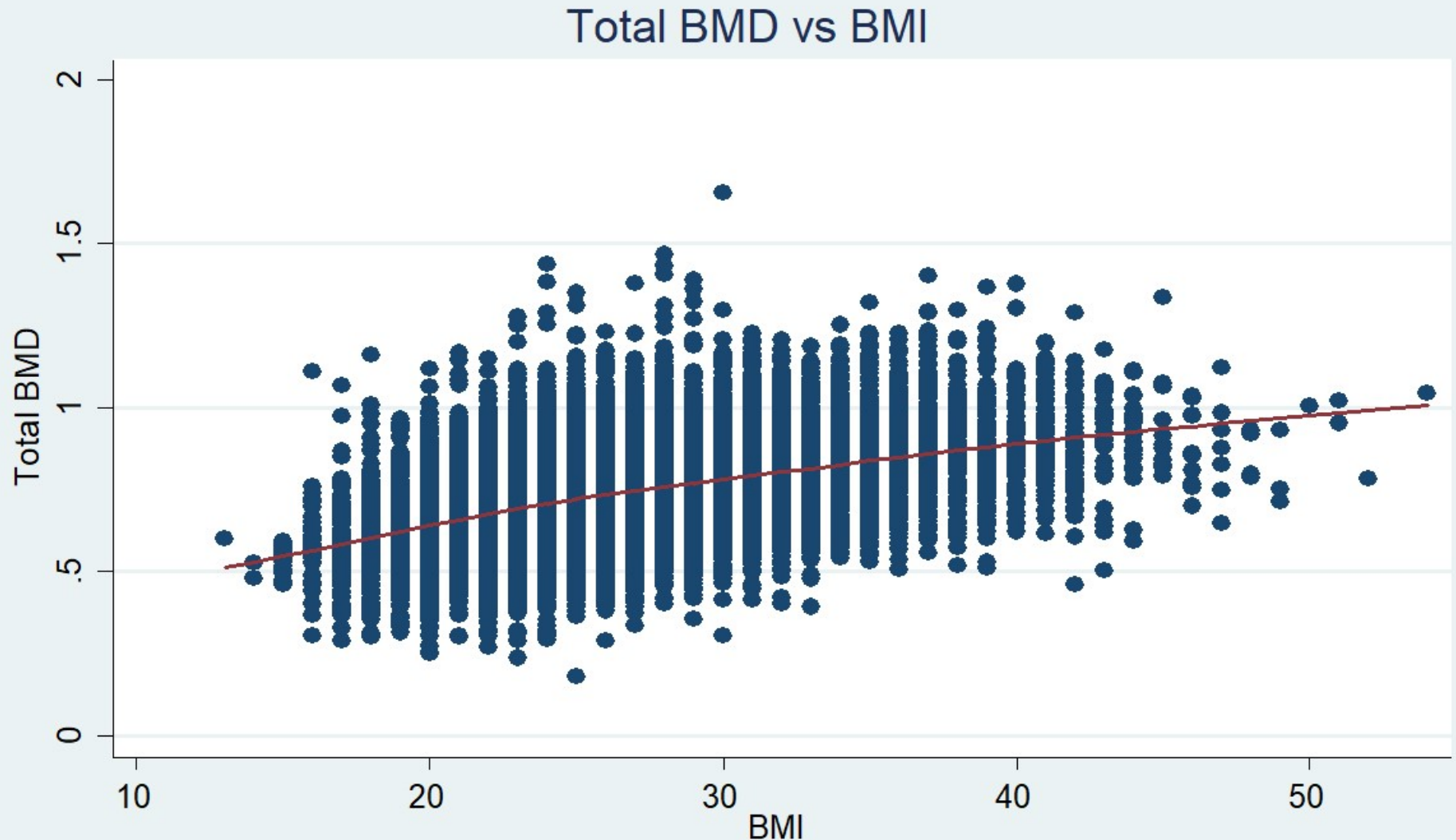
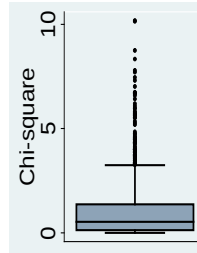
$$\text{BMD}_t = b_0 + b_1 * \text{BMI}_t \text{ implies}$$

$$\text{BMD}_t - \text{BMD}_{t-1} = b_1 * (\text{BMI}_t - \text{BMI}_{t-1})$$

So change in BMD is predicted by change in BMI.

Ex 2: BMD/BMI (time varying predictor)

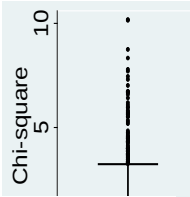
Does BMI predict total BMD? LOWESS plot





Example 2: xtgee

```
. xtgee totbmd bmi, i(id) robust
```



```
GEE population-averaged model
Group variable:                id
Link:                          identity
Family:                        Gaussian
Correlation:                   exchangeable

Number of obs      =      26,829
Number of groups   =       8,468
Obs per group:
    min =           1
    avg  =          3.2
    max  =           5

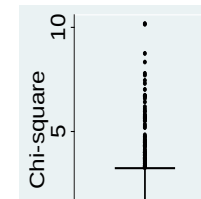
Wald chi2(1)       =      1639.11
Prob > chi2        =       0.0000

Scale parameter:    .0146148
```

(Std. Err. adjusted for clustering on id)

		Robust				
totbmd		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]

bmi		.0091548	.0002261	40.49	0.000	.0087116 .009598
_cons		.4890844	.0060705	80.57	0.000	.4771865 .5009823



Example 2: Standardize

```
. egen bmi_std=std(bmi)
. egen totbmd_std=std(totbmd)
```

```
. xtgee totbmd_std bmi_std, i(id) robust
                        (Std. Err. adjusted for clustering on id)
```

		Robust				
totbmd_std		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
-----+-----						
bmi_std		.3218237	.007949	40.49	0.000	.3062439 .3374035
_cons		-.0317306	.0096224	-3.30	0.001	-.0505903 -.012871

- A one standard deviation change in BMI is associated with a .3 standard deviation change in total BMD.
- So a small to moderate sized effect using the usual rules of thumb (0.2 = small, 0.5 = medium 0.8 = large).

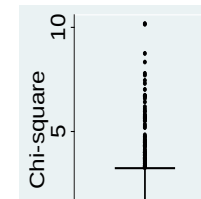
Example 2: Check linearity

Assess linearity in BMI

```
. xtgee totbmd_std c.bmi_std##c.bmi_std, i(id) robust
```

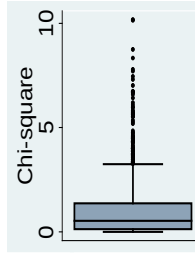
bmi_std		.3362406	.0077491	43.39	0.000	.3210527	.3514284
c.bmi_std#c.bmi_std		-.0179974	.0041768	-4.31	0.000	-.0261838	-.0098111
_cons		-.0131305	.0103411	-1.27	0.204	-.0333986	.0071377

Since a quadratic term is statistically significant, the linearity in BMI assumption is not correct. Is it an important deviation? A plot of the predicted values versus BMI shows that the quadratic effect is minimal.



Longitudinal analysis strategy

- Assess if a predictor is time-varying or time-invariant (use x_t sum if you don't know)
- Time-varying (like BMI) – just include it as a predictor.
- Time-invariant (like obesity at baseline) – include it in the model as well as the interaction of that variable with the time variable. A longitudinal relationship is tested by testing the interaction.



Summary

- Approximately normally distributed outcomes can be handled with mixed models (`mixed`) or generalized estimating equations (`xtgee`).
- Mixed models have the advantage of handling multiple levels of clustering and more explicit modeling of sources of variability and correlation. Better with missing data.
- Generalized estimating equations (when using the robust option) makes fewer assumptions.

