INSTRUCTOR: Good morning. Good morning. So, anybody check *The New York Times* yesterday? What did you see?

AUDIENCE: [INAUDIBLE]

INSTRUCTOR: People, what people?

AUDIENCE: I can't remember their names. [INAUDIBLE]

INSTRUCTOR: [LAUGHS]

AUDIENCE: [INAUDIBLE] I can't remember their names.

INSTRUCTOR: Yeah, the Crick and Watson people.

AUDIENCE: [INAUDIBLE].

INSTRUCTOR: Exactly. So, perfect timing, *The New York Times* had an article in yesterday's paper. Francis Crick's correspondence with Maurice Wilkins during the critical year when Crick and Watson went down and saw the X-ray crystallography.

By the way, I made a mistake. I said that Rosalind Franklin showed it to Crick and Watson. Actually it was Maurice Wilkins who showed it to Crick and Watson when Rosalind Franklin was away. Which, was itself a slightly complicated thing to be doing because it was really Rosalind Franklin's work.

But in any case, there was correspondence, some heated correspondence that went back between Crick and Wilkins and others. And it was believed that the correspondence had been lost, had been thrown out. But in fact, it turns out that in the papers of Sydney Brenner, another great person of that period, Crick's correspondence had got misfiled in Sydney's files.

Sydney had donated his files to the Cold Spring Harbor Laboratory on Long Island. And they went through the files in the past several months and found them. So we actually now have, as *The New York Times* reported yesterday, the letters with

Crick and Watson and Maurice Wilkins about just that period I was telling you about.

It doesn't radically change any of the story. But it really shows you the attitude. And if you read the *New York Times* article, you'll find all sorts of juicy quotes about the attitude back and forth there, including the first model Crick and Watson made where they totally screwed up because they had misunderstood some number. Anyway, it's interesting stuff.

And the reason I bring up this history is because science is done by real people. It's a business of passion. It's a business of trying to-- you know -- science is wonderful. It's objective in a certain sense. And it's also about convincing others. You know, a scientific result doesn't mean anything unless you can convince the community. So it's an inherently human activity to bring people's attention to things, make things clear.

Anyway, that was kind of cool. I invite you all to go look at The Times article. You don't realize how much work we have to go to in 7.01 to arrange these things to come out just at the right time during our curriculum. But we pay off The New York Times and they do our bidding.

So last time we were talking about-- I want to briefly go back to the Semiconservative Model, which I ended with last time, of DNA replication, the work of Matt Meselson and Frank Stahl, these graduate students at Caltech. So you remember, our DNA double helix immediately suggests the secret of life, the way that you copy information to daughter cells. Each strand is a sufficient template for the other strand. If you just unzipped them, each would be able to serve as a template for replication for the other strand. Beautiful. It's called Semiconservative because you've conserved. You used one strand. And you've made a new strand on the other.

It seems obvious, but we can't take things for obvious in science. Because the alternative model, alternative, which we know today is of course wrong, is that somehow the cell comes along, feels this double helix as a template, and somehow builds two new strands that are the same as that double helix. They build a new

double helix with both strands being new. That's nuts-- why would you do it? It's so obvious you could use one strand as the template for the other.

But this is what Meselson and Stahl had to rule out. They had to rule out that that double helix stayed intact, and maybe the cell sent some enzymes around to feel its shape and somehow construct another double helix like it. That would be a non-conservative model. You weren't using any old strands. The two old strands stayed together. And you made two new strands. That's what they were trying to distinguish between, this semiconservative model or not.

So I just remind you that their really cool, cool idea-- see, they couldn't use a radioactive tracer that was different on the new strand than the old strand in the conventional sense. Because, of course, they're made out of the same atoms. But what they did do, as we talked about last time, was they take the DNA. They grow it up in heavy nitrogen. They then shift the bacteria to light nitrogen. And, if in fact the Semiconservative Model is right, then the new DNA after one generation of growth will have a lighter density.

Very simple, except that they had to go invent a way to measure density. They had to invent this centrifugation process where they spin really, really, really, really hard. And the salt gets a little denser here, and a little less dense here, and a little less dense here. And it's not a very huge difference. But if you know the density of DNA, and you arrange your salt concentration at just the right density, you can spin it really hard so that there's some gradient in density in the salt.

And the heavier stuff will band here. The lighter stuff from one generation of growth will band there. And normal DNA would band there. And that's a pretty convincing proof. After no generations it's all in 15-15. After one generation it's all intermediate. After two generations some of it is now 14-14. Some of it is 14-15. And onward like that.

Obvious, and it's a gorgeous experiment, just a gorgeous experiment. And this idea of density centrifugation, which they invented for this purpose, has been used for many other purposes since.