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PROFESSOR: OK, so we're going to leave off where we were last time talking about buffers. And I'm a big fan of buffers, actually, and buffers are extremely useful in my research because they keep the p h of things constant. So if you're going to do any kind of biology research or biochemistry research, you need to know about buffers. And as I'll mentioned later, also your body needs to be buffered appropriately, you don't want a large changes in p h in your body or things won't function properly. So buffering is very important.

So let's go over buffers. So if we talk about an acid buffer, that's something that's buffering on the acidic side of the p h range. And in that, you want to have play on both sides. So if you have a strong acid, it can be neutralized, the p h stays the same. If you had a strong base, that would be neutralized so the p h stays the same. So what happens, you have to have an acid and its conjugate base in the mixture to have a good buffer.

So what the weak acid is going to do is it will transfer protons or hydrogen ions to hydroxide ions that are supplied by the strong base to neutralize that strong base that was added. So you need to have an acid in there that's capable of giving up a proton to neutralize the hydroxide ion that was added. You also need to have a conjugate base. The conjugate base is going to accept protons if an acid is added, thereby neutralizing the effect of that added acid. So again, you need a weak acid and its conjugate base, you need both to have a good buffer.

So I've been talking about weak acids and weak conjugate bases, so why would a strong acid and the salt of its conjugate base not make a good buffer? What do strong acids do? They dissociate almost completely, and that's not going to do you any good. You want to be able to shift that equation both directions. So a strong acid goes to completion is going to drive it to the right, and for a good buffer you want to be able to switch things around that if you add a strong acid, then you neutralize that, you add a strong base, you neutralize it. So you need the conjugate to be effective as a base, and a strong acid has an ineffective conjugate base. It's not good as a base at all, so that won't work. So buffers are made up of weak acids and their conjugate bases, or weak bases and their conjugate acids. They need to be in the weak range or there's no buffering capacity.

So let's look at a base buffer example. The only difference here is that a basic buffer is going to buffer on the basic end of the p h range. So here's an equation. We have a base in water forming a conjugate of that weak base and hydroxide ions. So let's think about what happens if a strong acid is added. Well if a strong acid is added,

then this base, NH_3 , can accept protons from the incoming acid and make more NH_4^+ , thereby removing the strong acid from the solution and neutralizing the pH .

If on the other hand a strong base is added, NH_4^+ or ammonium ions can donate the proton forming its conjugate base in water, and again, the pH remains about the same. So the base and its conjugate acid can both react, neutralizing the pH .

So in the base buffer acid, a weak base, b , will accept protons supplied by the strong acid, removing a strong acid from the solution. The conjugate acid of that weak base, which again, would be a weak acid, can transfer protons to the hydroxide ions added by the strong base, again, neutralizing the effect there.

So a buffer is a mixture of a weak acid base conjugate pair that will stabilize the pH serving as a source or a sink for the added protons. So that's how a buffer works.

So, I mentioned buffering is very important. It's very important in your blood. Your blood is buffered in the range of pH 7.35 to 7.45, and you have a buffering pair and a conjugate acid base pair that's in your blood that does to work. So nature has its own buffering system design to keep the pH of your blood constant.

Well what happens if the pH of your blood changes? So let me just tell you about one disease that can change the pH of your blood. This is from a vitamin B12 dependent enzyme called methylmalonic coa mutase, and this enzyme is your friend. I think that most of you are excited about the idea of having all your fat go to energy, so you should be all fan of this enzyme. So it breaks down from fatty acids - you get methylmalonyl coa, which is converted to succinyl coa and goes into the citric acid cycle. But if this step is blocked, if there's some kind of genetic disease associated with that particular enzyme, you get a condition called methylmalonic aciduria.

So this is excreted in the body, it can't be converted to the succinyl coa, so it has to be excreted from the body, and it has an acidic pH . And so when it's excreted, it will actually, there's a large amount of it, and it can change the pH of blood. So even though you have this buffering system, it can overwhelm the buffering system and cause a change in the pH , which can lead to neurological disorders and sometimes death.

So they can look for this in newborns, they can do a test, and I was -- one of the tests is -- it's not in every state, but it is in Massachusetts, so my daughter, Samantha, had this test. But they can simply look at the urine of a newborn and look at the pH and whether any of this is being excreted. And some infants that have this condition can excrete like a gram of this acid a day. So it's really large quantities of acid that are excreted and it goes beyond the buffering capacity.

So, I'm going to tell you a little story and it sort of emphasizes some of the importance of genetic research. So before the human genome project, scientists were trying to find the gene to figure out what was wrong with these patients that had this condition. And here are all the amino acids translated from the gene. This is not a small protein, that's a lot of amino acids. And they found that the problem was right here, or one of the main problems is right here. There's a glycine residue, which glycine is the smallest amino acid and that had been changed to something else and that led to the disease.

Now I want you to imagine if you were parents of a small child and you found out your child had this condition and then you had heard that there were advances, they now know what caused it, and so, they went to the doctor and the doctor said, yes, your child, the DNA is wrong, and so let's substitute a different amino acid for glycine here. OK. What does that do for you? Like why is that a problem? Well, they didn't know why it was a problem, they just knew that it had the wrong amino acid in there.

And so, the next step was to try to understand what was actually going on. So what happened in this case was that the vitamin B12 cofactor had changed its conformation when it bound to the protein. And instead of having this sort of loop structure here, it had more of a tail. So this base here had moved down, and so there was a different shape to the vitamin than had been expected.

So when the first structure was solved of one of these enzymes, it found that here's kind of what the vitamin B12 looked like, it had this extended region which no one was expecting, and so that had to fit into the protein. So this is the domain of the protein that binds the vitamin, and it had a large hole, and you put these together and that's great, it fits and you have happy enzyme. Well, how do you create a hole -- nature supposedly abhors a vacuum, so how do you have this hole? Well, what nature did was it put the smallest amino acids there are, glycines, right along here to make room for this to fit together.

So, what was happening in this genetic case is that the switch of a glycine to an arginine did this to the hole. So, what people were trying to do is treat these patients with extra B12, you give them injections of it, you have a lot more B12, and you want the B12 to bind and get the activity back going again. But really, no matter how much vitamin B12 you added to it, it wasn't really going to do much good, it just wasn't going to fit.

So instead, there was a suggestion that instead of giving the whole vitamin, perhaps you could just give a truncated version of the vitamin, which was commercially available, and that that might bind and restore activity of the protein. So this is what was suggested once you knew what the problem actually was.

So this is just an example of a genetic disease, and it's not that common, but as I said, it is tested for here in Massachusetts. And how knowing something about what the problem is can lead to a potential solution. But for most of you, your blood is doing just fine, you don't have a genetic condition which is pumping too much acid into your bloodstream, so that nature's buffering capacity is working quite well.

So buffers are important. It's great to have my important statements emphasized up there. We've been rehearsing at home. OK. So let's do a sample buffer problem. All right, suppose we have an acid, 0.1 moles of an acid, and 0.5 moles of its conjugate base added in the form of a salt. And so they're put into water and diluted to 1.0 liter. And you're given information about the K_a of the acid, 1.77×10^{-4} , and you're asked to calculate the pH. So what do you do?

All right, first, it's always good to write the equation that you're talking about. And so you have acid in water forming hydronium ions and the conjugate base. So here, the acid is giving up a proton to the water, forming H_3O^+ and its conjugate base.

Now we want to think about what happens at equilibrium. So we know how many moles we have and we know what the total volume is. And in this table we should be using molarity, but the math here is pretty easy because we have 1 mole and 1 liter or 1, and 0.5 moles in 1 liter or 0.5 for molarity. And now at equilibrium what's going to happen, well, when this equilibrates some of this will go away and more of these are going to be formed.

So we have minus x over here, plus x and plus x over there, and we add it all together you get $1 - x + x + 0.5 + x$. So the important thing to remember is in buffering problems, you have the acid and the conjugate. So we're used to seeing these tables where we only have something over here and it's all zero on the other side. But in a buffering problem, you have things on both sides from the very beginning. And that's a really important point, and that alone, if you can remember that, will get you a long way through this unit. So you remember that in a buffer you got to have both an acid in its conjugate base or a base in its conjugate acid.

So here we're talking about an acid in water, it's an acidic buffer, and so we can use our K_a value -- we want to know what the concentrations are at equilibrium to calculate our pH . So we can use our K_a and we can set it up, so we have on the top products over reactants, and we we're not including water in this because it's dilute in solution and so it's not changing very much. And now we can plug in our values, so we have $0.5 + x$, x over $1 - x$.

All right, now this is just written again from the last slide, we can try an approximation, which is it that x is small compared to 1 molar or 0.5 molar. And so we can get rid of the plus x and the minus x down here and just have one x term, which makes it simpler to solve, but we'll have to go back and check that approximation in a few minutes.

So making that approximation, we can calculate x as 3.54×10^{-4} molar, and now we need to check that assumption. Well, you can probably guess it's going to be OK, because something times 10^{-4} compared to 0.5 and 1, that's probably going to be OK that it's small. But our assumption here is that it needs to be less than 5%, and here it's 0.1%. So you could just take this value of x , divide it by the smaller of the two, 0.5, times 100, and calculate the percent ionization. If it's less than 5% you're OK, if it's more you need to use the quadratic equation to solve the problem.

So x here is our concentration of hydronium ion, which is great, because then we can easily calculate the pH . So pH again is minus log of the hydronium ion concentration, and so the pH here is 3.45. And again, significant figures, we'll be talking about this as we go through. The volume had two, it was 1.0 liters, and so we're going to have two significant figures after the decimal point, because the volume was limiting insignificant figures.

All right, now let's consider what happens if some strong acid had been added in the solution. So the volume is still going to be 1 liter, because the acid was added in before we went up to the 1 liter mark.

So strong acids, they go to completion. So, if we added 0.1 moles of that strong acid, it will react with equal number of moles of the conjugate base to form the

conjugate acid. So we can just do subtractions here. We don't have to worry about setting up any kind of equilibrium, we assume it goes completely.

So for the conjugate base we had 0.5 moles before, and it's going to be reacting then with a strong acid, so 0.1 of those will react, leaving us with 0.4 moles of the conjugate, and that's in 1 liter. So now we have 0.4 molar. For the acid, we had 1 mole to begin with, but now we formed more as they reaction has taken place, and so we have 0.1 more. Now we have 1.1 moles again in 1 liter.

So now we can do the same thing again. So after this has happened, after we have added the strong acid, then a new equilibrium is going to be reached. And so we can plug in this table as well. So we have 1.1 now over here, and 0.4 on the other side. As equilibrium is approached, you lose some of the acid as it reacts with water and ionizes and you form more of the H_3O^+ and more of the conjugate. So we have 1.1 minus x , x , and 0.4 plus x .

So again, the trick here is just to remember that there is a reaction with a strong acid that has been added, and you need to figure out the new molarities, and then go back to your equilibrium table with those new molarities.

So here we can set up with a K_a again, and do the same problem that we did before. And so, we can make the assumption again that x is small, try it out and see if it works. x turns out to be 4.87×10^{-4} molar -- so again, it's a small number. And so, it turns out to be 1.1 -- less than 1% of 0.4. If it's less than 5% of the smaller number, you don't have to worry about the bigger number, and so your assumption is OK, you don't need to use the quadratic equation. And so, then we can calculate at the end that the pH is now 3.31, again, two significant figures after the decimal place because of the volume. So addition of 0.1 moles of a strong acid changed our pH from 3.45 to 3.31. So we buffered pretty well. There was a change in pH , we added acid and the pH did go down, but not by an enormous amount. And so, that's because this turned out to be a pretty decent buffer here, so we didn't have a really huge effect.

So, those are -- that's an example of a buffer problem.

So, let's think for a minute about designing a buffer. Suppose you wanted to create a buffer at a particular pH , what do you need to think about? Well, you need to think about the ratio of your acid to the conjugate, and you need to think about the $\text{p}K_a$ of the acid, and the pH that's desired.

So here is a generic equation for an acid in water, so we have our acid, H_a , in water forming hydronium ions and our conjugate base. And now we're going to do a little derivation to come up with an equation that would be useful to you in thinking about buffers and designing buffers.

So, we can write a generic term for K_a . K_a equals products over reactants, and so we have our hydronium ions are conjugate base over our acid. And now we can take this term and rearrange it. So we can pull a hydronium ion concentration over to one side. And now we're going to take the logs of both sides, so we get the log of hydronium ion concentration, the log of K_a , and the log of H_a concentration over a minus concentration, and now we're going to multiply everything by negative sign, so we have minus logs of things. And I'm just going to move this now up to the top of the screen, and we have this equation.

So what is minus log of hydronium ion concentration? pH . What's minus log of K_a ? pK_a . So, we have pH equals pK_a minus the log of a concentration of your acid over the concentration of your conjugate base. And these are equilibrium concentrations for that, because remember, we derived it from our equilibrium expression for K_a . But a lot of times when you're working buffer problems, you know the concentrations that you added of these things, not necessarily the concentrations of equilibrium.

And if we rewrite this expression in terms of the initial concentrations or original or o concentrations, then we have pH is approximately equal to pK_a minus log of the initial concentrations of your acid over your conjugate base. And this is known as a Henderson Hasselbalch equation. And people love the Henderson Hasselbalch equation, and it can be incredibly useful to you in solving these problems. But I'm going to emphasize when it's OK to use it and when it's not OK to use it, because people try to apply it to everything, and it's for buffer problems, and people apply it to all sorts of things that are not buffer problems. So I want to make sure that it's clear when you can use it and when you can't use it. And it's fine to use it and you should use it when it's acceptable, but not at other times. It's one of the few equations in acid base, so people get very excited by it.

All right, so remember that it's really equal when they're at equilibrium concentrations, and this is just an approximation that we're saying that those are initial concentrations. So when is it OK to say well, the equilibrium concentration is more or less the same as the initial concentration. And that's true when x , which is in this particular example your hydronium ion concentration, is small compared to your initial concentration of the acid and the conjugate base that you added to the buffer. So, and when x is small, then pretty much, the equilibrium concentration equals the initial concentration. So there's not really very much change if x is a really small number.

So, a lot of the time this is true. Remember, we're making buffers from weak acids and weak conjugate bases, and the definition of a weak acid is that it only loses a tiny fraction of its protons. It only ionizes slightly in water. And a weak base typically only accepts a fraction of the protons it can accept. It's a weak base, so it's not doing a whole lot of chemistry there. So this approximation is good a lot of the time. So just you know when you can and can not use it, we're going to give a rule and say it's the same rule as before. When we say when x is small or your hydronium ion concentration is small compared to the acid or the conjugate base, when it's less than 5%, that's what we're going to call small, so the same rule we've been using all along. When x is small, this approximation works pretty well. And you can plug in your concentrations right there -- your initial concentrations not your equilibrium concentrations.

All right, so let's use Henderson Hasselbalch and design a buffer system if we want a pH of 4.6. And a good rule to remember is that a buffering solution is most effective when it's plus or minus 1 away from the pK_a . So that's a good thing too I keep in mind for research as well. If you're really far away from the pK_a , it's not going to be a good buffering system, and this is a mistake the people make in the lab sometimes, so you may run into that in some of your laboratory courses.

So we want a buffer about pH 4.6. So we can look at our ionization constants of acid, and of course, we're always doing everything at room temperature in this unit, and so we can look at what pK_a 's are of some weak acids, and acetate, acetate is

an easy buffer to get your hands on, acetate is quite available, and it has a good pK_a of 4.75. So that's great, we can use that in designing our buffer. So, acetic acid has the right pK_a , and we're all set, we can prepare a buffer. But we'll need to add the acid and the conjugate, and we need to know how much acid and how much of the conjugate to add.

So we can use Henderson Hasselbalch equation for this. We're creating a buffer, and so this is an equation we can use for buffers. We know what pH we want, we know the pK_a of the thing we're going to use, and we want to figure out how much of the acid to use and how much of the conjugate to use. We need to know the ratio of one to the other to set up our buffer ideally. So we can plug our numbers in and calculate that.

So, we can rearrange this if you want so that the unknown is on one side and we have to pK_a and the pH on the other side. And so, we have here our pK_a minus our pH and we get -1.5. Now we need to inverse log and come up with the ratio, and the ratio that we want is 1 : 4. So we want to have a ratio from our acid to the conjugate of 1 : 4.

Well how much exactly are we going to add them, we know the ratio now, how much are we going to add? Well, you could use 1 : 4 molar and 1 molar, for example, that would have the correct ratio. But how do you know if that's going to be good? Well, the ratio is more important than the exact amounts, however, the amounts get to this issue of sort of the capacity of the buffer -- how resistant it is to changes in the pH . So if you use too low concentrations of both, it won't be all that resistant. So if you need to have a better buffering capacity, the higher concentrations that you should use. And you can use Henderson Hasselbalch then to calculate what sort of the minimum amount you use, the minimum amount to have that 5% rule work.

So in the example I told you about this condition, the buffer in the blood was pretty good, but the acid with so much that it overwhelmed buffering capacity. So if there had been larger concentrations of the buffer, that would have certainly helped in that case. So the higher the concentrations you use, the more resistant to change. And that's the idea of buffering capacity. So, and if you use too low concentrations, then your Henderson Hasselbalch equation won't even be valid. So we can go back and calculate what is sort of the minimum concentrations we need to use for Henderson Hasselbalch to be valid to meet that 5% rule. So for a pH of 4.6, a hydronium ion concentration is a 2.5×10^{-5} .

And so then if we work our equation backwards, we want to be less than 5%, so we have this over the concentration of either one of those times 100% gives you 5%. So the concentrations need to be greater than 5 times 10^{-5} moles or you won't meet this 5% rule. So at least to be greater than that and they need to be in the right ratio. Other than that you're somewhat free to decide what you're going to do with that, and there may be other considerations involved if you're working with a certain concentration of protein, you might not want your buffer concentration to be too high, it might start interfering with enzyme assay, for example. And often buffers are somewhere around 100 millimolar, that's a pretty common concentration for buffers.

All right, so this slide we're doing really well. So we talked about weak acids in water, weak bases in water, and I'm trying to convince you that these are the same as the salt and water problems. So we're going to talk much more about salt and

water in a few minutes. And I told you about buffers, so we only have 2 more things to go. We need to talk about strong acids in water, and strong bases in water, and then you'll have all of the 5 types of problems to do the problem-set. And as I mentioned last time, it looks deceptively short, the number of questions on them, but the titration problems are long. So don't leave those to the last minute or there will not be a whole lot of sleep involved. So just a word of warning from the past. Everyone looks and go, "Oh, this is an easy problem-set, there aren't many problems." So, titration problems do take a lot of time. So let's talk about titration, so that as soon as class is over today, you can go work on those questions on the problem-set.

All right. So acid base titrations. How many of you in high school titrated an acid with a base? Large fraction of you, OK. So usually what titration problems are meant to do, that you have something known about an acid or a base, base say of known concentration, and an acid of unknown concentration or maybe unknown molecular weight, and you're titrating them out, titrating them together to find missing information. So you can determine concentration, sometimes you can determine a molecular weight.

All right, so here's what a plot looks like and some of the key terms involved in acid base titrations. So you have a p h on one side, and then volume of either base or acid added on the other side. So p h versus a volume. And the actual experiment here, you have a base that you're dripping, one drip at a time supposedly into your strong acid. And then you're looking to figure out when you're going to reach the either equivalence point or the end point, these are basically the same terms. It's also called the stoichiometric point, and often equivalence point is used as a more theoretical amount of volume is added, where as end point is the experimentally measured. So we're going to be talking a lot about equivalence points, because we have no lab associated with this course, so everything will be theoretical in terms of these, but they should be the same.

So, many times you will measure p h with the p h meter -- this just shows a p h meter. And for those of you who have done these experiments, this should look familiar. And for those of you who haven't, often what you're doing when you're dripping something in, you're waiting for an indicator dye to change color as an indication that you have reached the end point, and often you're adding, and it's clear, clear, clear for what seems to be forever, and just as you get incredibly impatient, you start adding it faster and you go all the way to this dark color. And what you want is this very, very, very light changed color that indicates the end point. So you usually go too slow and then go too fast and then have to do the experiment over again.

Those of you who know how to calculate theoretical values could sit down and do a calculation first and then go really fast right until you get around this point and add it really slowly, and be done with lab sooner. So, we'll talk about how you do the theoretical value, which could save you a lot of time if you ever run across these labs in any future class.

So, here are the two curves that you would see for either a strong acid with a strong base, or strong base with a strong acid. So if you're titrating a strong acid with a strong base, you're going to start down being very acidic, because all you have is your strong acid. And then as you add in base, the p h will go up. You'll reach this

point -- s is for the stoichiometric point, we also call this, again, the equivalence point, and then it'll continue to go up and then start to level off a bit more up here.

If you're going the other direction, you're starting with strong base, your p h is going to be high, and the p h will decrease as you add the acid. And then you get to the stoichiometric or equivalence point in the middle of this curve here. And then as you go down farther, more acidic, it starts to level off. So those are what the titration curves look like.

So let's do an example. We're going to have a strong base being titrated with a strong acid first. And our strong base is n a o h, and our strong acid is h c l. So let's calculate the p h at the equivalence point. Well, let's just calculate the p h at 5 mils - - I don't know whether it's equivalence point, actually. 5 mils of this have been added to the amount of base. So we have 25 mils of our strong base at 0.15 molar concentration, and we're adding 5 mils of our 0.34 molar acid.

So what we want to do is figure out how many moles of base we had to start with. So how many moles of o h minus -- again, n a o h is a strong base, so however much n a o h you add, is the amount of o h minus you get, and so we just put in the number of liters times the concentration to get moles. We don't need any equilibrium table here.

So then we want to figure out the amount of acid added when you're adding 5 mils of it. So again, h c l is a strong acid, so the amount of h c l added equals the amount of h 3 o plus, that's formed, goes to completion, and so we added 5 mils, the concentration was 0.34 molar, so we have 1.7×10^{-3} moles.

So now, the strong acid is going to react with the strong base, and we want to figure out how much of the base is left, how much hydroxide ion is left after it reacts with the hydronium ions. So it'll react 1:1, so we had 6.25×10^{-3} moles, and we added 1.7×10^{-3} moles of the acid, so we're going to have 4.55×10^{-3} moles left. And now we can calculate the molarity here, so we have the number of moles and the new volume, so we had 25 mils to the base to begin with. We've added 5 mils to the acid, so our new volume is 30, and so we have our new concentration.

And now we can calculate p h. First we'll calculate p o h, and then use 14 minus to get the new p h. So if you were making your own little titration curve, we could have volume of acid on one side and p h on the other side, and you have a point of 13 . 18. That's how much we have after you have 5 mils added. So we didn't, in this curve, we have not measured the zero point, but we know what one point after 5 mils of the acid has been added.

So now let's go right to the equivalence point -- so the way I draw it should indicate that was not an equivalence point. So we want to figure out how much we need to add of the acid to reach the equivalence point. So the equivalence point or the stoichiometric point means that you add the same amount of moles of your titrate as you had, and so they're going to be equal to each other. So if you're adding acid to a strong base, you've added enough acid that you now have equal number of moles to the number of moles of base that you had to begin with. So we know we have 6.25×10^{-3} moles of the base were present.

So at the equivalence point, you need to have that exact same number of moles of acid. So we know the concentration of the acid we have and the number of moles we need, and so we can calculate the volume, which is 18.4 millimeters, or 0.0184 liters. So what would the pH then be of the equivalence point? We're titrating a strong acid with a strong base, what should the pH be? The pH should be 7 . So somewhere around here we're going to be at 18 , so you can just try to draw a curve, and here we have a pH of 7 when we've gone to about 18.4 milliliters added.

So when you titrate a strong acid with a strong base, you form a salt that's neutral. Because the conjugates of a strong acid and a strong base are not basic or acidic. They're ineffective as acids or bases, so you're going to get a neutral salt. So if you're doing a problem with a strong acid and strong base, it's not a lot of calculations that need to be done at this point, you just need to recognize that your salt should be neutral.

So now, we can talk about what happens if you add an extra milliliter of your acid, after you've reached that equivalence point, which is something that people probably have done in doing these titrations not meaning to, gone well beyond the equivalence point.

So first we can find out the number of moles of the strong acid that we've added extra, so we added one mil of the strong acid, and so again, it goes to completion. The concentration, the acid, is 0.34 molar times our 1 mil, so we've added 3.4 times 10^{-4} extra moles of our acid, and so let's calculate then what the molarity is that we have added that was extra.

And even if you don't have a calculator, we've helped you out. Let's just take 10 more seconds.

I think this is a first, isn't it? Did I mention it's a good idea to start the problem-set early. So the trick here was about the volume. So we had 25 mils to begin with, then we added 18.4 to get to the equivalence point, and then we're 1 mil beyond the equivalence point. And the tricks to these parts of the problems are to remember all the things that have been added to get to the volume.

So the problem itself is not very tricky of having just an acid in water, but the one trick is in calculating the molarity, remembering all of the things that were added to get to this point. And so by the end of the problem-set this should be pretty familiar to you, but it's also something that you want to make sure that you check on an exam that you're not making any volume mistakes.

So again, here are the things that you want to remember to add in in calculating this. And then, if you calculate the pH of that, you get a pH of 2.1106 , so that's down somewhere in here. We've added 1 more mill, and we're at a pH of 2.1106 , and this can be a check as well. If you forgot to add some of your volume, you might get a pH that doesn't make a lot of sense. So that can be a double check. Always ask yourself when you have a strong base and you're adding acid, before you've added very much, your pH should be basic. At the equivalence point of a strong acid, strong base titration, it'll be 7 . And if you continue to add acid, then you should have a pretty low pH , you'll notice the curve drops off pretty fast. So it should be a dramatic change in pH by adding extra of your acid.

So always check your work. OK, so let's stop there, and we're going to weak acid, weak base titrations next time.