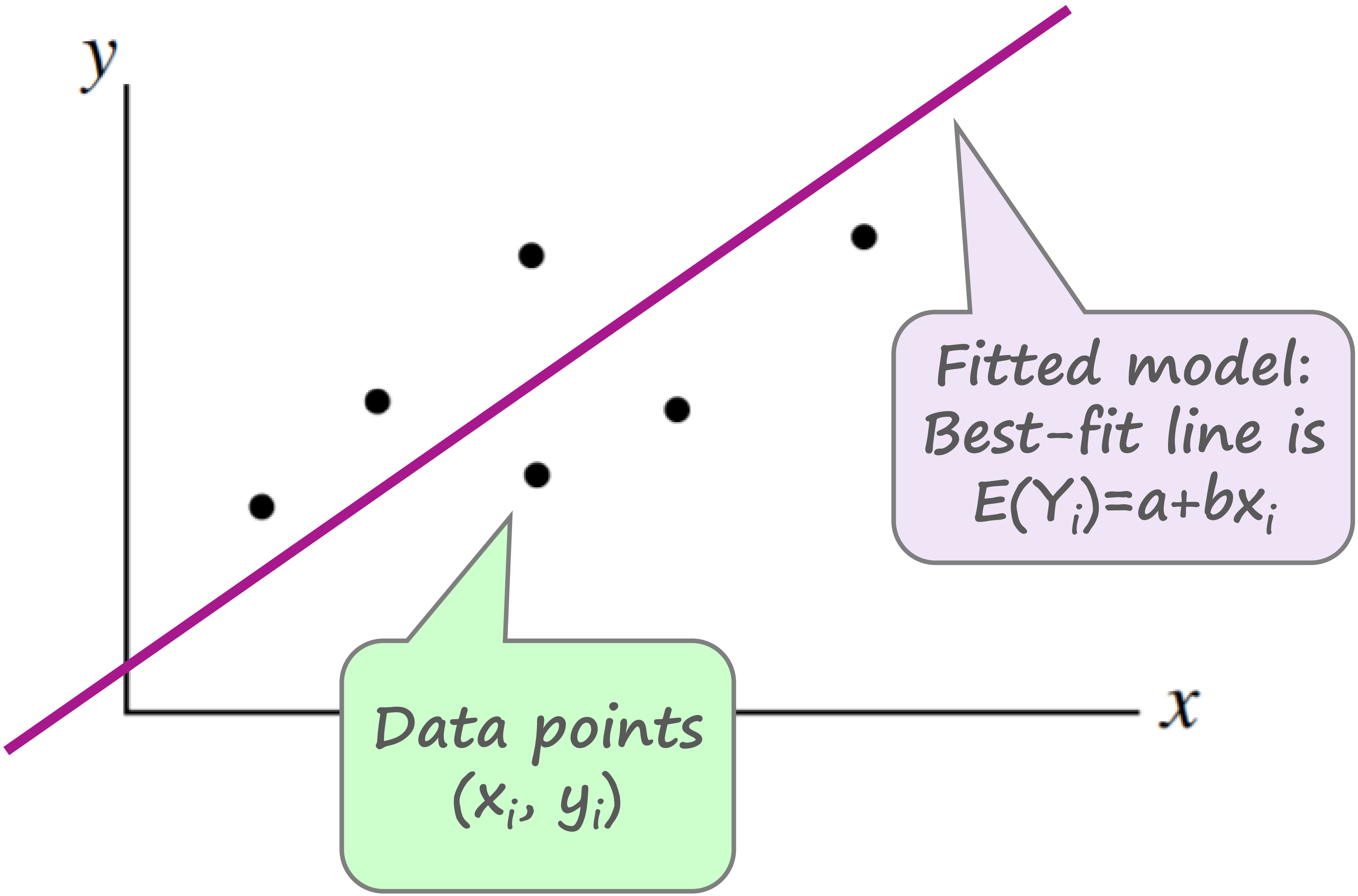
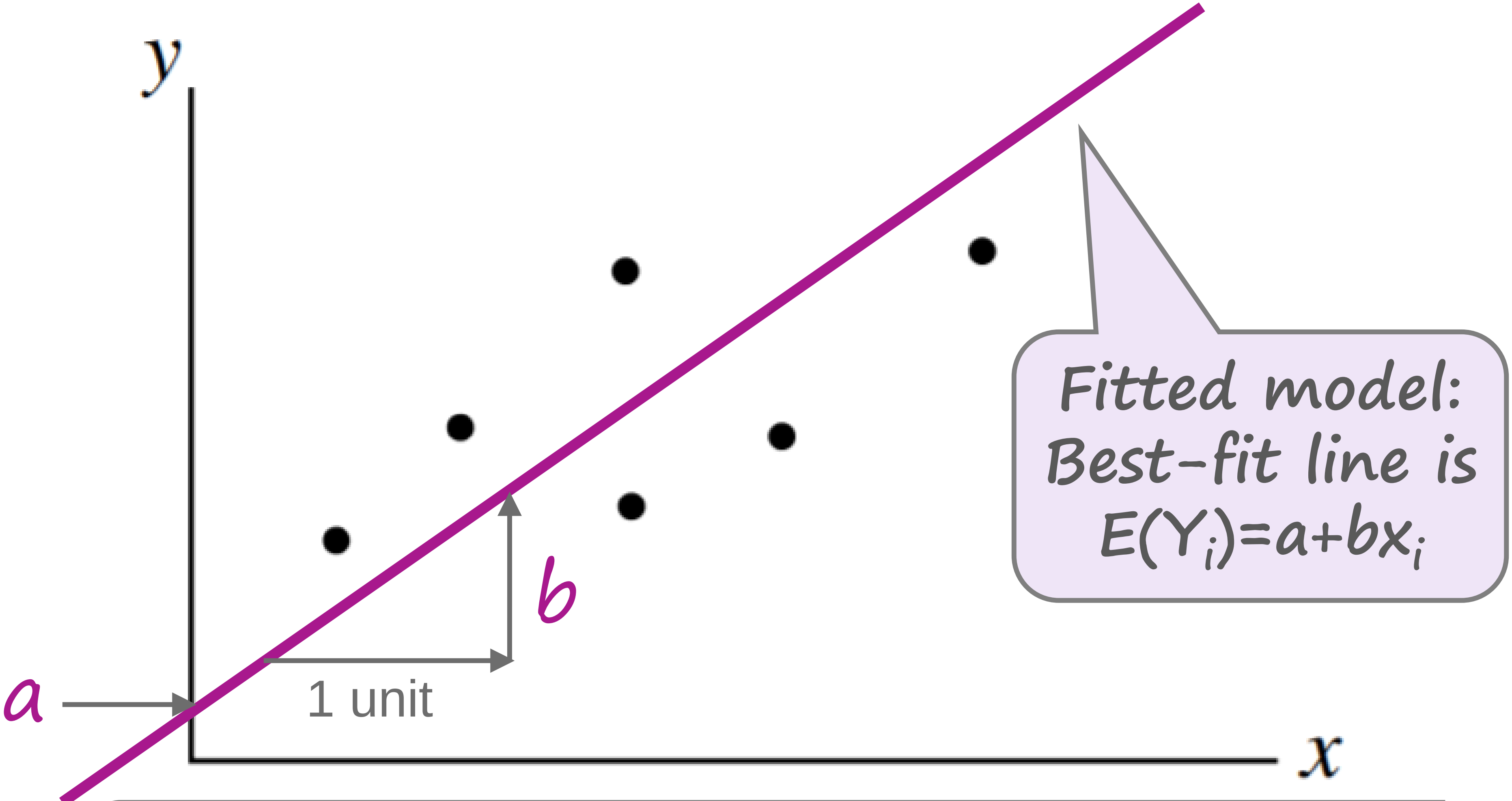
DIY Statistical Modelling

Demystifying the black box …

How do we fit a model?

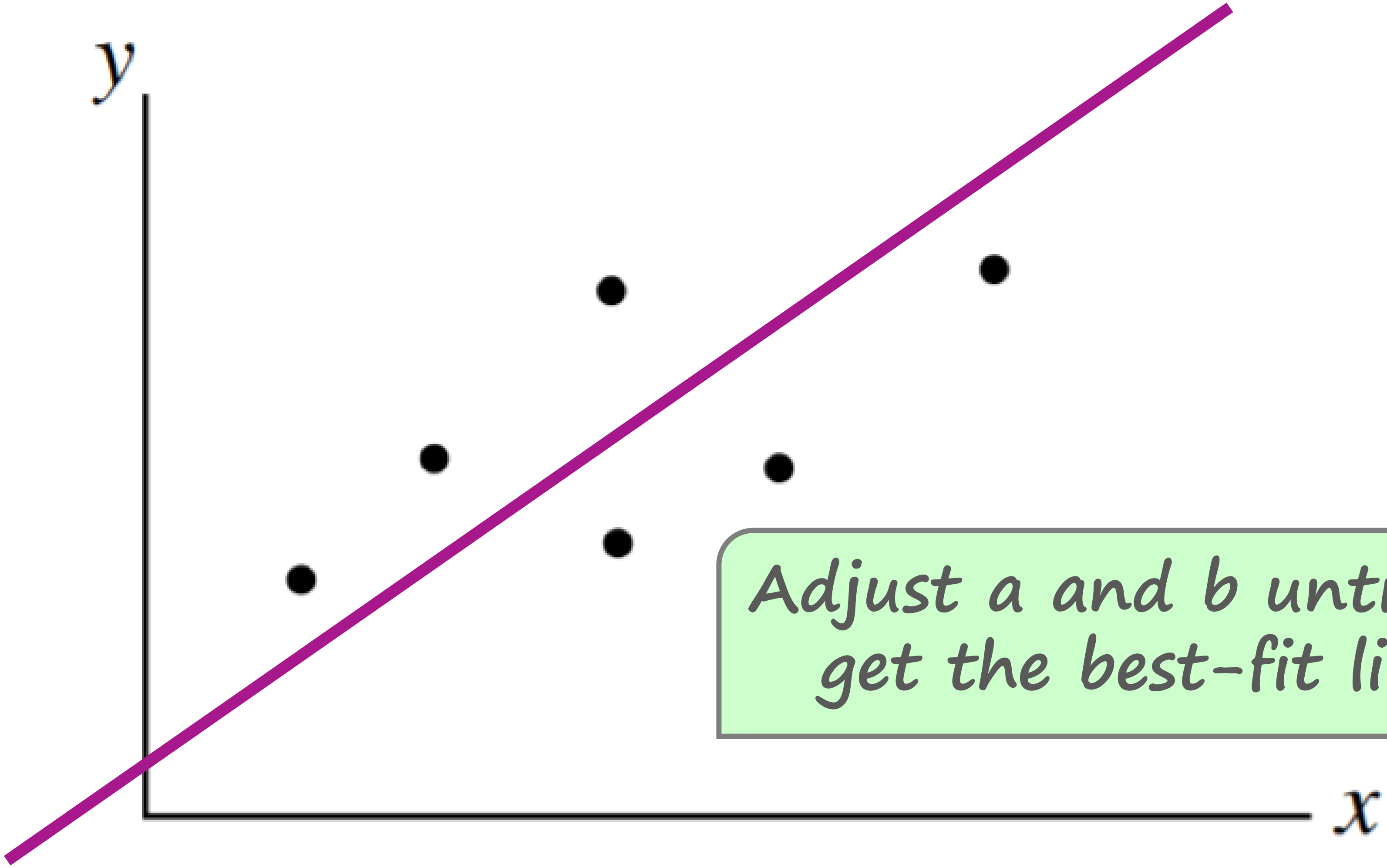


How do we fit a model?



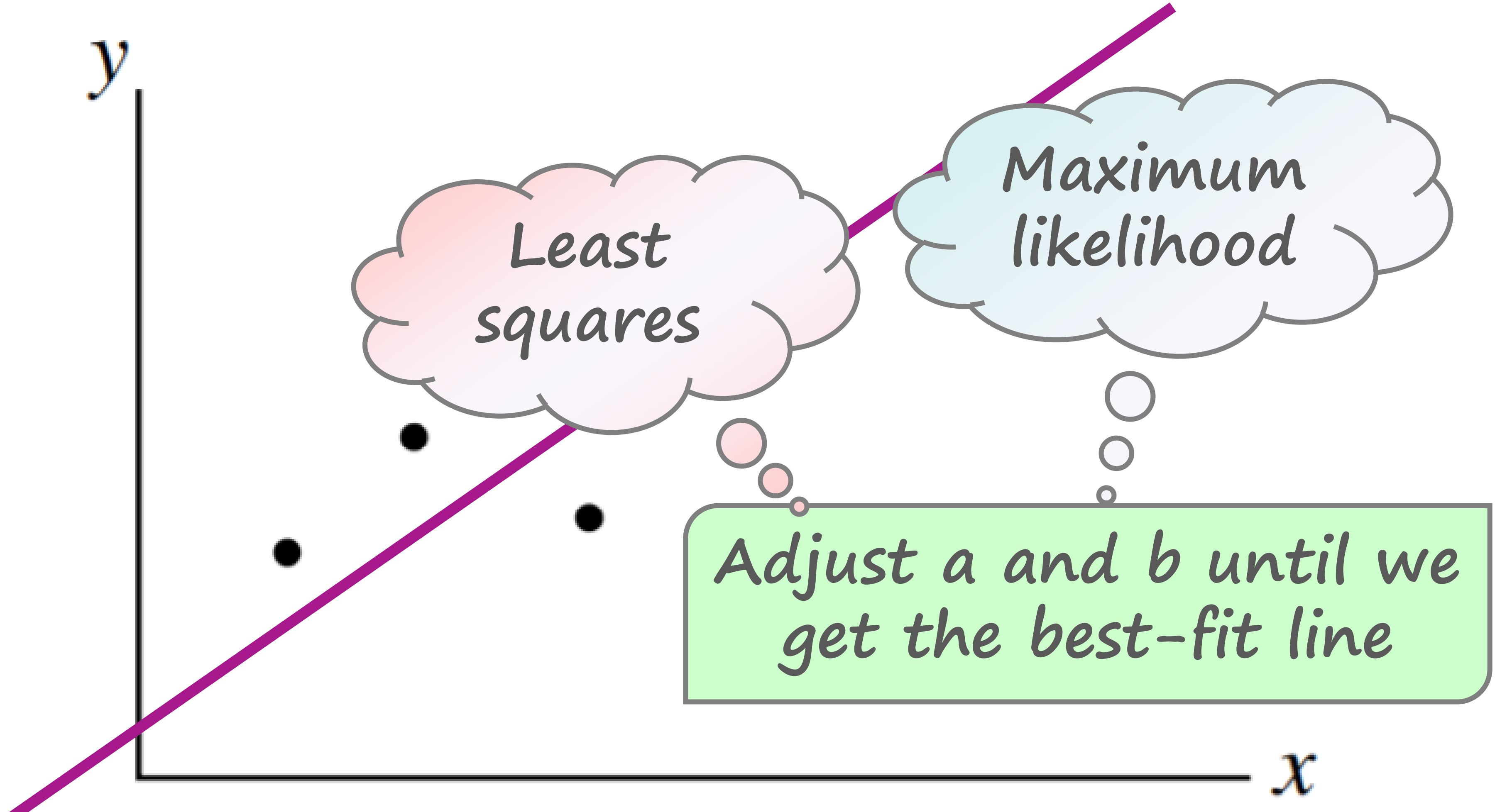
Fitting the model means estimating values for the unknown parameters, a and b

How do we estimate *a* and *b* ?



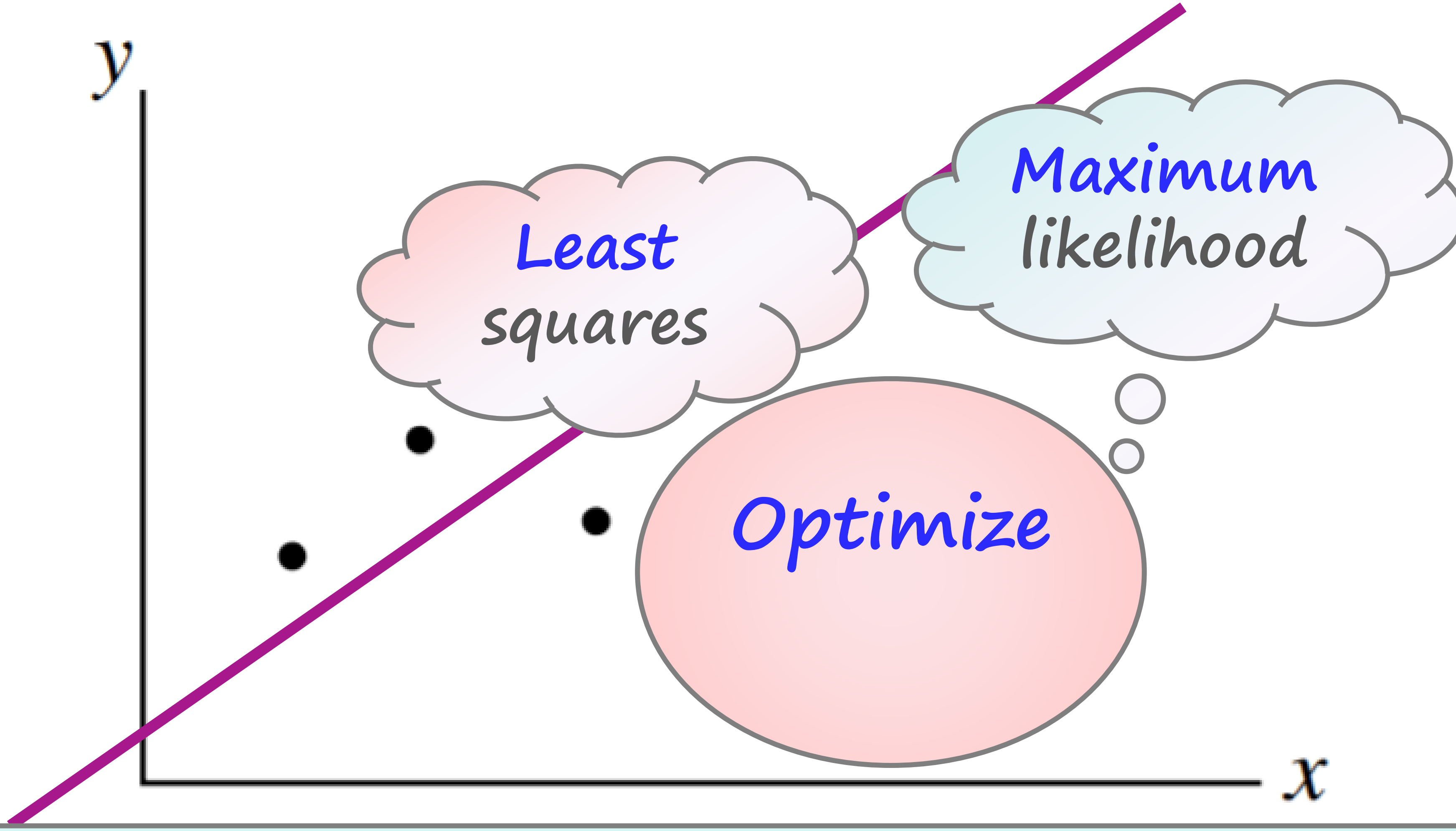
Adjust a and b until we get the best-fit line

What do we mean by ‘best fit’?



We need a criterion to optimize:
something we can measure that can become best

What do we mean by 'best fit'?



We need a criterion to optimize:
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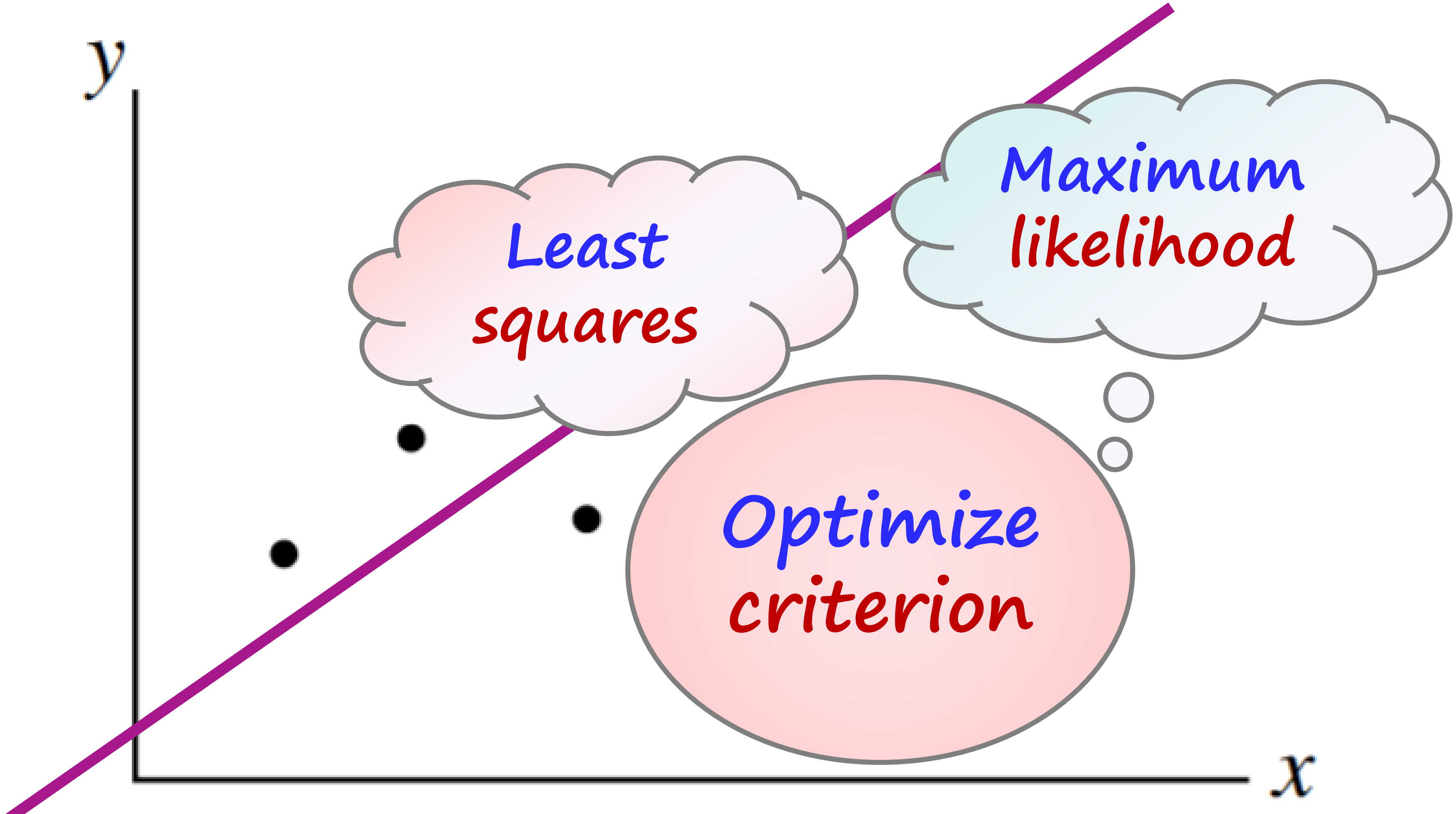
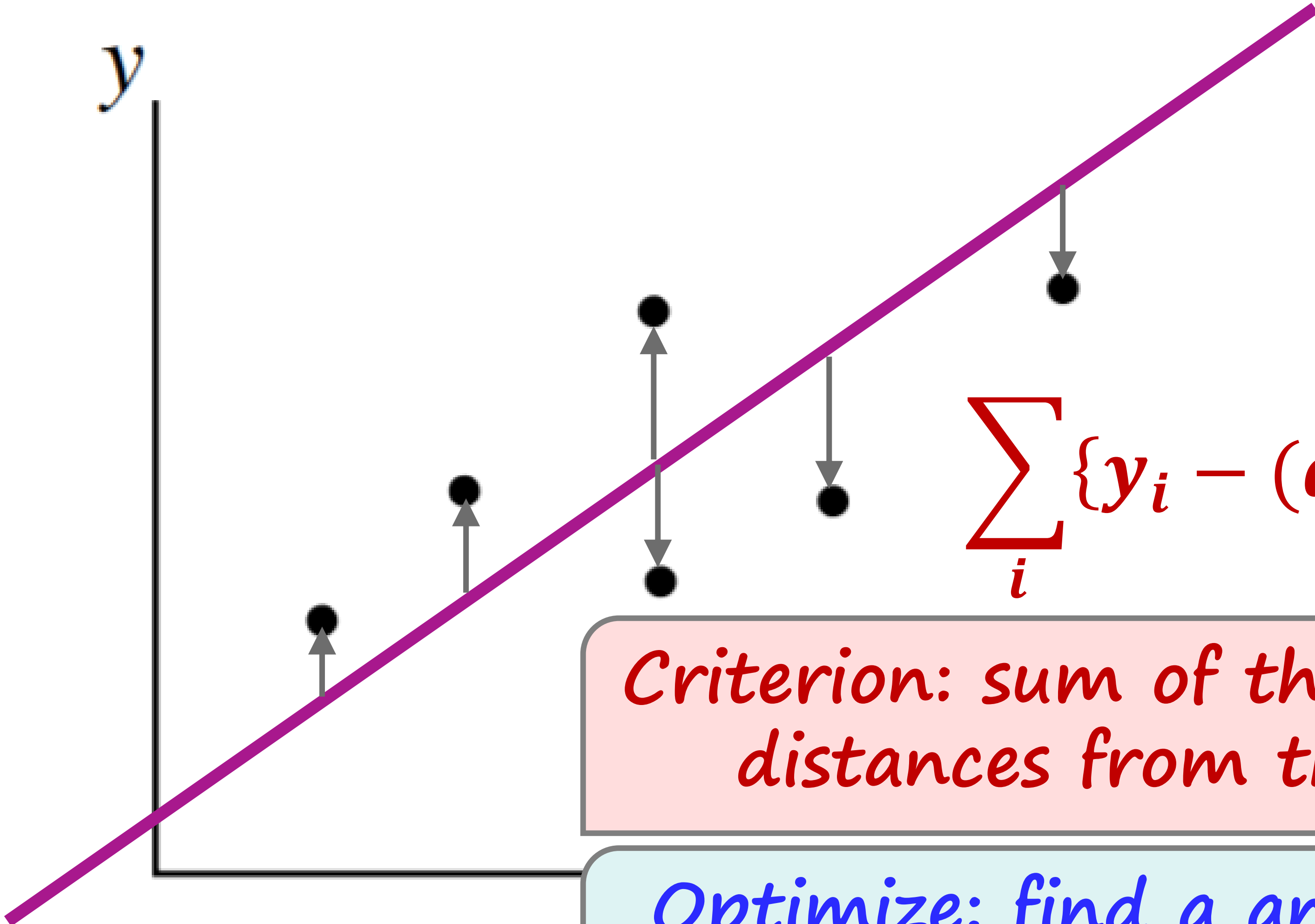
What do we mean by 'best fit'?



We need a criterion to optimize:
something we can measure that can become best

Least squares

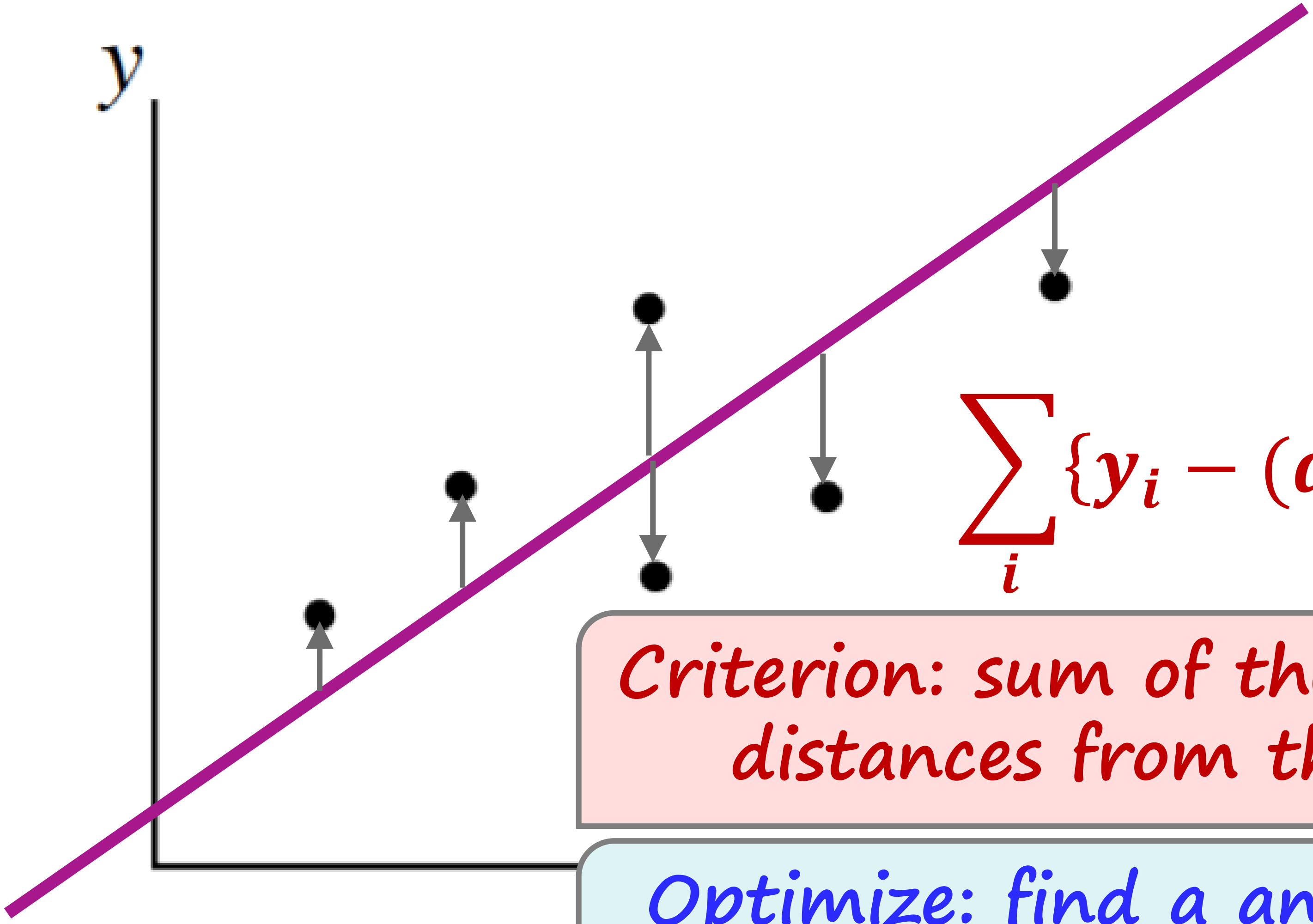


$$\sum_i \{y_i - (a + bx_i)\}^2$$

Criterion: sum of the squared distances from the line

Optimize: find a and b that minimize this sum of squares

Will we need anything else?

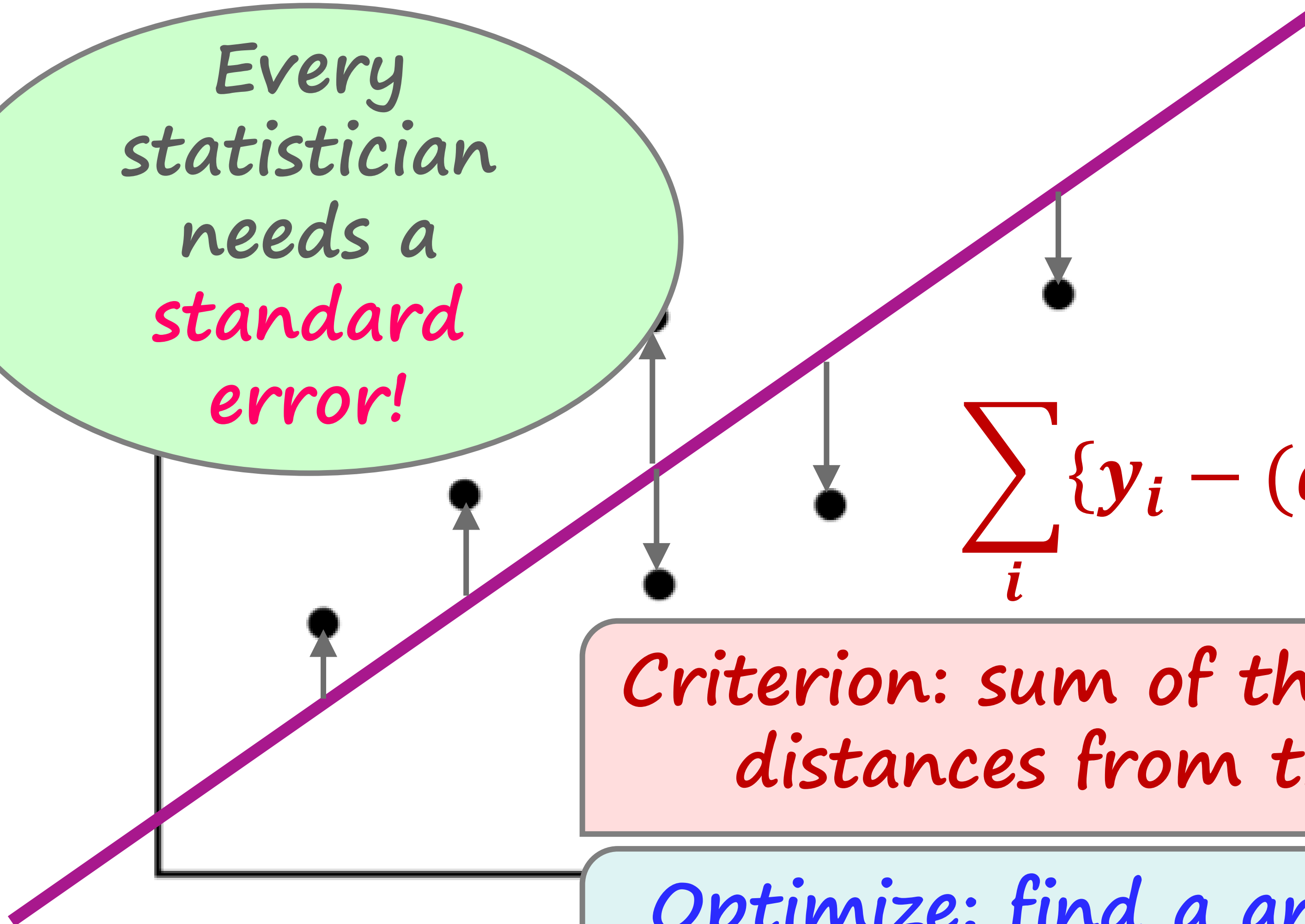


$$\sum_i \{\boldsymbol{y_i} - (\boldsymbol{a} + \boldsymbol{b}\boldsymbol{x_i})\}^2$$

Criterion: sum of the squared distances from the line

Optimize: find a and b that minimize this sum of squares

Will we need anything else?



Every statistician needs a **standard error!**

$$\sum_i \{y_i - (a + bx_i)\}^2$$

Criterion: sum of the squared distances from the line

Optimize: find a and b that minimize this sum of squares

Why do we need a standard error?

An estimate is useless without a standard error!

Would you eat this...?

This...?

Yum! (not)

???

Why do we need a standard error?

An estimate is useless without a standard error!

It's useless to try selling a possibly-dodgy item unless you include an assurance of goodness

Why do we need a standard error?

An estimate is useless without a standard error!

- **A standard error is quality assurance**

This item is
only a little bit
lethal!

Why do we need a standard error?

An estimate is useless without a standard error!

- **A standard error is quality assurance**

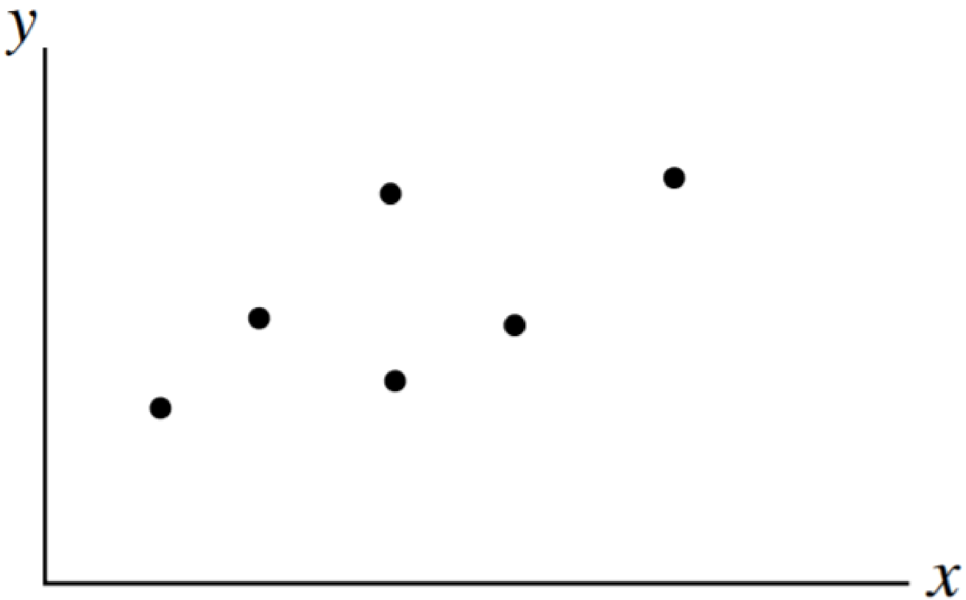
- **Anyone can propose an estimate:**

$a = 3.14$ $b = 1.23$

My estimates!

- **But we need the standard error to tell us what this estimate is worth, or how safe it is**

SE: pathway to inference (conclusions)

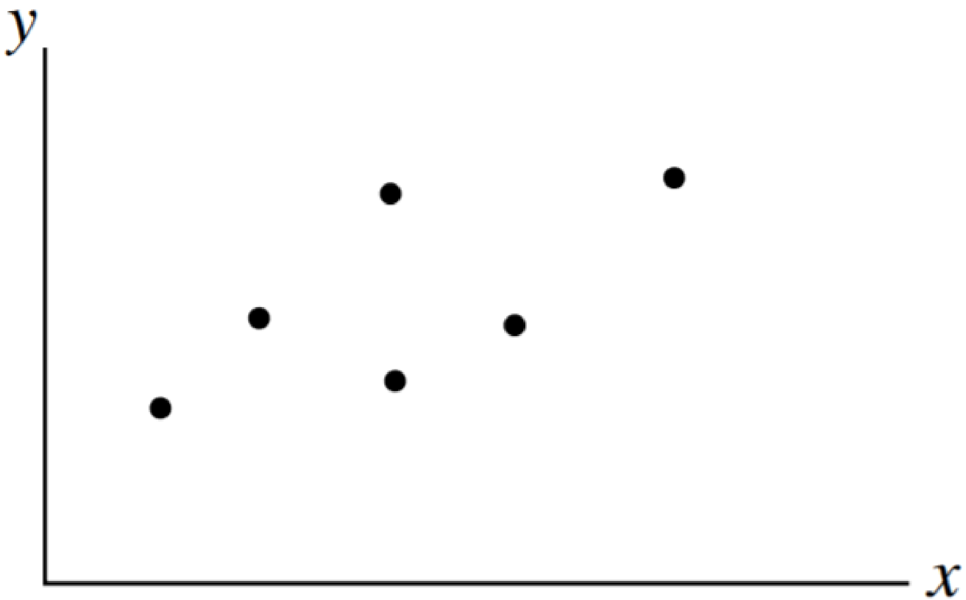


Is there a relationship between x and y?

Are we sure the slope b isn't zero?

- My estimate is b = 1.23, which isn't zero…
- But to answer the question "are we sure?", we need the standard error

SE: pathway to inference (conclusions)



Is there a relationship between x and y?

Are we sure the slope b isn't zero?

If my estimate is $b = 1.23$ …

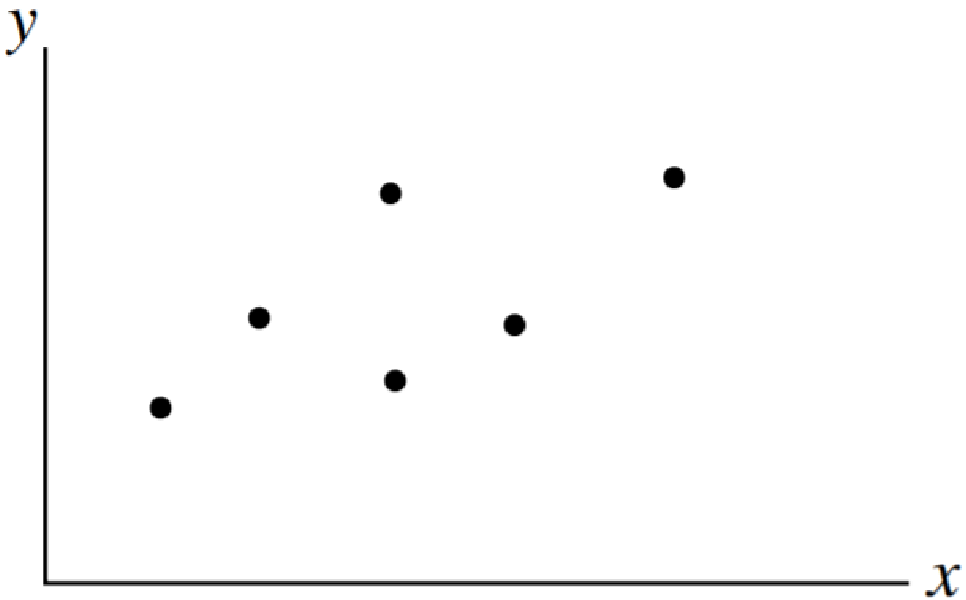
SE = 5.8

Poisonous!!
Don't trust this b!

SE = 0.2

Great stuff!
You can trust that b>0

SE: pathway to inference *(conclusions)*



Is there a relationship between x and y?

↓

Are we sure the slope b isn't zero?

Standard error → p-values and confidence intervals → Conclusions

So how can we do all this ourselves?

We need:

- **A criterion to optimize**
  - ➢ **e.g. least squares or maximu**

Next video!

- **Some way to optimize things**
  - ➢ **In R, if you can calculate it, you can optimize it**

- **Some way to generate a standard error**
  - ➢ **We can use the bootstrap**

Numerical optimization in R

- In R, if you can calculate it, you can optimize it
- Numerical optimizers repeatedly try out values of a and b to find their way downhill to the minimum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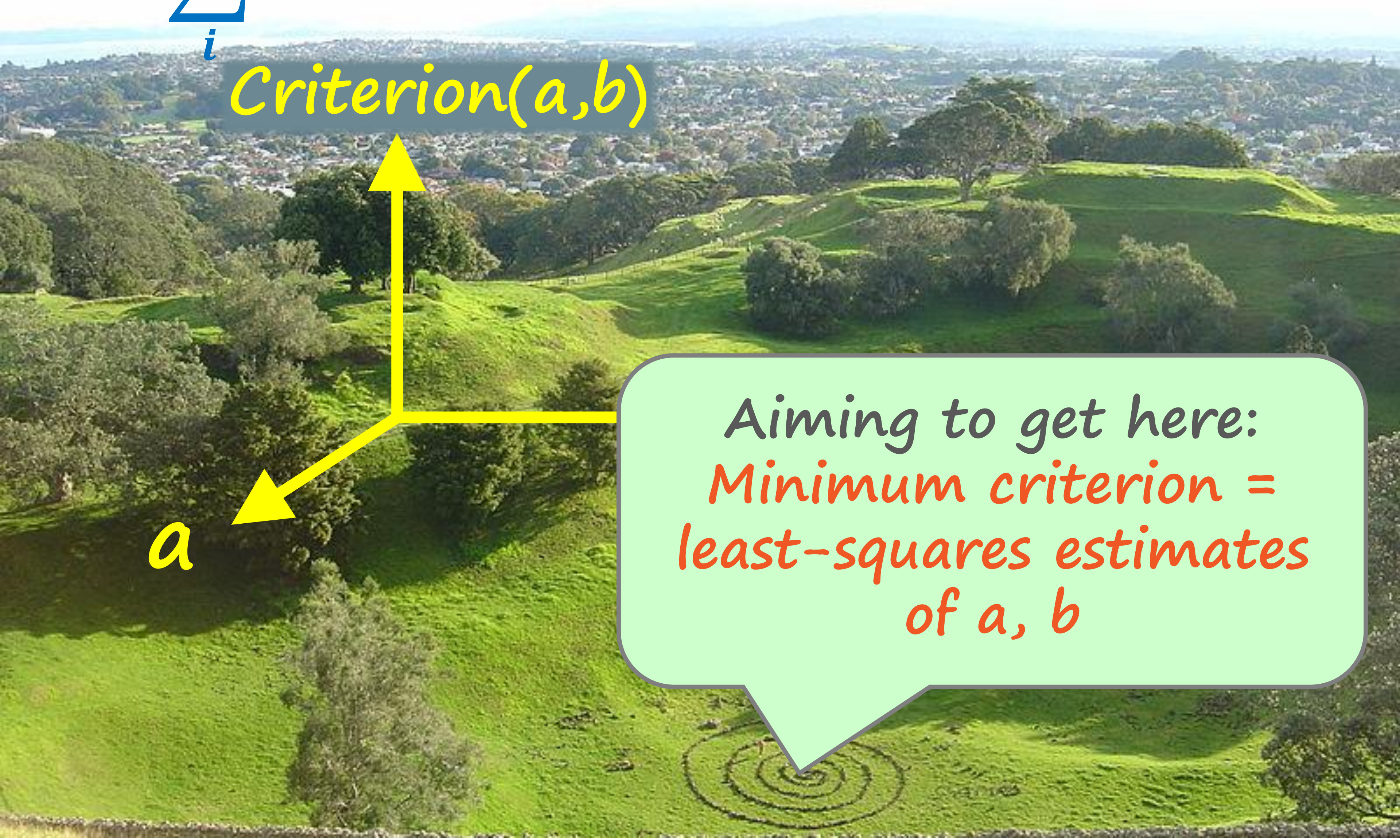
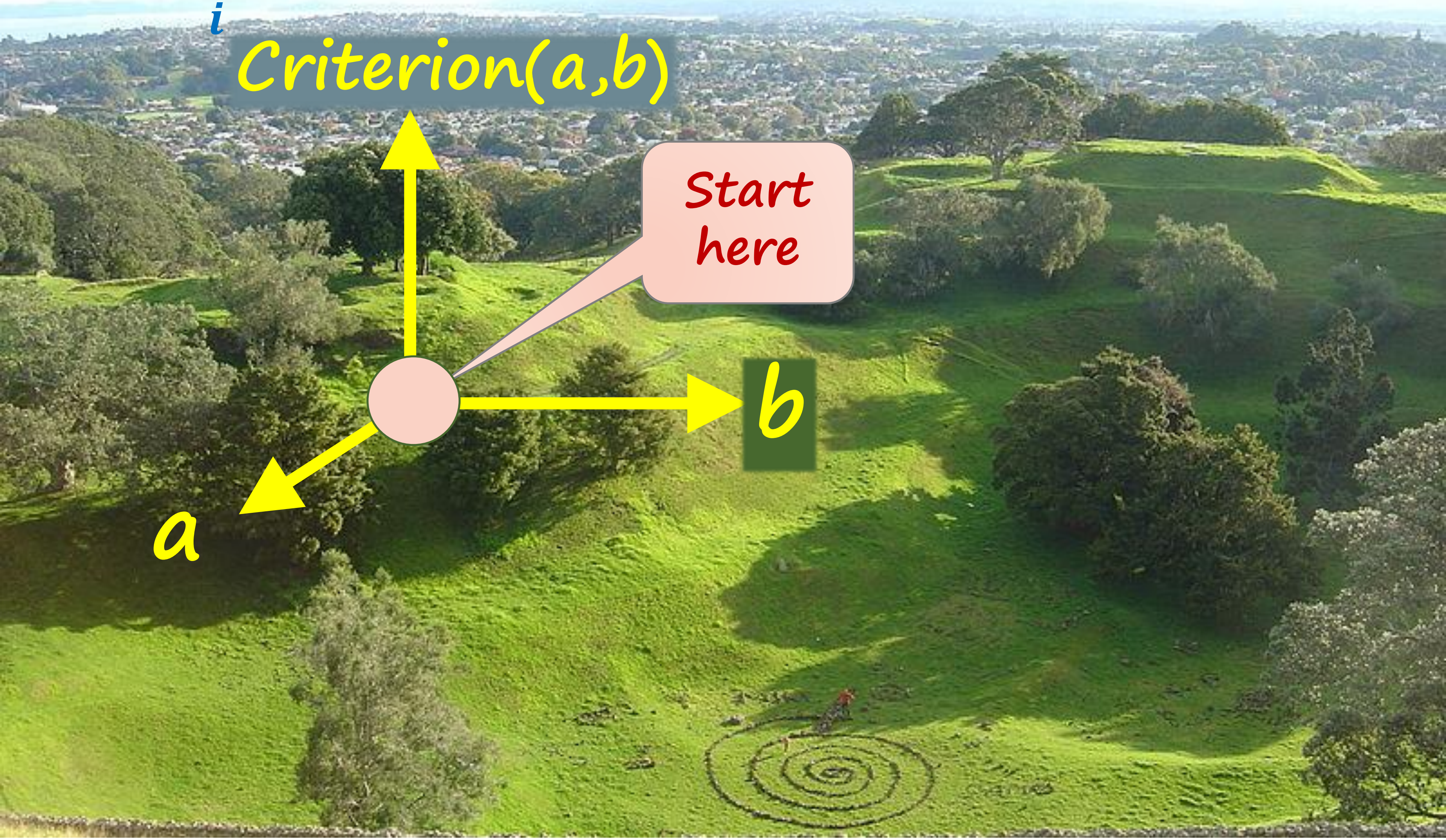
$$\sum_i \{y_i - (a + bx_i)\}^2$$



We want to fumble our way downhill to the bottom

$$\sum_i \{y_i - (a + bx_i)\}^2$$



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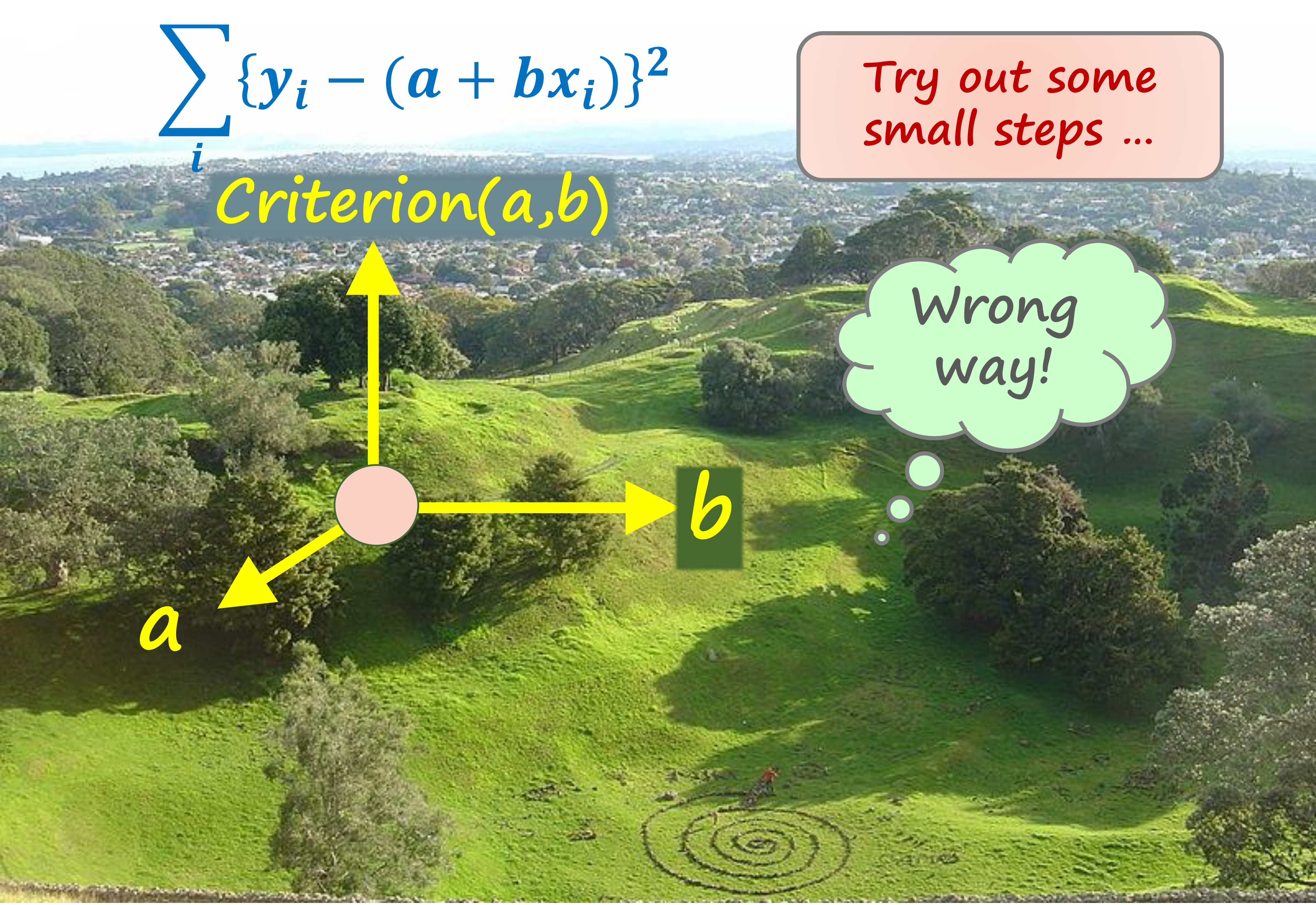

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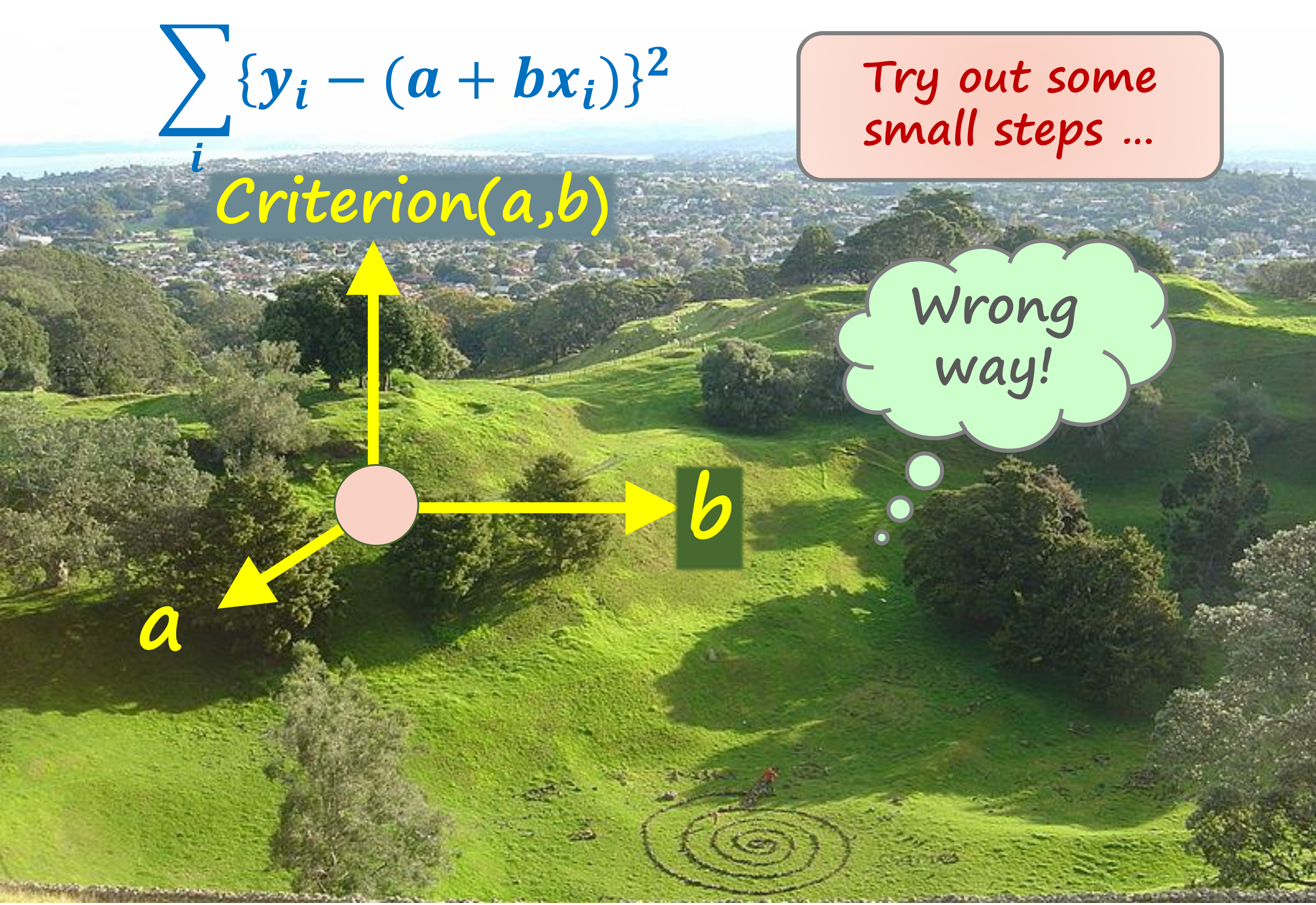

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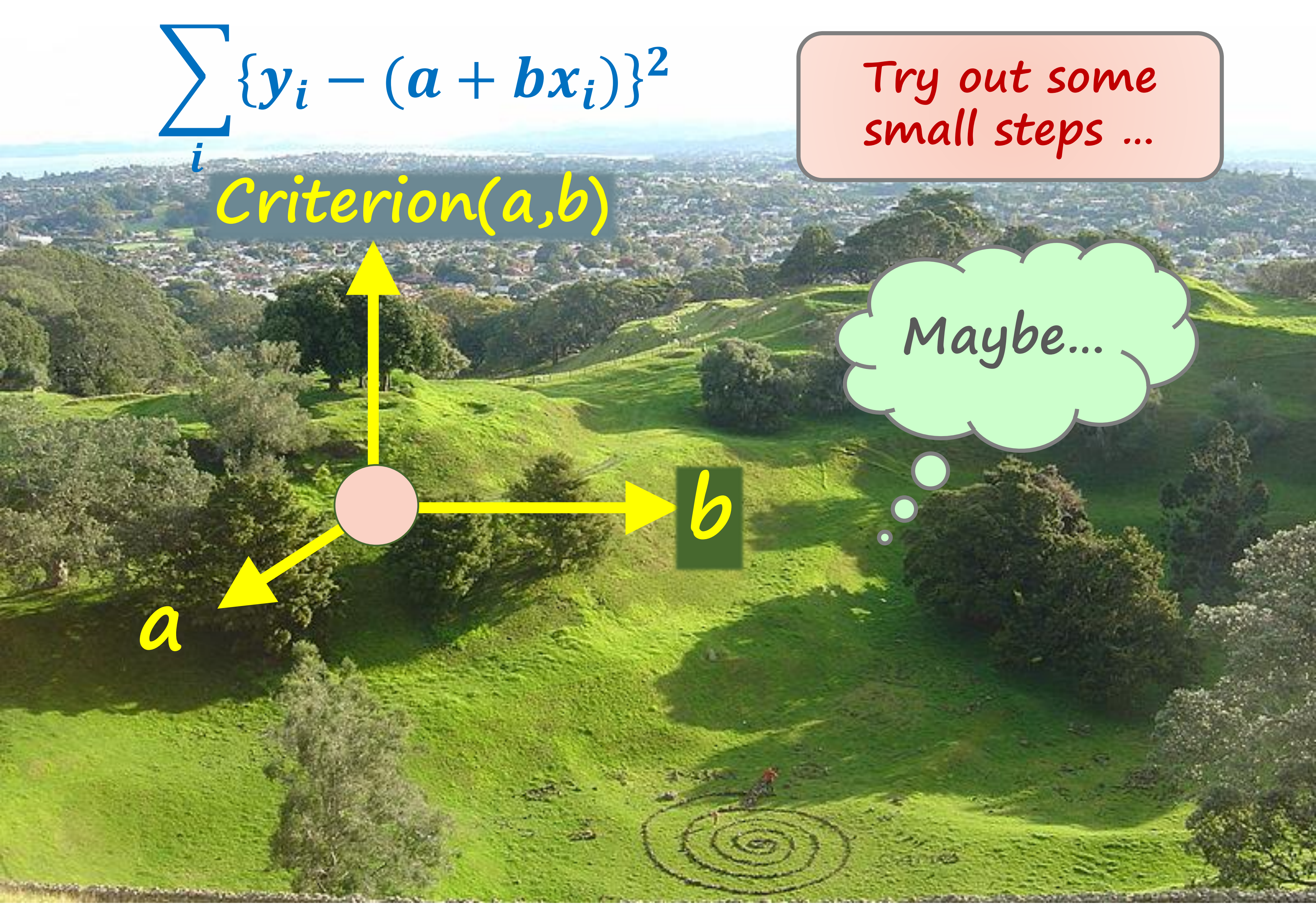
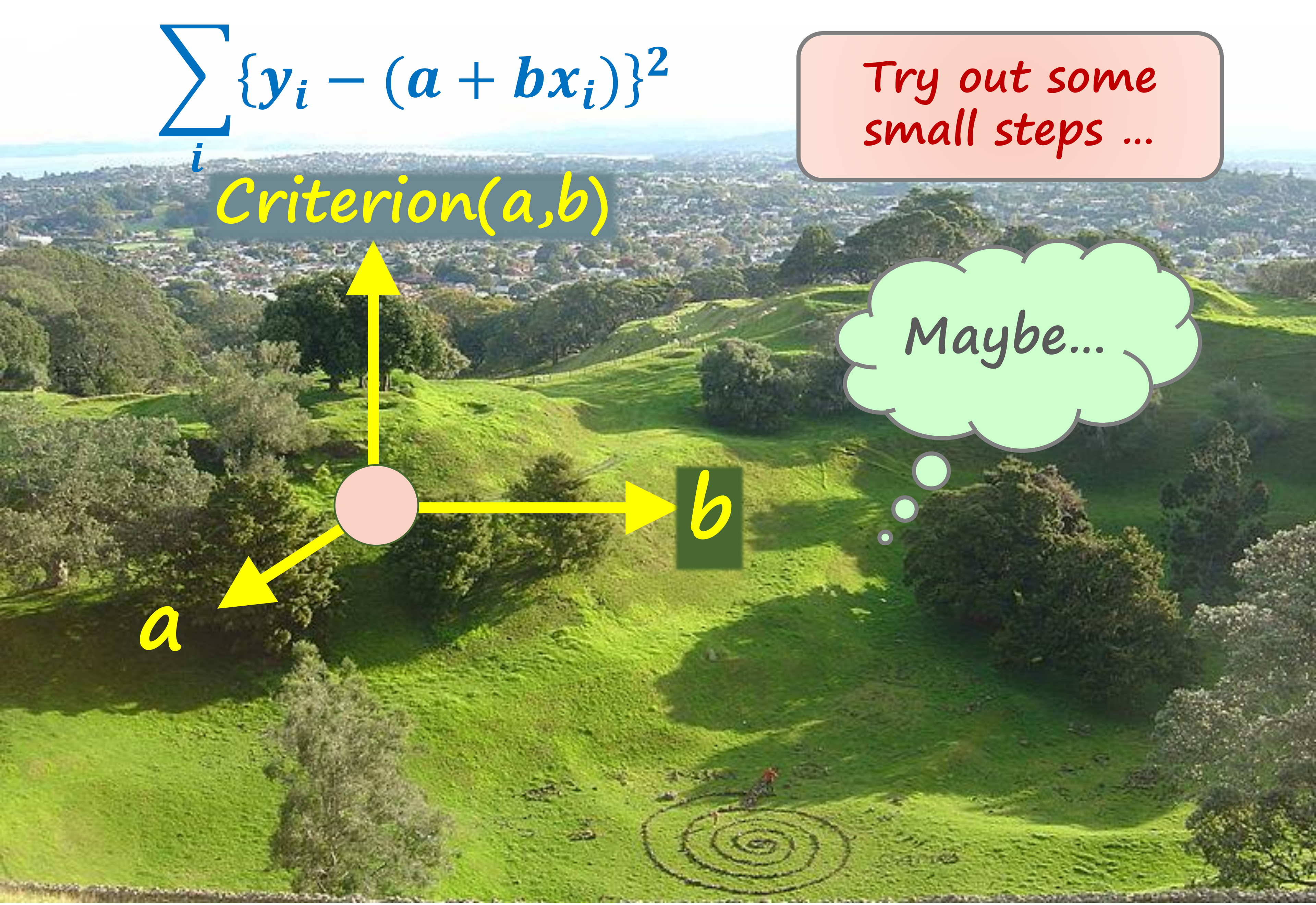
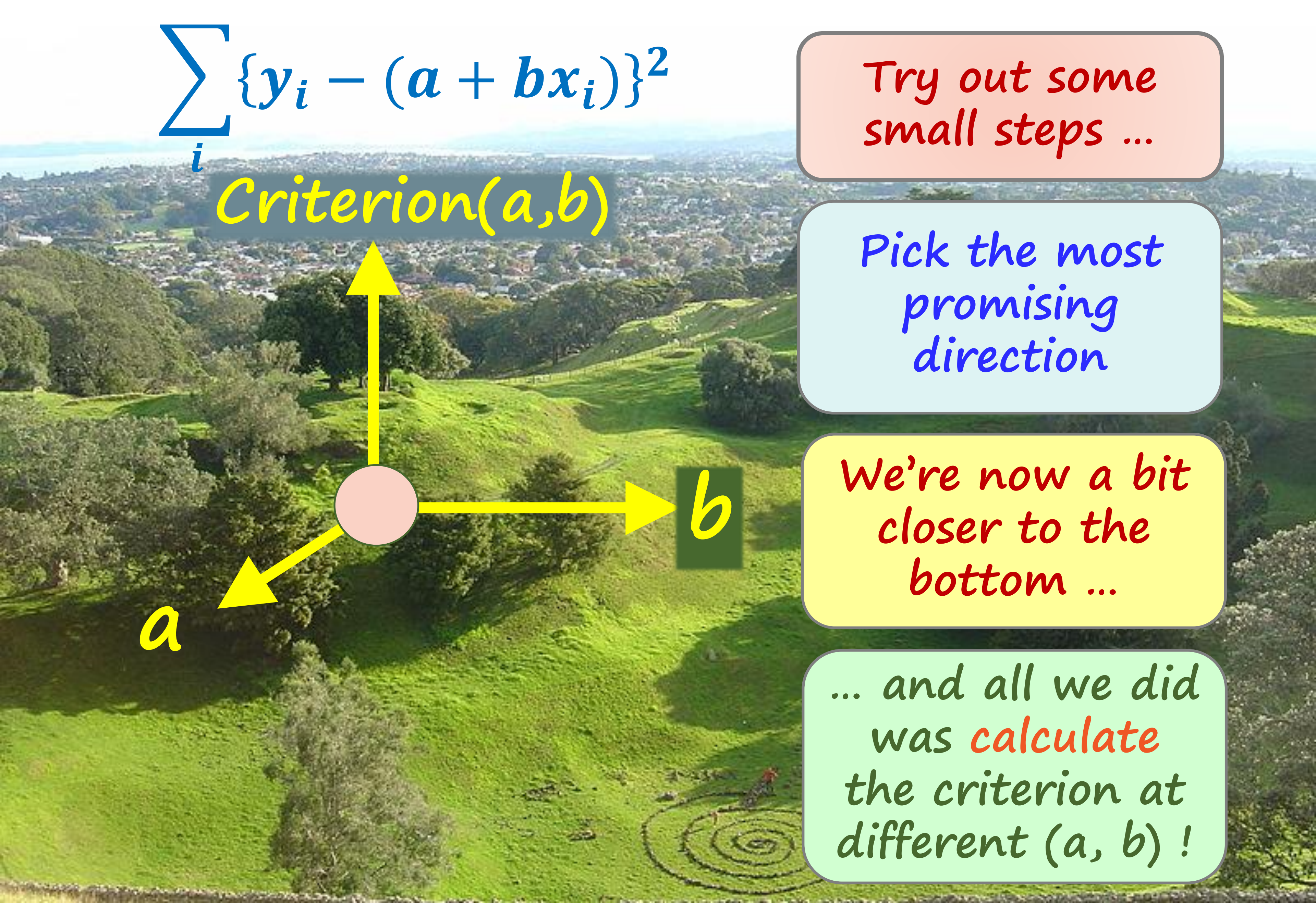


We want to fumble our way downhill to the bottom



We want to fumble our way downhill to the bottom

$$\sum_i \{y_i - (a + bx_i)\}^2$$



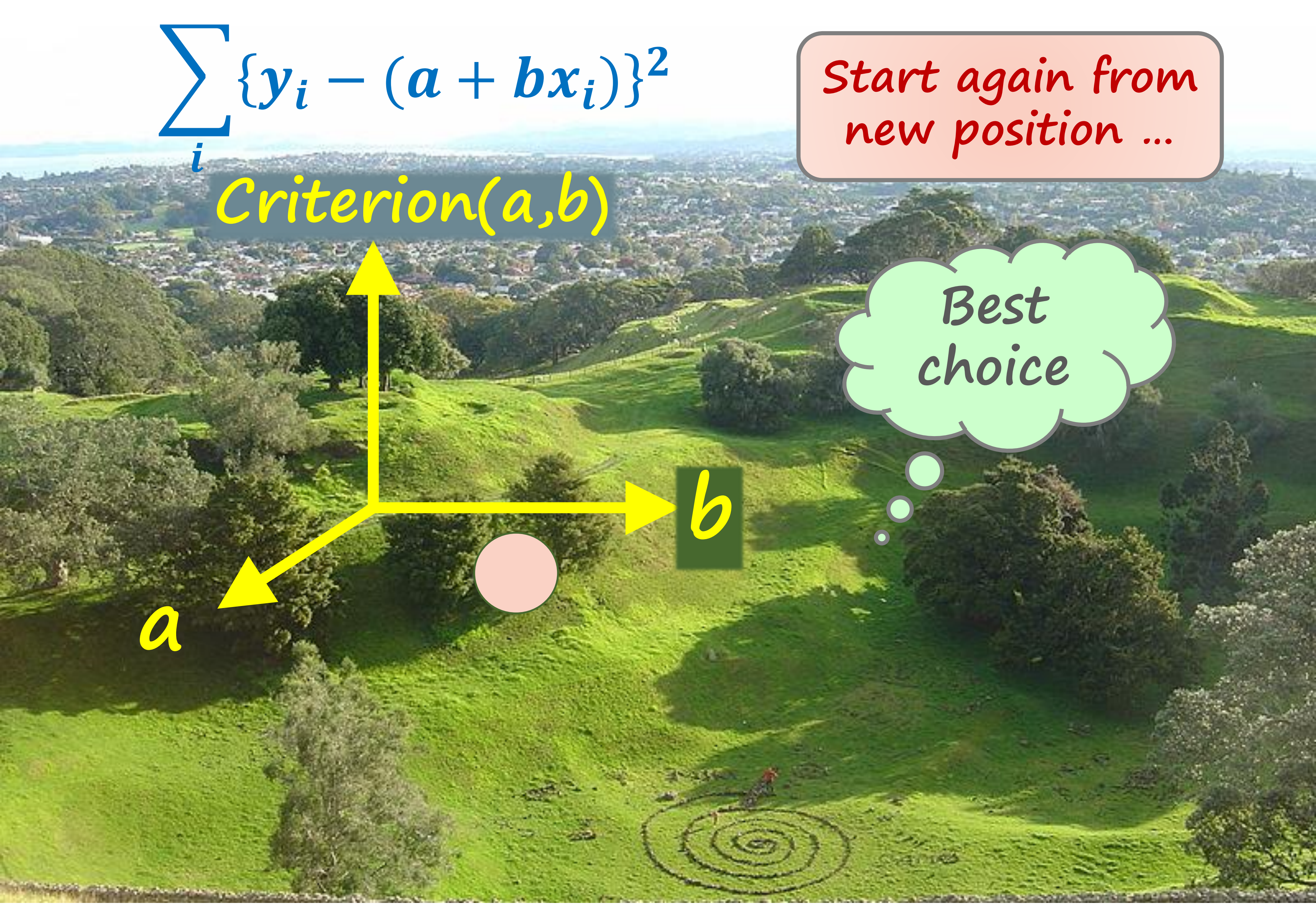
Try out some small steps …

Pick the most promising direction

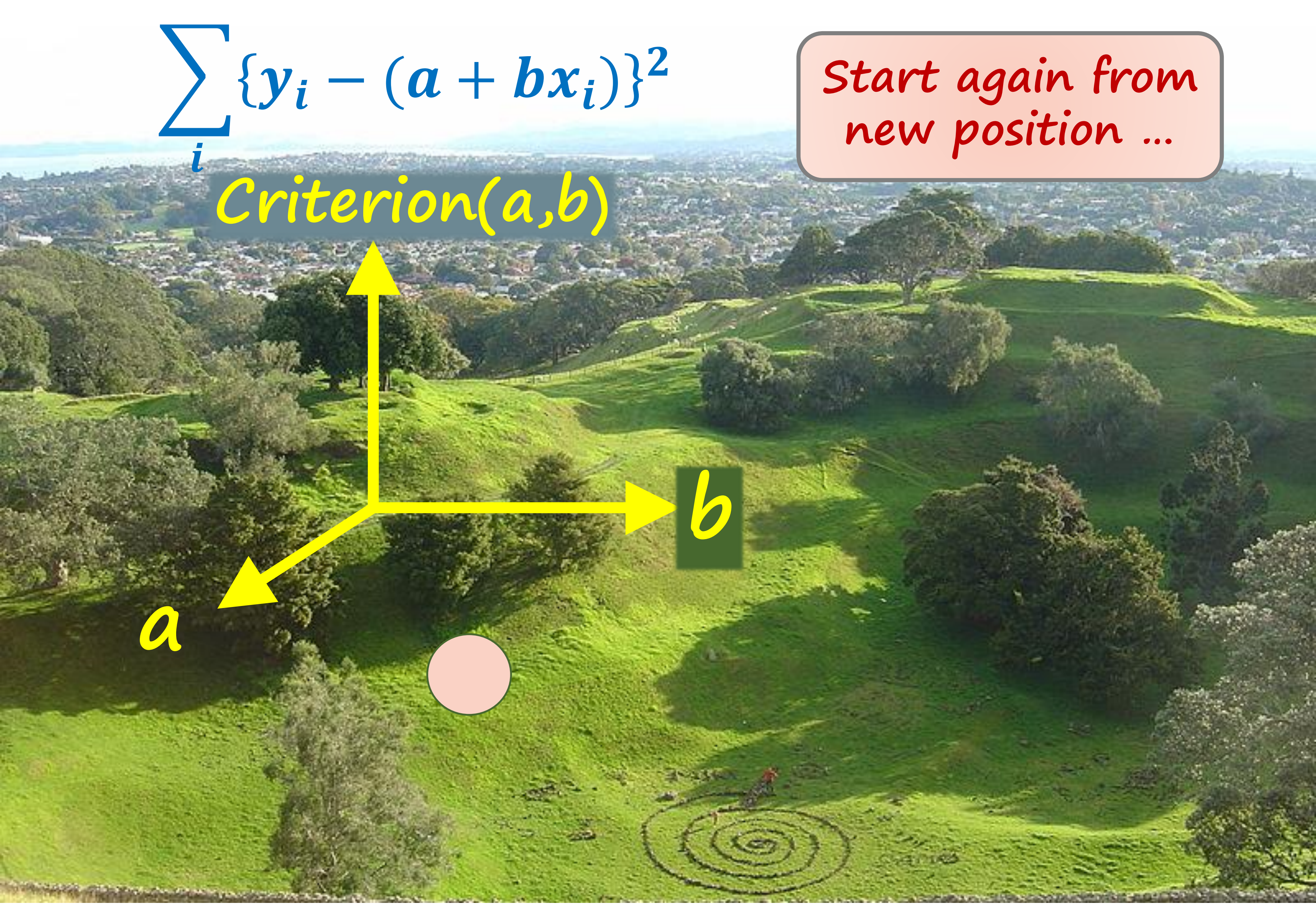
We're now a bit closer to the bottom …

… and all we did was calculate the criterion at different (a, b) !

We want to fumble our way downhill to the bottom

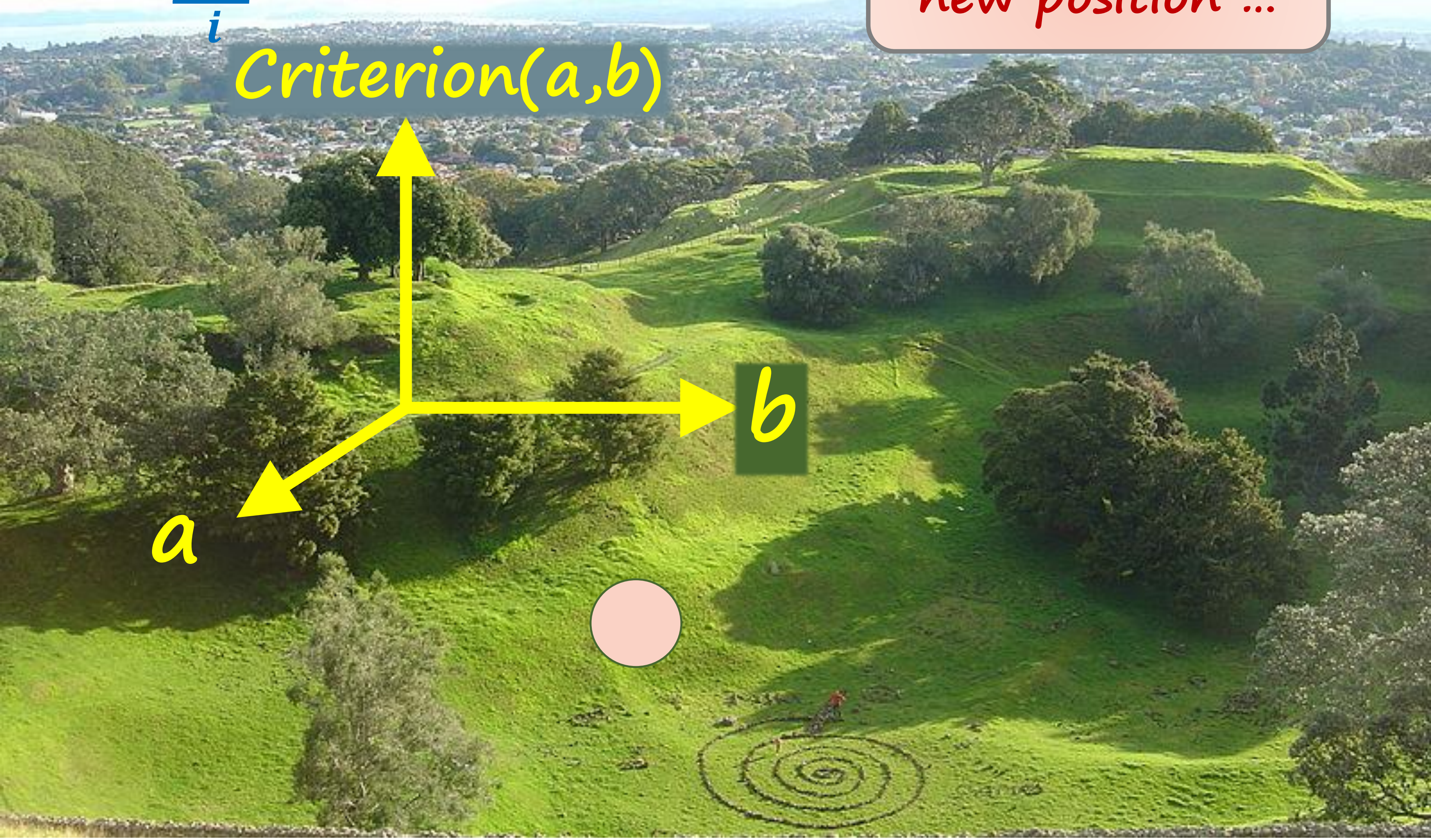


We want to fumble our way downhill to the bottom



We want to fumble our way downhill to the bottom

$$\sum_i \{y_i - (a + bx_i)\}^2$$



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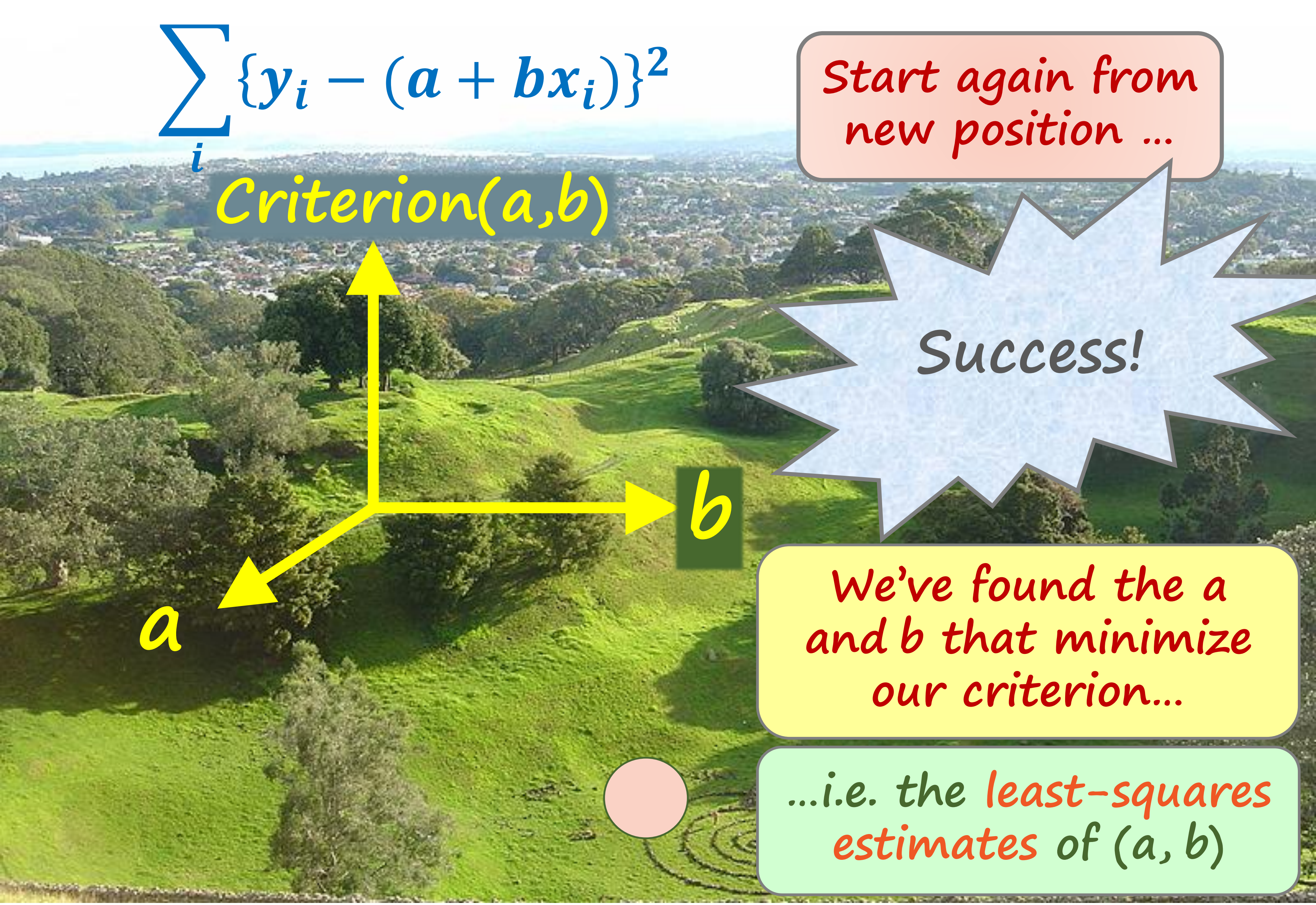


We want to fumble our way downhill to the bottom

How do we do this in R ?

Notice what we've achieved:

- **We can find the parameters (a, b) that optimize our criterion …**

- **… entirely by calculating the criterion at different choices of (a, b)**

  - **In R, if you can calculate it, you can optimize it**

To estimate parameters, we only need to be able to calculate some criterion that measures how good the fit is at each choice of parameters

How do we do this in R ?

- There are a few numerical optimizers in R:
  - nlm, nlminb, optim, …
- We recommend nlm as a good all-purpose optimizer to start with
  - nlm stands for non-linear minimization
- All it needs is:

1. A function to optimize: called the objective function or "criterion"
2. Somewhere to start: initial values of (a, b)

Minimize the criterion $f(a, b) = (a-1)^2 + (b-2)^2 + 3$:

```
findmin.func <- function(startvec=c(0, 0)){
        # Define the objective (criterion) as an inner function:
        objective.func <- function(pars){
                # The parameters have to be supplied as a vector:
                a <- pars[1]
                b <- pars[2]
                # Calculate the objective for this (a, b):
                return((a-1)^2 + (b-2)^2 + 3)
        }
         # Perform the minimization:
        nlm(f=objective.func, p=startvec)
}
```

Minimize the criterion $f(a, b) = (a-1)^2 + (b-2)^2 + 3$:

```
findmin.func <- function(startvec=c(0, 0)){
        objective.func <- function(pars){
                a <- pars[1]
                b <- pars[2]
                return((a-1)^2 + (b-2)^2 + 3)
        }
        nlm(f=objective.func, p=startvec)
}
```

Minimize the criterion $f(a, b) = (a-1)^2 + (b-2)^2 + 3$:

```
> findmin.func()
$minimum
[1] 3

$estimate
[1] 1 2

$gradient
[1] 0.000000e+00 1.110223e-12

$code
[1] 1

$iterations
[1] 2
```

Is this what you would expect?

Best values of a and b: the ones that minimize the objective

Check that the gradient is close to 0 at the minimum

What could possibly go wrong …?

```
findmin2.func <- function(startvec=c(0, 0)){
        objective.func <- function(pars){
                a <- pars[1]
                b <- pars[2]
                return(log(a-1)^2 + log(b-2)^2)
        }
        nlm(f=objective.func, p=startvec)
}
```

1. Bad start values!

```
> findmin2.func()
$minimum
[1] 1.797693e+308

$estimate
[1] 0 0

$gradient
[1] 0 0

$code
[1] 1

$iterations
[1] 0

There were 11 warnings (use warnings() to see them)
> warnings()
Warning messages:
1: In log(a - 1) : NaNs produced
2: In log(b - 2) : NaNs produced
3: In log(a - 1) : NaNs produced
4: In log(b - 2) : NaNs produced
5: In nlm(f = objective.func, p = startvec) :
  NA/Inf replaced by maximum positive value
```

1. Bad start values:

Solution is to choose better /alternative start values

```
> findmin2.func(startvec=c(5,5))
$minimum
[1] 3.430193e-12

$estimate
[1] 1.999999 2.999998

$gradient
[1]  2.436579e-08 -1.333134e-07

$code
[1] 1

$iterations
[1] 12
```

All looks good now

What could possibly go wrong …?

```
bad.func <- function(startvec=c(1, 1)){
        objective.func <- function(pars){
                a <- pars[1]
                b <- pars[2]
                return( (a-1)^2+ (b-2)^2 + 1/(a-b)^2 )
        }
        nlm(f=objective.func, p=startvec)
}
```

2. Some (a,b) combinations don't work: evaluate to NA or Inf

```r
fixed.func <- function(startvec=c(1, 1)){
	objective.func <- function(pars){
		a <- pars[1]
		b <- pars[2]
		obj <- (a-1)^2+ (b-2)^2 + 1/(a-b)^2
		# Print output so we can see what’s happening:
		print(c(a, b, obj))
		# Fix up the case where obj is NA or Inf by
		# redefining it as a very large positive number:
		if(is.na(obj) | is.infinite(obj))
			obj <- (abs(a)+abs(b))*1e10
		return(obj)
	}
	nlm(f=objective.func, p=startvec)
}
```

Your first task …

- Given a code template your first task is to complete the code and reproduce the output from the “lm” function
  - lm stands for linear model
  - lm is fitted in R by a least-squares criterion

- Coming next: how to use the bootstrap to compute a standard error for your least-squares estimates of (a, b) …

Standard error by bootstrap

We've said that the standard error is a type of quality assurance …

… but what does it really mean?

The standard error aims to measure the variability you'd see in estimates of (a, b) …

… if you conducted your whole estimation procedure again and again:

– starting with collecting your data

The standard error measures the variability you would see in your estimates of (a, b) …

… if you ran your whole estimation procedure over and over:

– starting with collecting your data

So in an ideal world we would have:

- Lots and lots of data sets;
- Each one has the same characteristics as our real data (same sample size and study design);
- We'd estimate (a, b) from each one…
- and just measure the variance in our estimates!

- Lots of data sets
- Each one has the same design as our real data
- Estimate (a, b) from each data set…
- Measure the variance in our estimates

This is exactly what the bootstrap aims to do

We only have ONE real data set …

… but if we resample from it, we could artificially create new data-sets that mimic our real data:

- Same sample size
- Same target population

Standard error by bootstrap

Original data

	X	Y
1	315.0	6.0
2	316.9	2.0
3	317.6	7.8
4	318.4	8.9
5	319.0	10.6
6	319.6	-14.9

Standard error by bootstrap

Original data

	X	Y
1	315.0	6.0
2	316.9	2.0
3	317.6	7.8
4	318.4	8.9
5	319.0	10.6
6	319.6	-14.9

	X	Y
6	319.6	-14.9
2	316.9	2.0
2	[illegible]	[illegible]
1	[illegible]	[illegible]
3	[illegible]	7.8
6	319.6	-14.9

Bootstrap replicate 1

	X	Y
5	319.0	10.6
5	319.0	10.6
1	[illegible]	[illegible]
4	[illegible]	[illegible]
5	[illegible]	10.6
2	316.9	2.0

Bootstrap replicate 2

	X	Y
3	317.6	7.8
1	315.0	6.0
2	[illegible]	[illegible]
1	[illegible]	[illegible]
3	[illegible]	7.8
2	316.9	2.0

Bootstrap replicate 3

B1

	X	Y
5	319.0	10.6
1	315.0	6.0
4	318.4	[illegible]
4	318.4	[illegible]
3	317.6	7.8
2	316.9	2.0

B2

	X	Y
3	317.6	7.8
5	319.0	10.6
1	315.0	[illegible]
4	318.4	[illegible]
5	319.0	10.6
1	315.0	6.0

B3

	X	Y
3	317.6	7.8
4	318.4	8.9
4	318.4	[illegible]
1	315.0	[illegible]
3	317.6	7.8
6	319.6	-14.9

B4

	X	Y
5	319.0	10.6
2	316.9	2.0
2	316.9	[illegible]
6	319.6	[illegible]
3	317.6	7.8
6	319.6	-14.9

And on and on and on!

Each bootstrap data-set mimics our real data:

- **Same sample size**
- **Same target population**

	X	Y
5	319.0	10.6
1	315.0	6.0
4	318.4	9
4	318.4	.9
3	317.6	7.8
2	316.9	2.0

$a_1\ b_1$

	X	Y
3	317.6	7.8
5	319.0	10.6
1	315.0	.0
4	318.4	.9
5	319.0	10.6
1	315.0	6.0

$a_2\ b_2$

	X	Y
3	317.6	7.8
4	318.4	8.9
4	318.4	9
1	315.0	0
3	317.6	7.8
6	319.6	-14.9

$a_3\ b_3$

	X	Y
5	319.0	10.6
2	316.9	2.0
2	316.9	0
6	319.6	.9
3	317.6	7.8
6	319.6	-14.9

$a_4\ b_4$

	X	Y
2	316.9	2.0
4	318.4	8.9
5	319.0	6
1	315.0	.0
3	317.6	7.8
1	315.0	6.0

$a_5\ b_5$

	X	Y
6	319.6	-14.9
5	319.0	10.6
6	319.6	9
4	318.4	.9
6	319.6	-14.9
2	316.9	2.0

$a_6\ b_6$

	X	Y
6	319.6	-14.9
2	316.9	2.0
2	316	2.0
1	315.	6.0
3	317.6	7.8
6	319.6	-14.9

$a_7\ b_7$

	X	Y
5	319.0	10.6
5	319.0	10.6
1	315.	.0
4	318.4	8.9
5	319.0	10.6
2	316.9	2.0

$a_8\ b_8$

Each one gives us an estimate of (a, b) ...

Our bootstrap estimates of the standard errors of a and b are:

$$\text{se}(a) = \text{sd}(a_1, a_2, \ldots\ldots, a_B)$$

$$\text{se}(b) = \text{sd}(b_1, b_2, \ldots\ldots, b_B)$$

2	316.9	2.0
6	319.6	-14.9
3	317.6	7.8
6	319.6	-14.9

5	319.0	10.6
1	315.0	6.0
3	317.6	7.8
1	315.0	6.0

		.6
6	319.6	-14.9
4	318.4	8.9
6	319.6	-14.9
2	316.9	2.0

	X	Y
6	319.6	-14.9
2	316.9	2.0
2	316	2.0
1	315.	6.0
3	317.6	7.8
6	319.6	-14.9

$a_7 \; b_7$

	X	Y
5	319.0	10.6
5	319.0	10.6
1	315.	.0
4	318.4	8.9
5	319.0	10.6
2	316.9	2.0

$a_8 \; b_8$

Each one gives us an estimate of (a, b) …

Equivalently:

se(a) = sqrt(var($boot\$a$))

se(b) = sqrt(var($boot\$b$))

2	316.9	2.0
6	319.6	-14.9
3	317.6	7.8
6	319.6	-14.9

	X	Y
6	319.6	-14.9
2	316.9	2.0
2	316	2.0
1	315.	6.0
3	317.6	7.8
6	319.6	-14.9

a_7 b_7

5	319.0	10.6
1	315.0	6.0
3	317.6	7.8
1	315.0	6.0

	X	Y
5	319.0	10.6
5	319.0	10.6
1	315.	.0
4	318.4	8.9
5	319.0	10.6
2	316.9	2.0

a_8 b_8

		.6
6	319.6	-14.9
4	318.4	8.9
6	319.6	-14.9
2	316.9	2.0

Each one gives us an estimate of (a, b) ...

For 95% confidence intervals:

quantile($boot\$a$, $probs$=c(0.025,0.975))

quantile($boot\$b$, $probs$=c(0.025, 0.975))

2	316.9	2.0
6	319.6	-14.9
3	317.6	7.8
6	319.6	-14.9

5	319.0	10.6
1	315.0	6.0
3	317.6	7.8
1	315.0	6.0

6	319.6	-14.9
4	318.4	8.9
6	319.6	-14.9
2	316.9	2.0

	X	Y
6	319.6	-14.9
2	316.9	2.0
2	316	2.0
1	315.	6.0
3	317.6	7.8
6	319.6	-14.9

a_7 b_7

	X	Y
5	319.0	10.6
5	319.0	10.6
1	315.	.0
4	318.4	8.9
5	319.0	10.6
2	316.9	2.0

a_8 b_8

Each one gives us an estimate of (a, b) ...

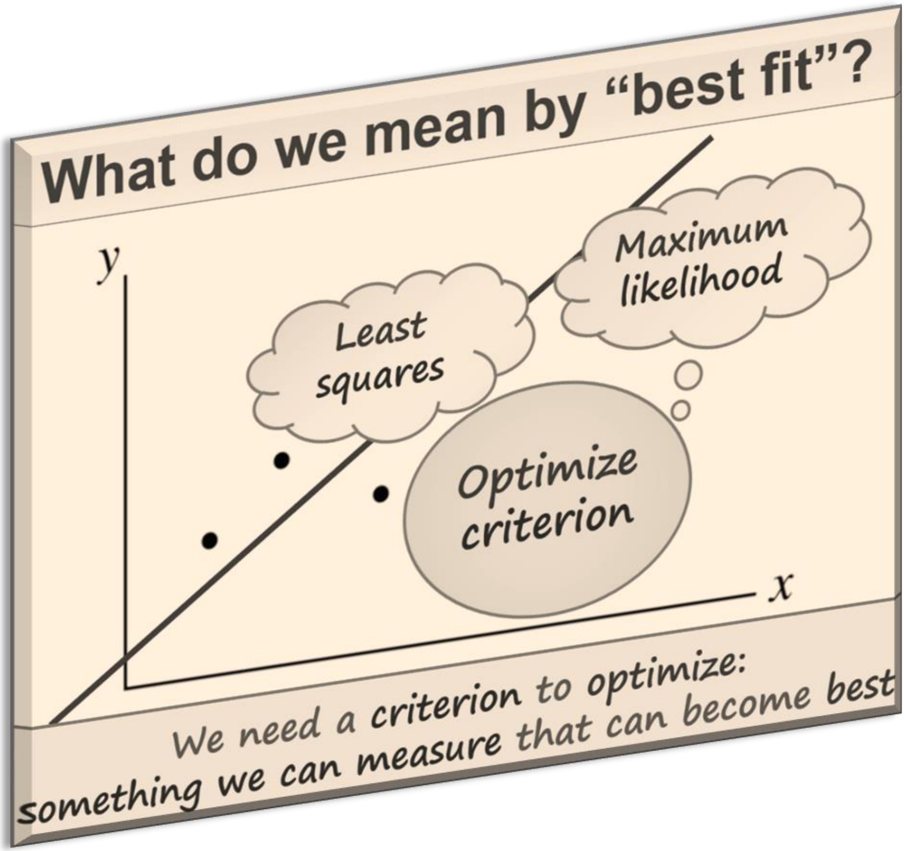
```
bootstrap.func <- function(dat, B=1000, startvec=c(0, 0)){
  # Create empty boot.res for storing your results:
  boot.res <- data.frame(rep=1:B, a=rep(NA, B), b=rep(NA, B))
  # Loop for bootstrap replicates:
  for(i in 1:B){
        # Sample the rows at random with replacement:
        resampleRows <- sample(1:nrow, size=nrow, replace=T)
        # Create the data for the resample:
        dat.boot <- dat[resampleRows, ]
        # Fit the model to this replicate:
        fit.boot <- leastSquares.func(dat.boot, startvec)
        # Enter the estimated values into row i of boot.res:
        boot.res$a[i] <- fit.boot$estimate[1]
        boot.res$b[i] <- fit.boot$estimate[2]
   } # End of loop
  # Find the confidence intervals:
  CI.a <- quantile(boot.res$a, probs=c(0.025, 0.975))
  CI.b <- quantile(boot.res$b, probs=c(0.025, 0.975))
}
```

```r
bootstrap.func <- function(dat, B=1000, startvec=c(0, 0)){
  n <- nrow(dat)
  boot.res <- data.frame(rep=1:B, a=rep(NA, B), b=rep(NA, B))
  for(i in 1:B){
        resampleRows <- sample(1:n, size=n, replace=T)
        dat.boot <- dat[resampleRows, ]
        fit.boot <- leastSquares.func(dat.boot, startvec)
        boot.res$a[i] <- fit.boot$estimate[1]
        boot.res$b[i] <- fit.boot$estimate[2]
   }
  # Find the confidence intervals:
  CI.a <- quantile(boot.res$a, probs=c(0.025, 0.975))
  CI.b <- quantile(boot.res$b, probs=c(0.025, 0.975))
  return(list(a=CI.a, b=CI.b))
}
```

DIY Modelling – we're nearly there!

- We can fit the model: i.e. estimate a and b

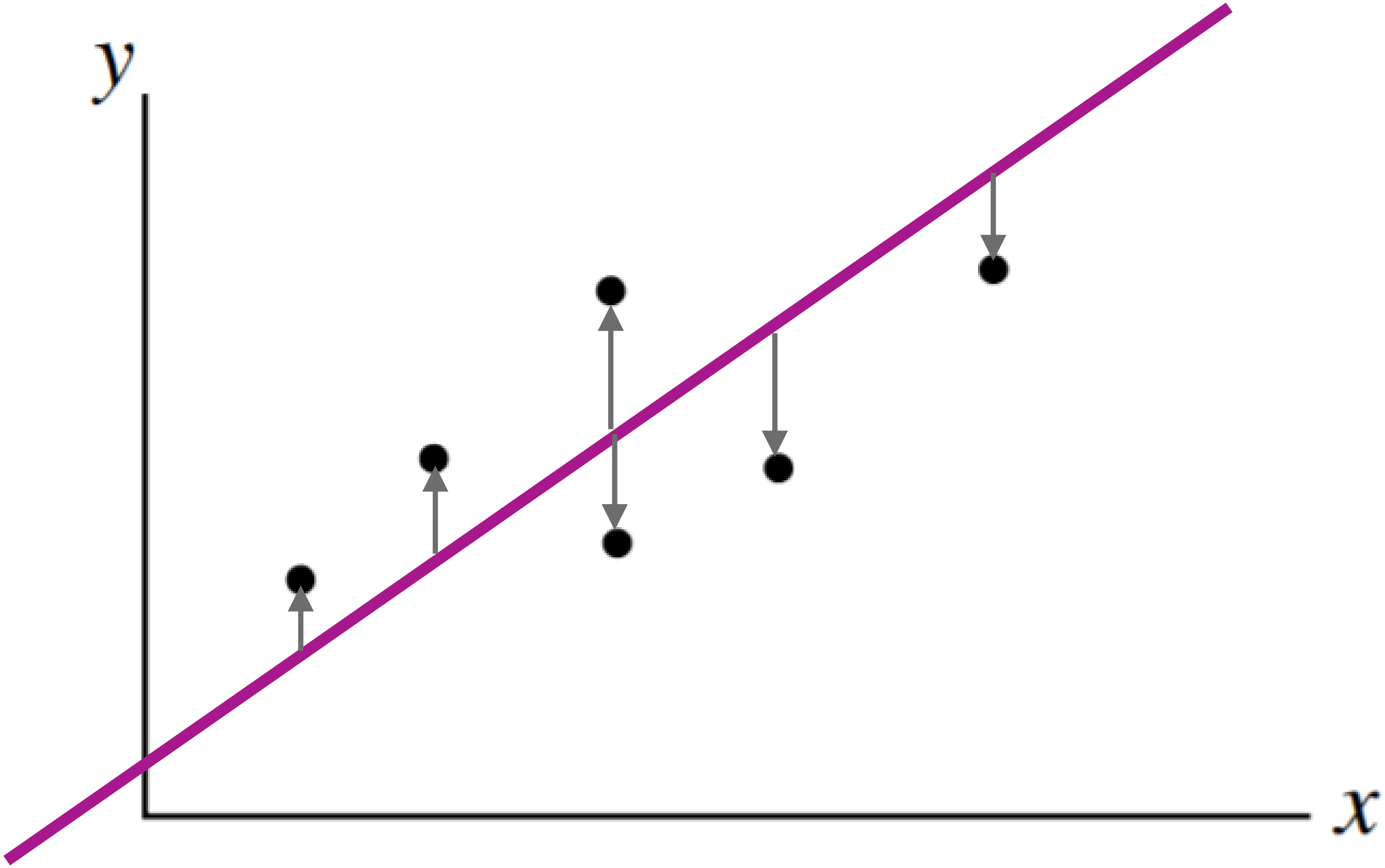
- We can compute their standard errors



One more thing:

Can we improve on the Least Squares criterion?

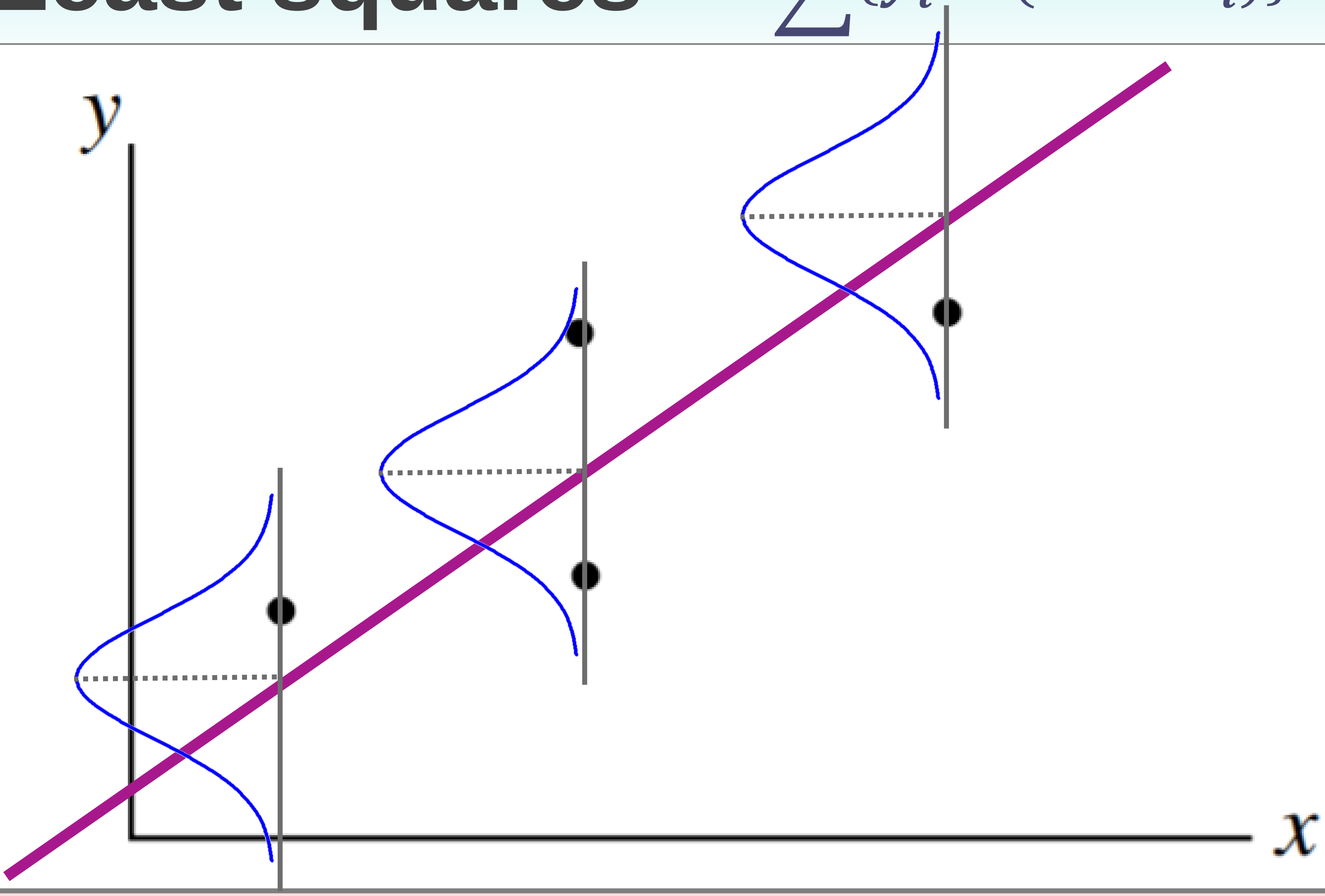
Least squares $\sum\{y_i - (a + bx_i)\}^2$



Least squares assumes the data are scattered symmetrically and evenly about the line

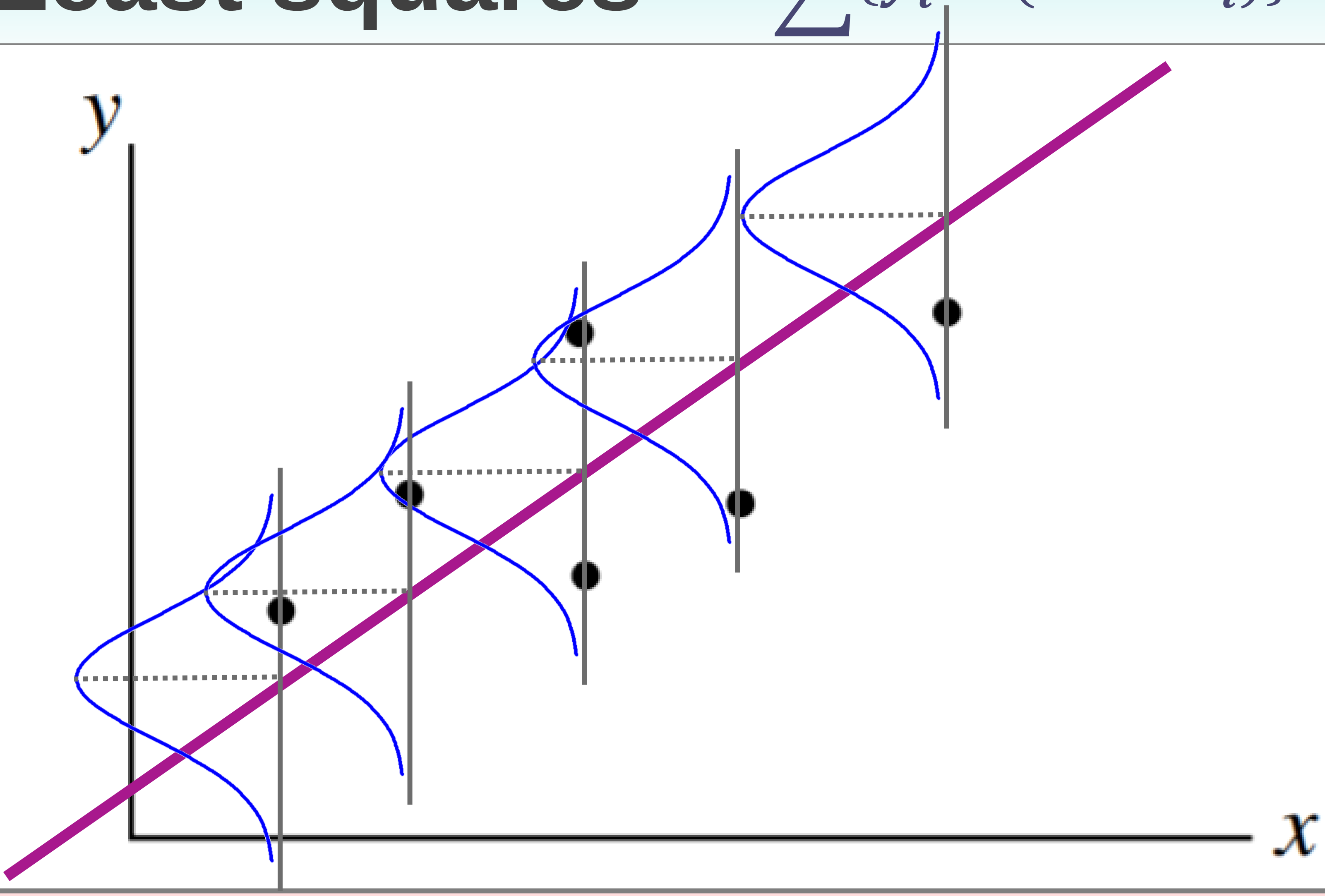
Least squares

$$\sum \{y_i - (a + bx_i)\}^2$$



Least squares assumes the data are scattered symmetrically and evenly about the line

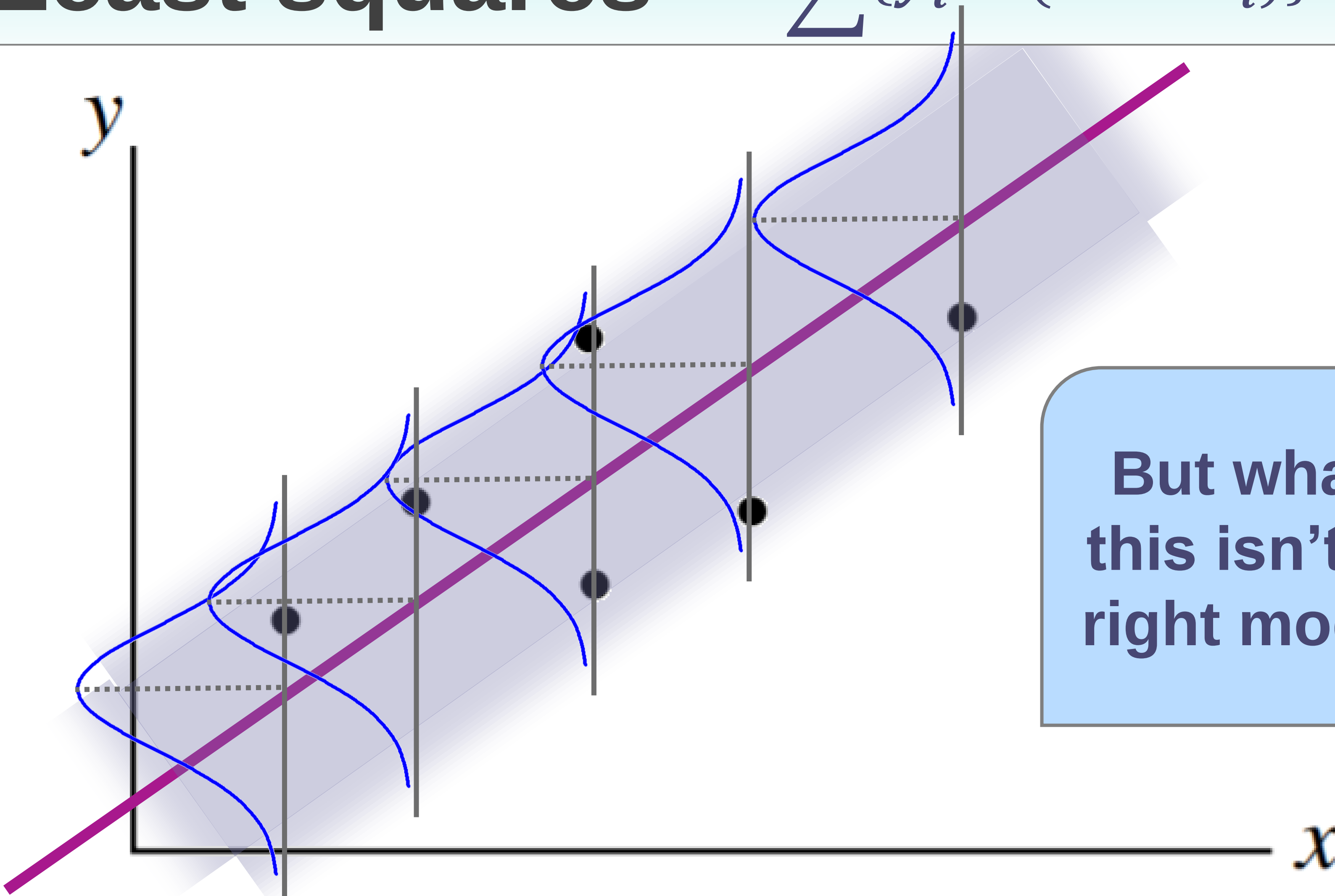
Least squares $\sum \{y_i - (a + bx_i)\}^2$



Least squares assumes the data are scattered symmetrically and evenly about the line

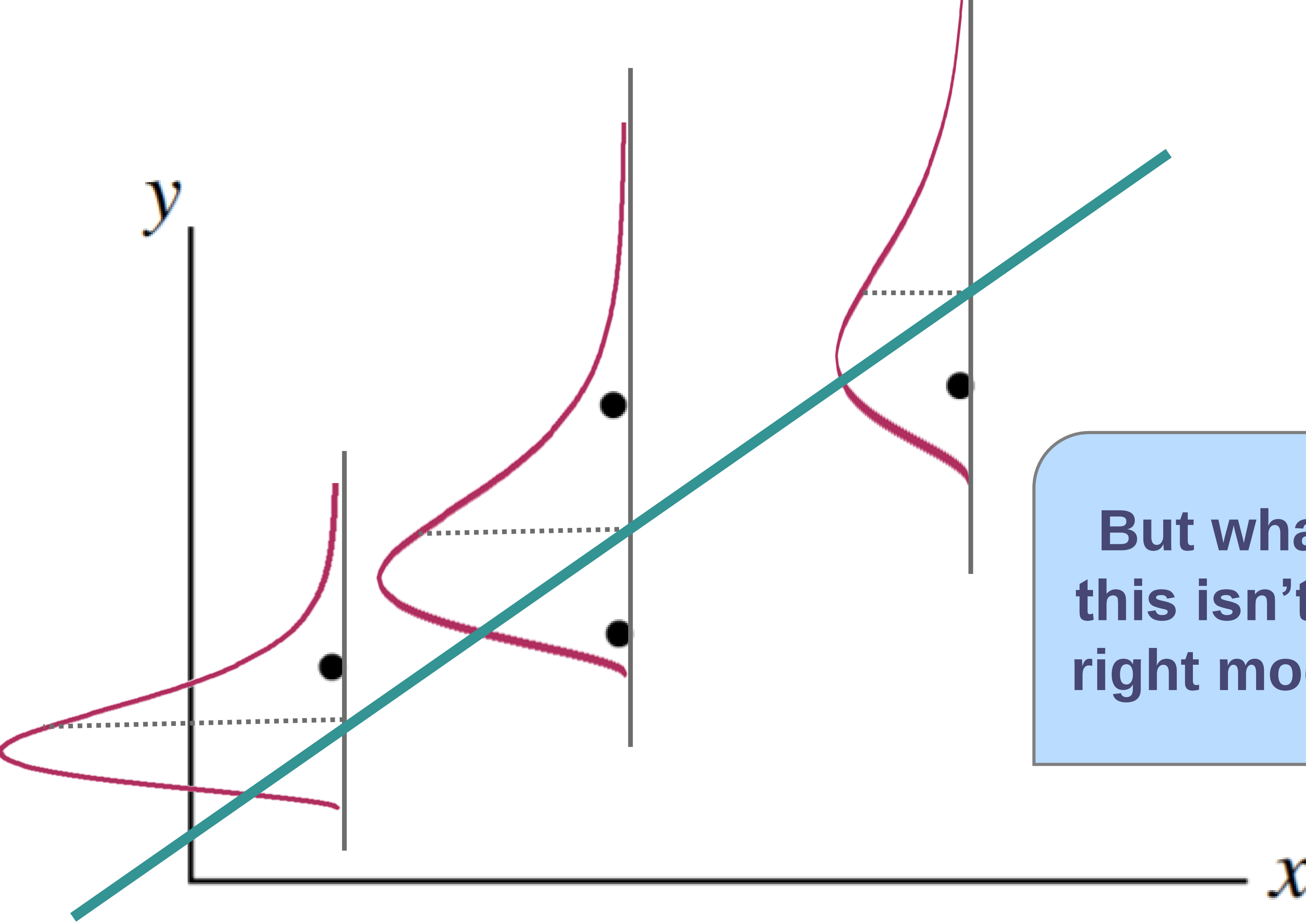
Least squares

$$\sum\{y_i-(a+bx_i)\}^2$$



But what if this isn't the right model?

Least squares assumes the data are scattered symmetrically and evenly about the line

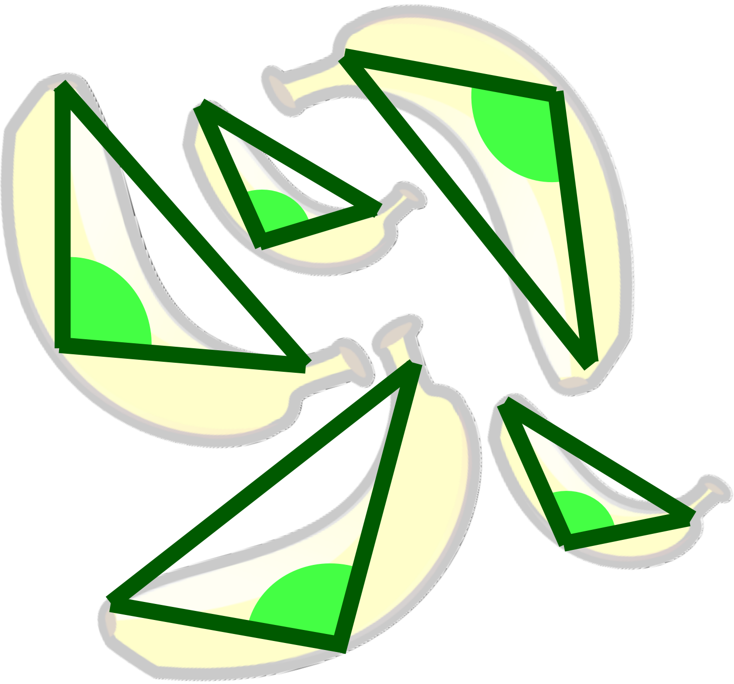


But what if this isn’t the right model?

Often a better model would allow right skew and/or scatter that increases along the line

Or maybe there isn’t even a line...

How bent is a banana?

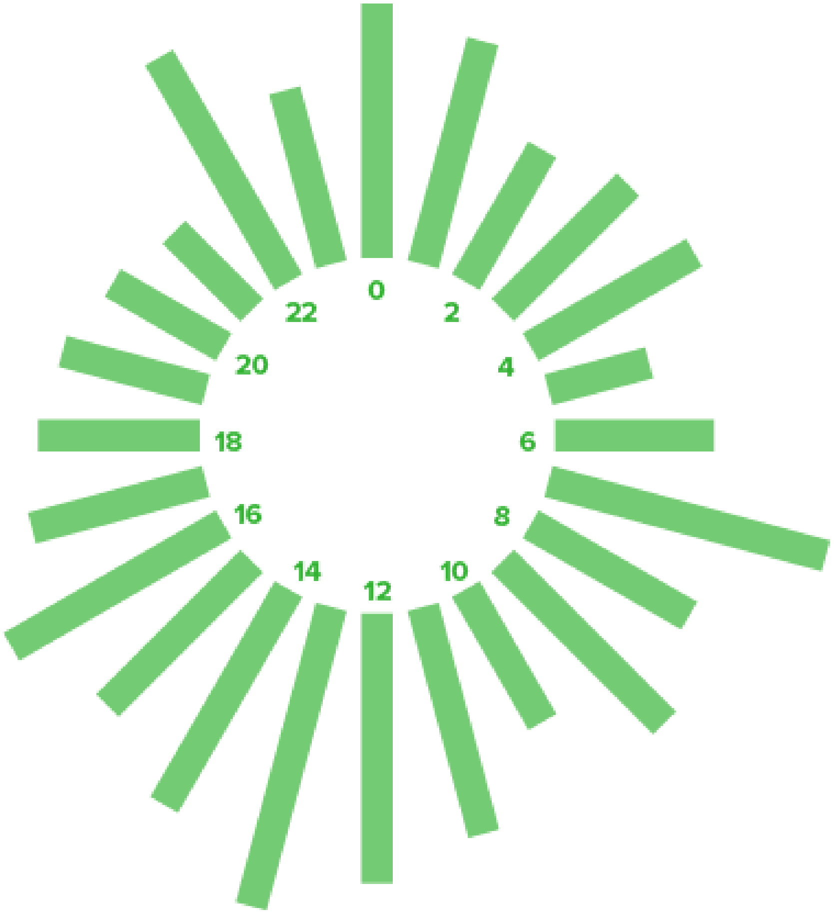


How many kiwi are there in the Coromandel?

We often want to fit models that don’t involve scatter about a line at all

Or maybe there isn't even a line...

What time of day do I receive emails?



We often want to fit models that don't involve scatter about a line at all

Maximum likelihood estimation

All these models have one thing in common:

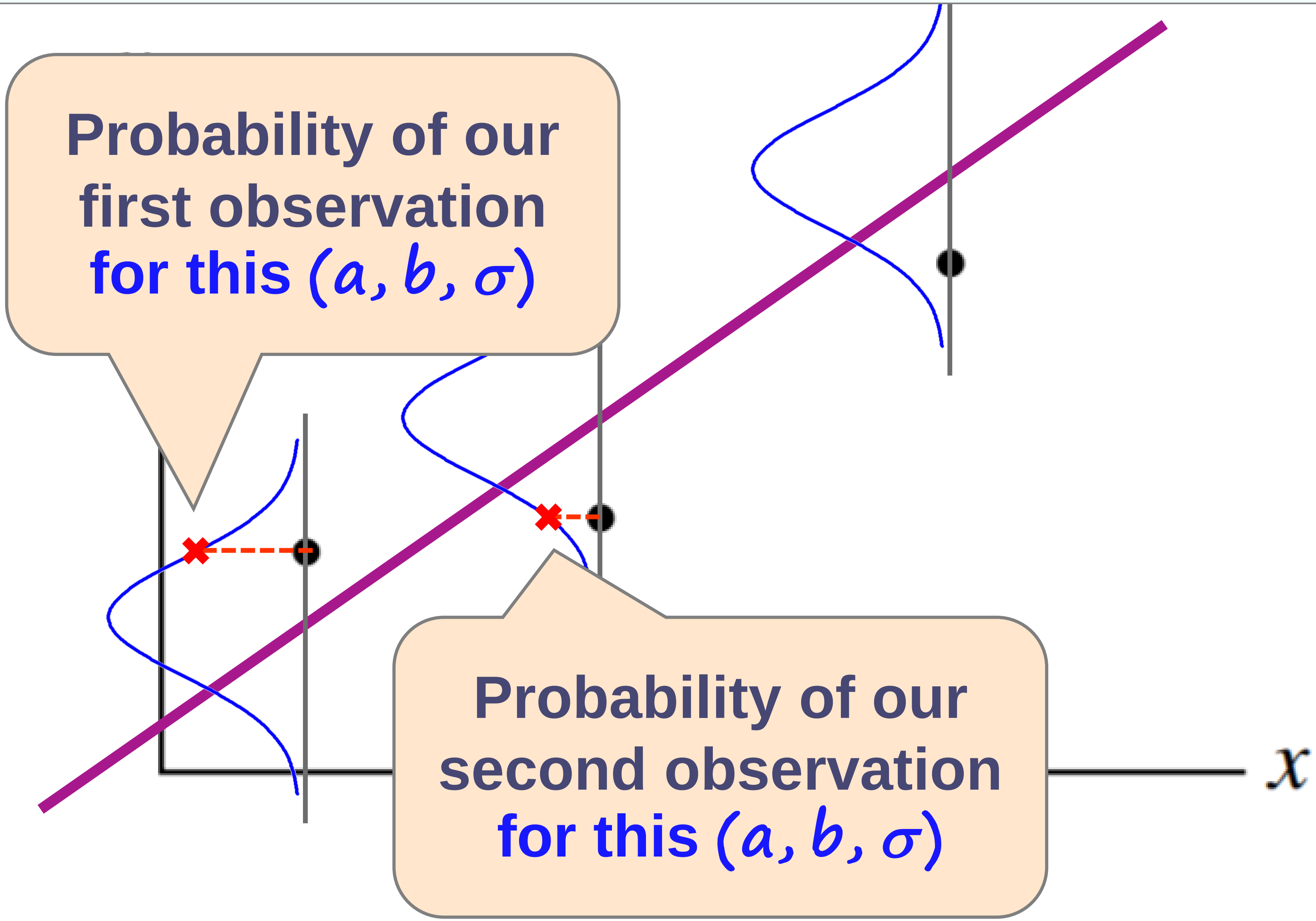
… a statistical distribution or stochastic process that we imagine our data are generated from

… under which we can calculate the probability of our data…

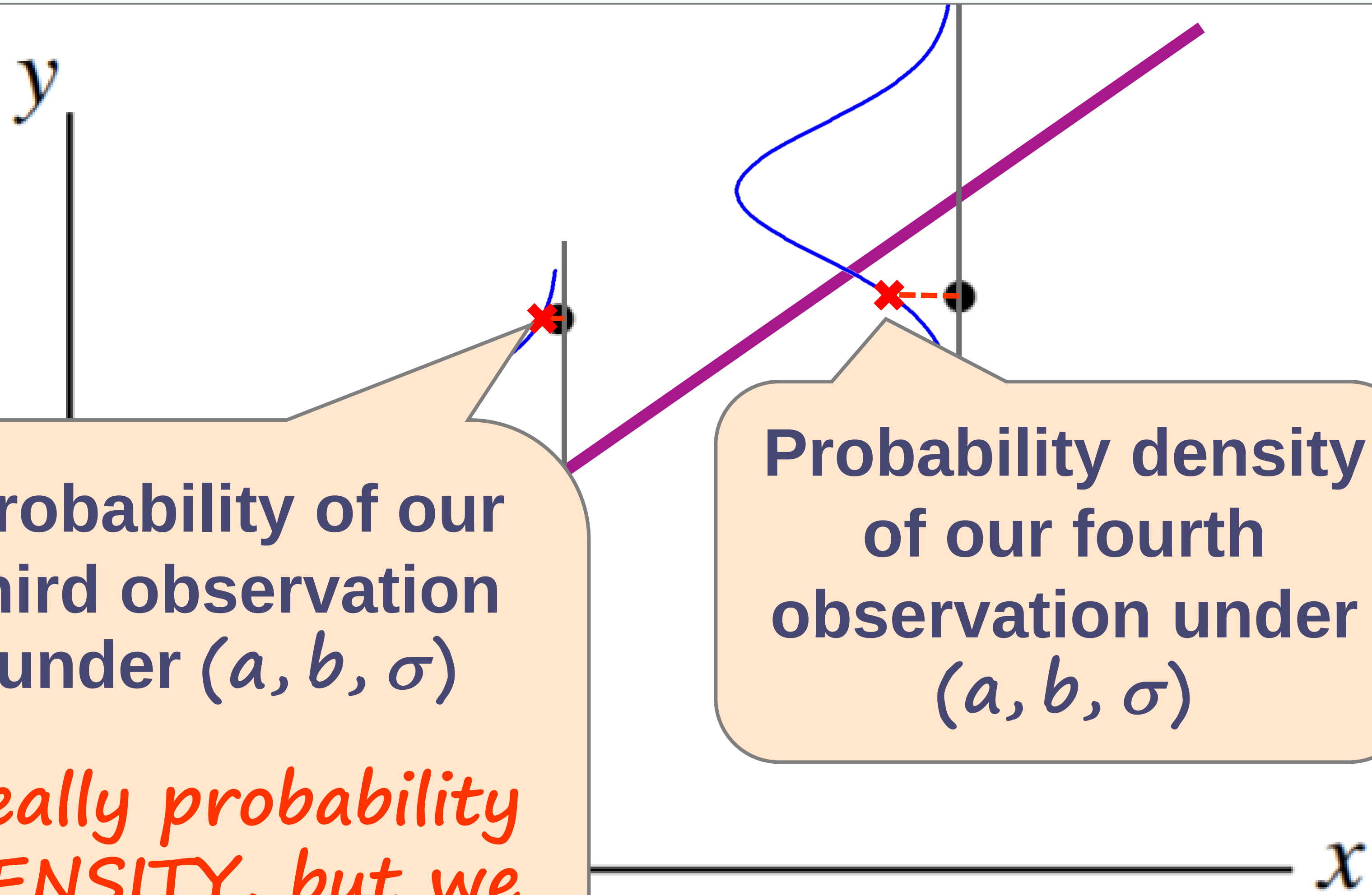
Why not use this probability as our fit criterion?

- **Good parameter values are those which give our data high probability**
- **a and b are good estimates if they make our data highly likely**

Maximum likelihood estimation



Maximum likelihood estimation

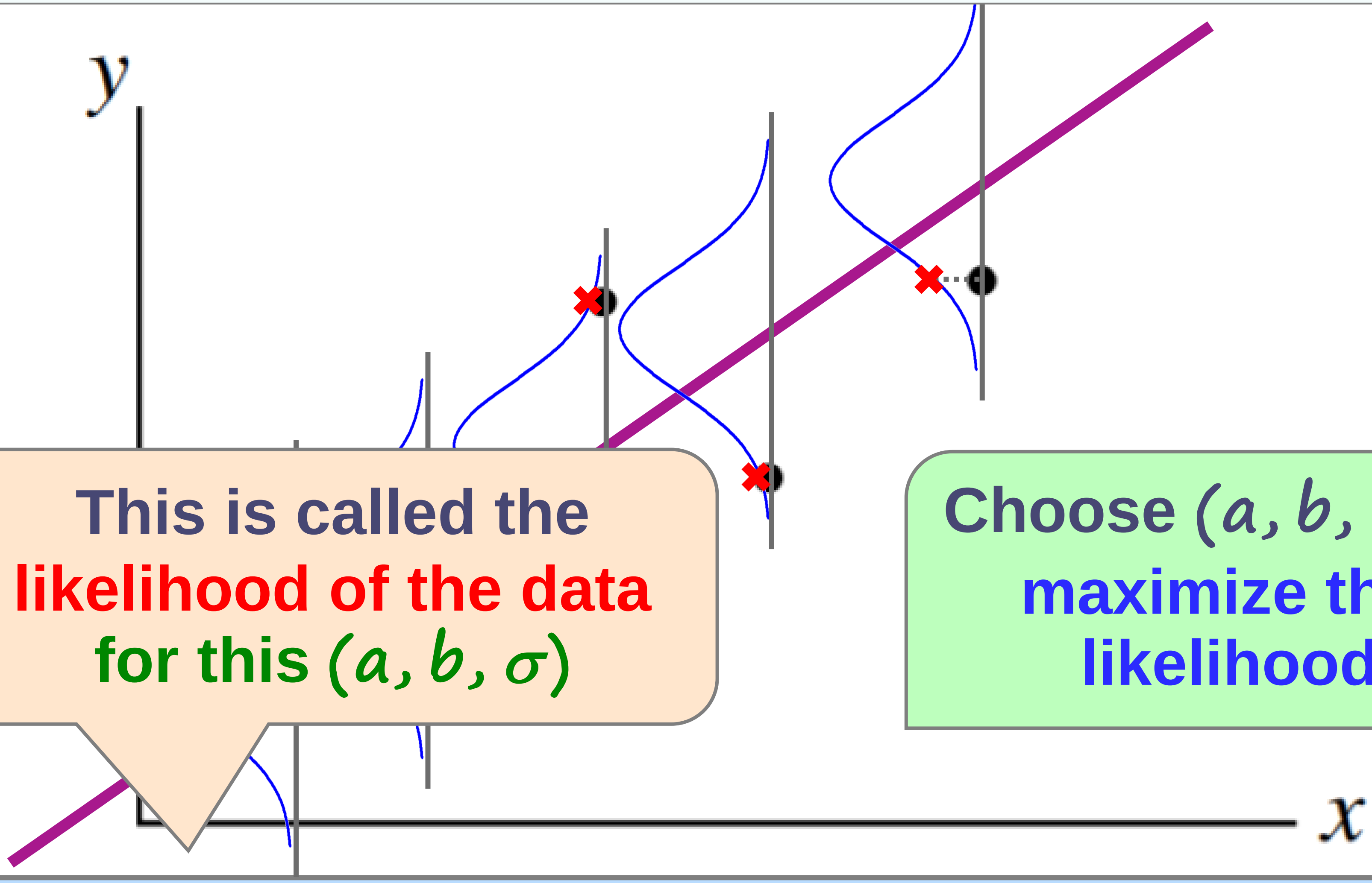


Probability of our third observation under (a, b, σ)

Really probability DENSITY, but we can think of it like a probability

Probability density of our fourth observation under (a, b, σ)

Maximum likelihood estimation



This is called the **likelihood of the data** for this (a, b, σ)

Choose (a, b, σ) to **maximize this likelihood**

Multiply together to get the overall probability density of the observations for this (a, b, σ)

Maximum likelihood estimation

In practice we don't multiply the probabilities:

- **Multiplying tens or hundreds of small numbers will create computational problems**

- **Instead, take logs and add:**

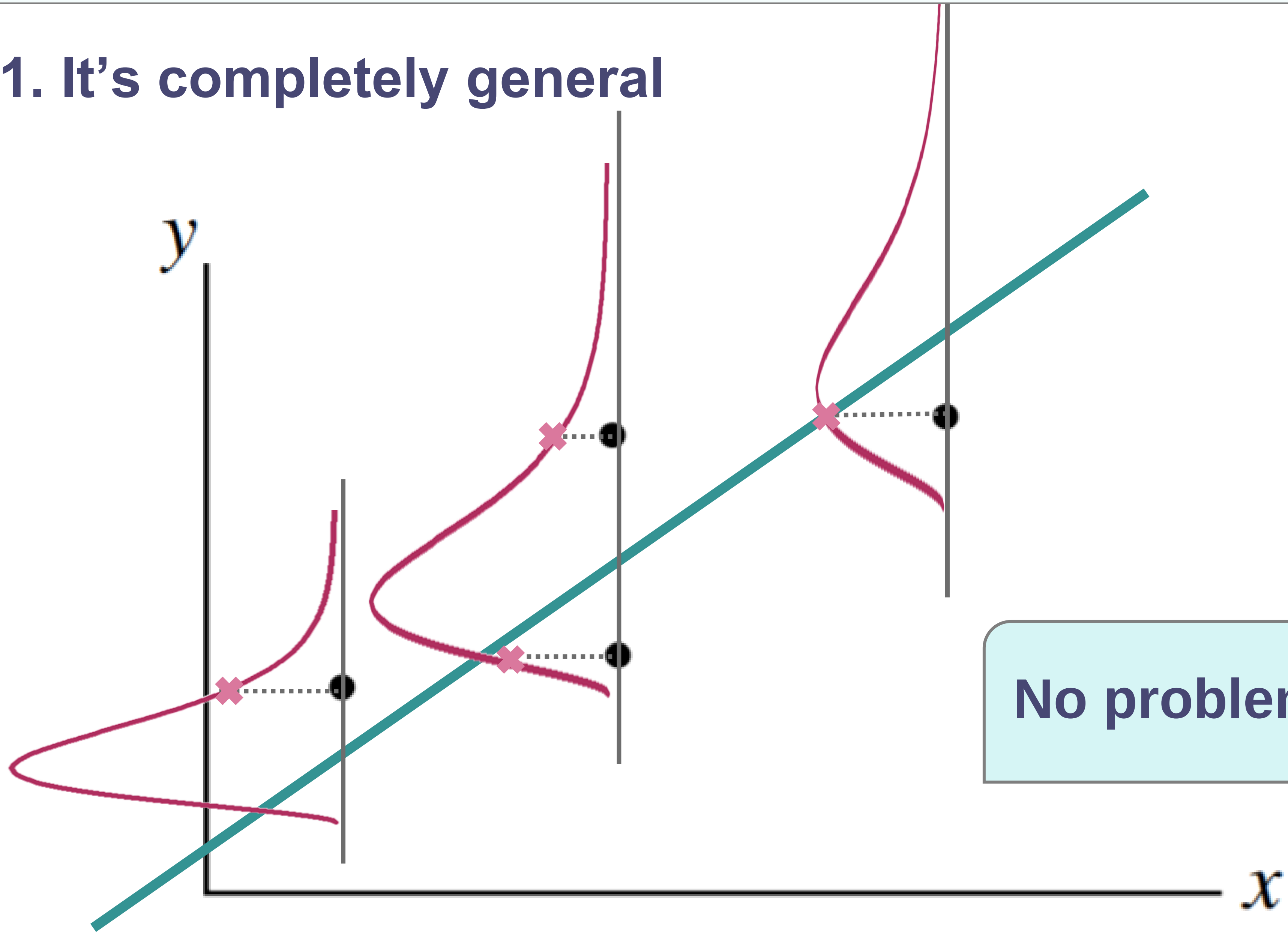
$$\log\left\{\prod_i P(y_i)\right\} = \sum_i \log\{P(y_i)\}$$

- **The log-likelihood is maximized at the same (a, b, σ) as the likelihood**

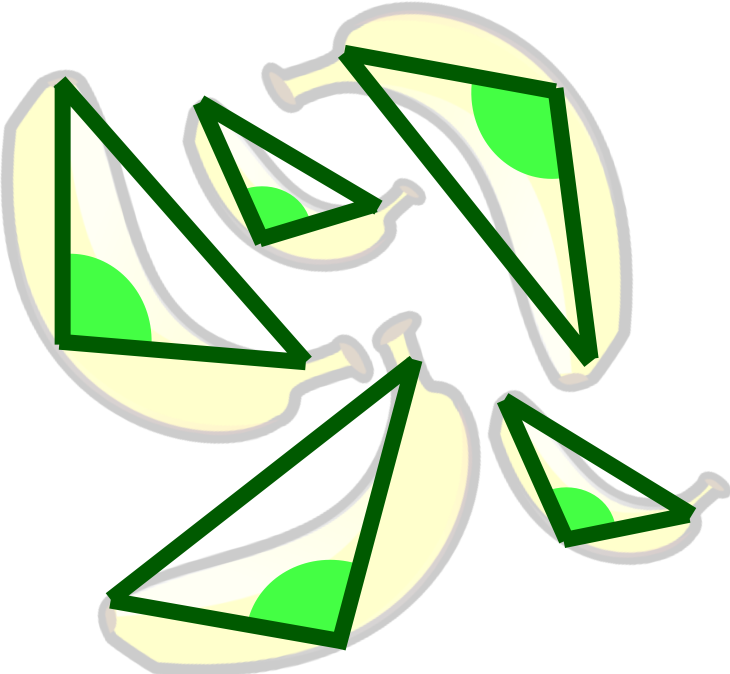
- **Can be easily computed**

Why use maximum likelihood?

1. It's completely general



No problem!



Maximum likelihood works for everything!

Why use maximum likelihood?

2. It's usually the best possible choice:

- **Maximum likelihood estimation yields the lowest possible standard error**

The standard error measures the variability you would see in your estimates of (a, b) …

… if you conducted your whole estimation procedure over and over

Some estimation procedures are more efficient than others!

Maximum likelihood in R

- **You can only minimize functions in R, not maximize them**

- **So minimize the negative log likelihood**

- **Least squares objective is:**

sum((yData – yPredicted)^2)

- **Maximum likelihood objective is:**

– sum(dnorm(yData, mean=yPredicted, sigma, log=T))

Negative log-likelihood is a sum …

…. of log-likelihoods for each observation

Maximum likelihood in R

- **You can only minimize functions in R, not maximize them**

- **So minimize the negative log likelihood**

- **Least squares objective is:**

  sum((yData – yPredicted)^2)

- **Maximum likelihood objective is:**

– sum(dnorm(yData, mean=yPredicted, sigma, log=T))

“dnorm” means use the probability density from the Normal distribution

Maximum likelihood in R

- **You can only minimize functions in R, not maximize them**

- **So minimize the negative log likelihood**

- **Least squares objective is:**

  sum((yData – yPredicted)^2)

- **Maximum likelihood objective is:**

– sum(dnorm(yData, mean=yPredicted, sigma, log=T))

- **For the Normal distribution, maximum likelihood gives the same answers as least squares!**

Want to change your model?

- **Easy!**

- **Normal model objective is:**

– sum(dnorm(yData, mean=yPredicted, sigma, log=T))

- **Poisson model objective is:**
  - – sum(dpois(yData, rate=yPredicted, log=T))

- **You can calculate the standard error by bootstrap as before**

DIY Modelling: Your tasks

- The code template contains incomplete R code to fit an “lm” model by least squares and find the standard error by bootstrap

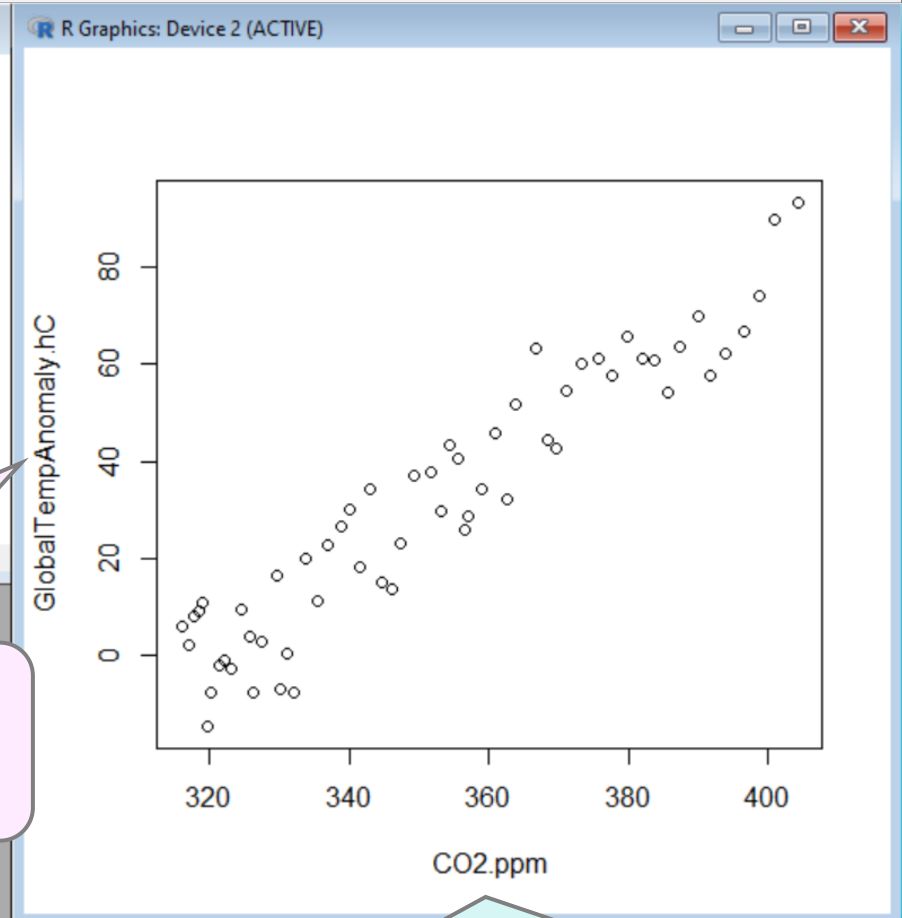
- First job: complete the code
  - Apply it to the Climate Data provided
  - Demonstrate you get the same estimates as lm, and similar standard errors / CIs
  - Write new code to fit the same model by maximum likelihood (Normal scatter model)
  - Demonstrate you get the same answers again

1. Climate data 1959-2016

GlobalTemperatureAnomaly.csv : call it temp.dat

R Console

```
> temp.dat <- read.csv(file.choose())
> head(temp.dat)
  CO2.ppm GlobalTempAnomaly.hC
1  315.97                 5.96
2  316.91                 2.04
3  317.64                 7.75
4  318.45                 8.88
5  318.99                10.68
6  319.62               -14.95
>
> with(temp.dat, plot(CO2.ppm, GlobalTempAnomaly.hC))
>
```



Global temperature anomaly in hC (hundredths of ºC)

Looks like good data for an “lm” model

Annual mean atmospheric CO_2 in ppm (parts per million)

2. Wombat data

Wombats.csv : call it wombat.dat

- The northern hairy-nosed wombat lives in just two locations in Queensland
- One of the world's rarest mammals: about 250 total
- Every few years there is a burrow survey to estimate the population size

- Sticky tapes erected outside burrows catch wombat hairs as the wombats go out for the night

2. Wombat data

Wombats.csv : call it wombat.dat

Photos: Dr Alan Horsup

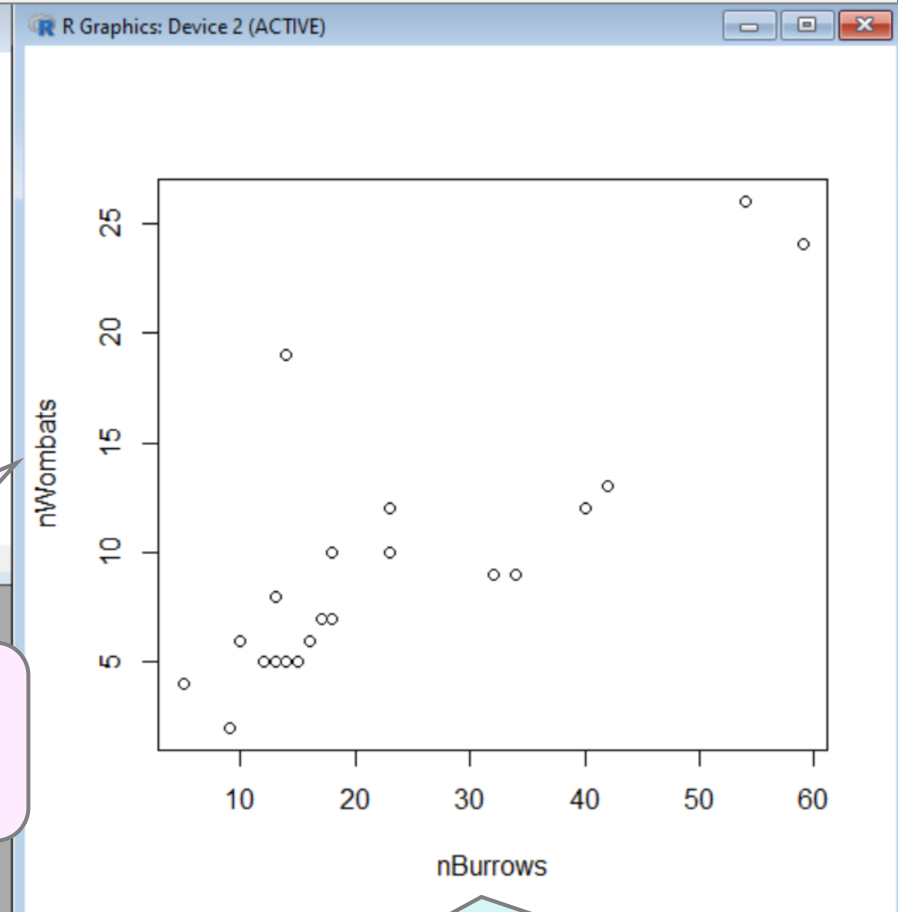
- **Sticky tapes erected outside burrows catch wombat hairs as the wombats go out for the night**

2. Wombat data

Wombats.csv : call it wombat.dat

R Console

```
>
> wombat.dat <- read.csv(file.choose())
> head(wombat.dat)
  location nBurrows nWombats males females
1     Bend       32        9     3       6
2     Camp       59       24    12      12
3     Cave       34        9     7       2
4  Coombes       23       10     4       6
5    Davis       15        5     2       3
6   Dexter       18        7     5       2
> with(wombat.dat, plot(nBurrows, nWombats))
> |
```



Number of different wombats sampled from that location

Looks like good data for a Poisson glm

#burrows in each location (location = cluster of burrows)

2. Wombat data

Wombats.csv : call it wombat.dat

```
> wombat.dat <- read.csv(file.choose())
> head(wombat.dat)
  location nBurrows nWombats males females
1     Bend       32        9     3       6
2     Camp       59       24    12      12
3     Cave       34        9     7       2
4  Coombes       23       10     4       6
5    Davis       15        5     2       3
6   Dexter       18        7     5       2
```

Maybe these columns could be suitable for some other type of model…?

DIY Modelling: your second task

- **Write MLE code to reproduce the following GLM using the Wombat data:**

glm(nWombats ~ nBurrows, family=poisson(link=log))

  - **Fit the GLM with poisson and quasipoisson:** glm(…, family=poisson) and glm(…, family=quasipoisson)
  - **Demonstrate your MLE code gives the same estimates as both poisson and quasipoisson**
  - **Investigate how the standard errors compare: are the bootstrap standard errors similar to the poisson or the quasipoisson ones? Why?**
  - **Write up all your findings in your report and submit your code on Canvas**

DIY Modelling: your third task

- **Do something else!**
- **Your ‘something else’ should use your DIY modelling skills in some way**
  - Code your own models

Ideas for your Something Else:

- Formulate a model for the extra columns in wombat.dat: code it and compare with R
- Find a context (data and/or model) where maximum likelihood is demonstrably better than least-squares
- Refresh theory from Stats 310 about how to calculate the standard error analytically: code it and compare it with your bootstrap results
- Code up the parametric bootstrap and compare with nonparametric bootstrap for both of the data-sets supplied

Report and video

- **Submit a brief project report (4 pages max)**
- **Compare output from R (lm / glm) with output from your own code (least-squares / MLE)**
  - Clearly show how the outputs demonstrate that your code matches the results from the R functions
  - Make sure you've answered all specific questions with each data-set (e.g. poisson *vs* quasipoisson standard errors)
- **Describe your Something Else and show output** (include points of interest, e.g. if a slope is significant)
- **On your video, show your code running in real time** (just the fitting code; the bootstrap may take too long)

Assessment: 8% total

- **Code that successfully answers the questions set for Tasks 1 and 2: 4% instructor**
  - We must be able to run your code successfully
- **Your Something Else: 4%**
  - 50% peer, 50% instructor

Good luck! ☺