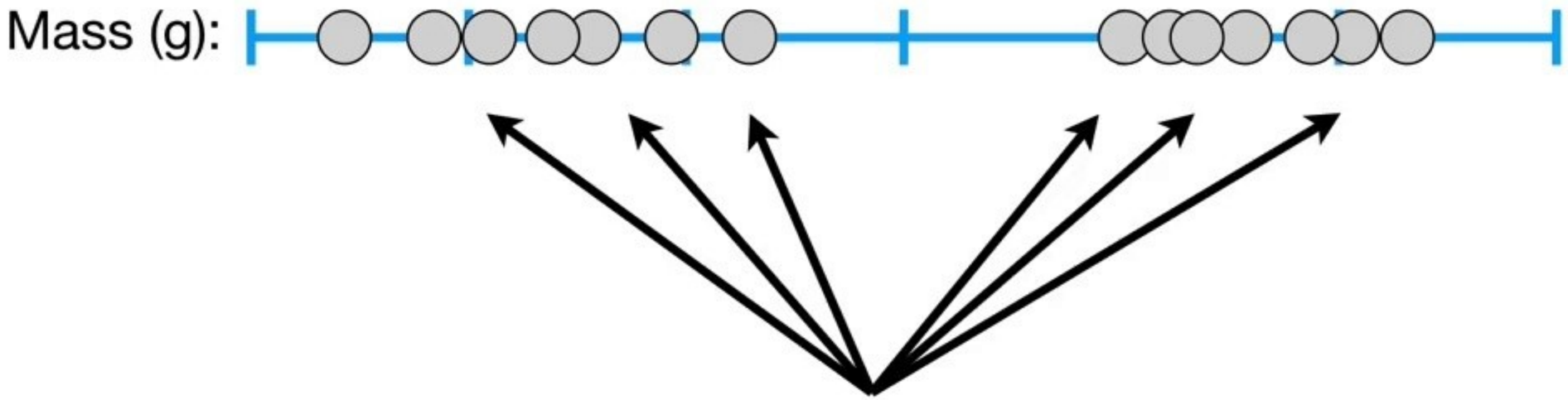
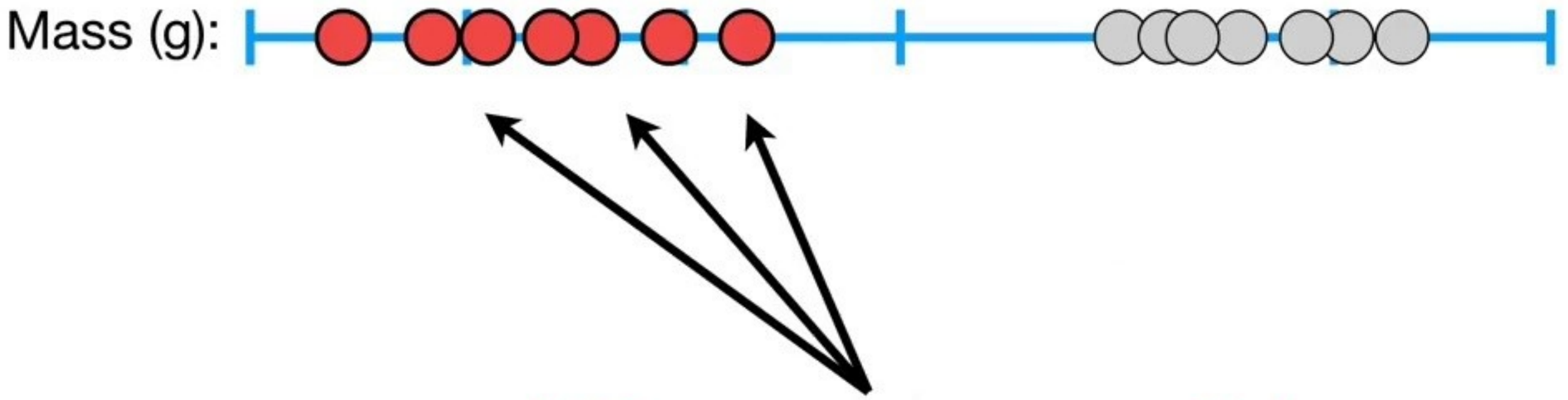
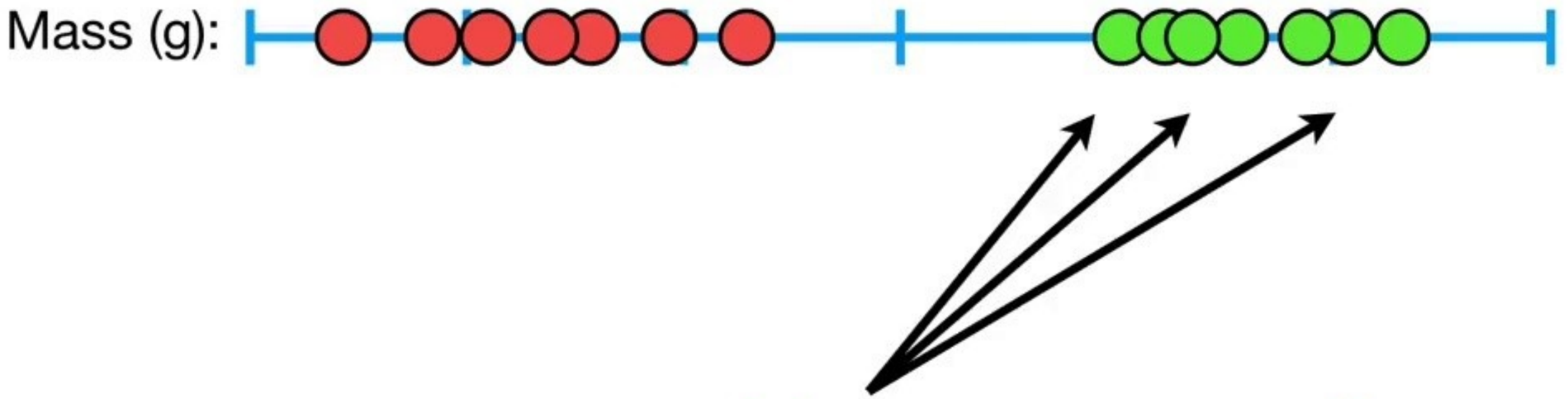


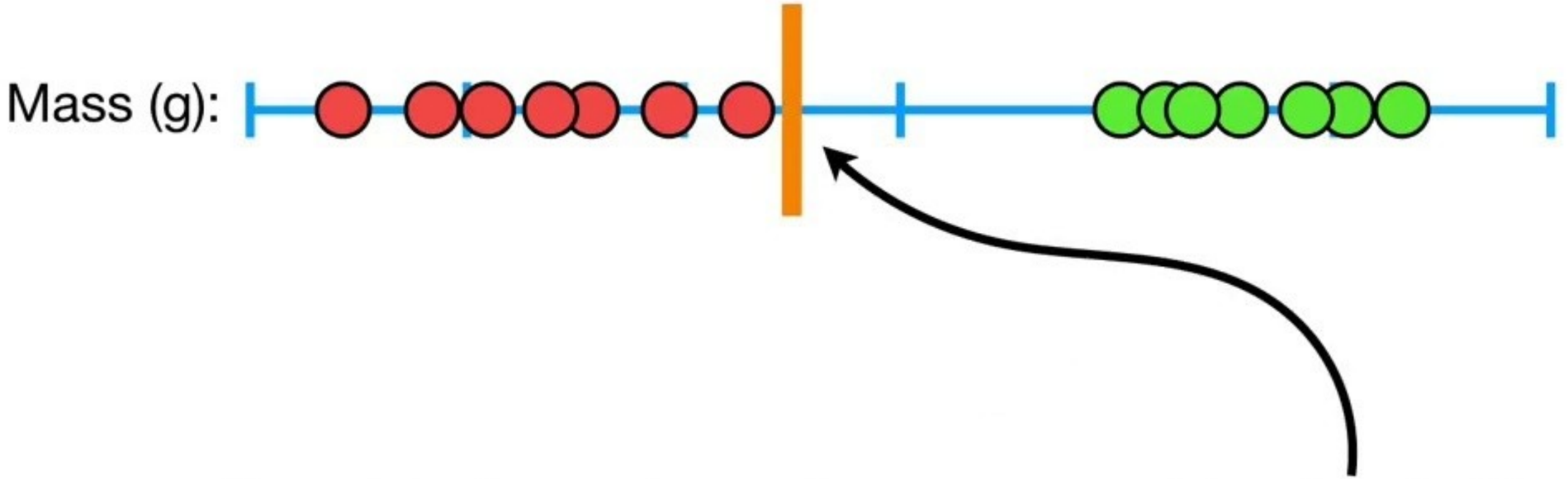
Let’s start by imagining we measured
the mass of a bunch of mice…

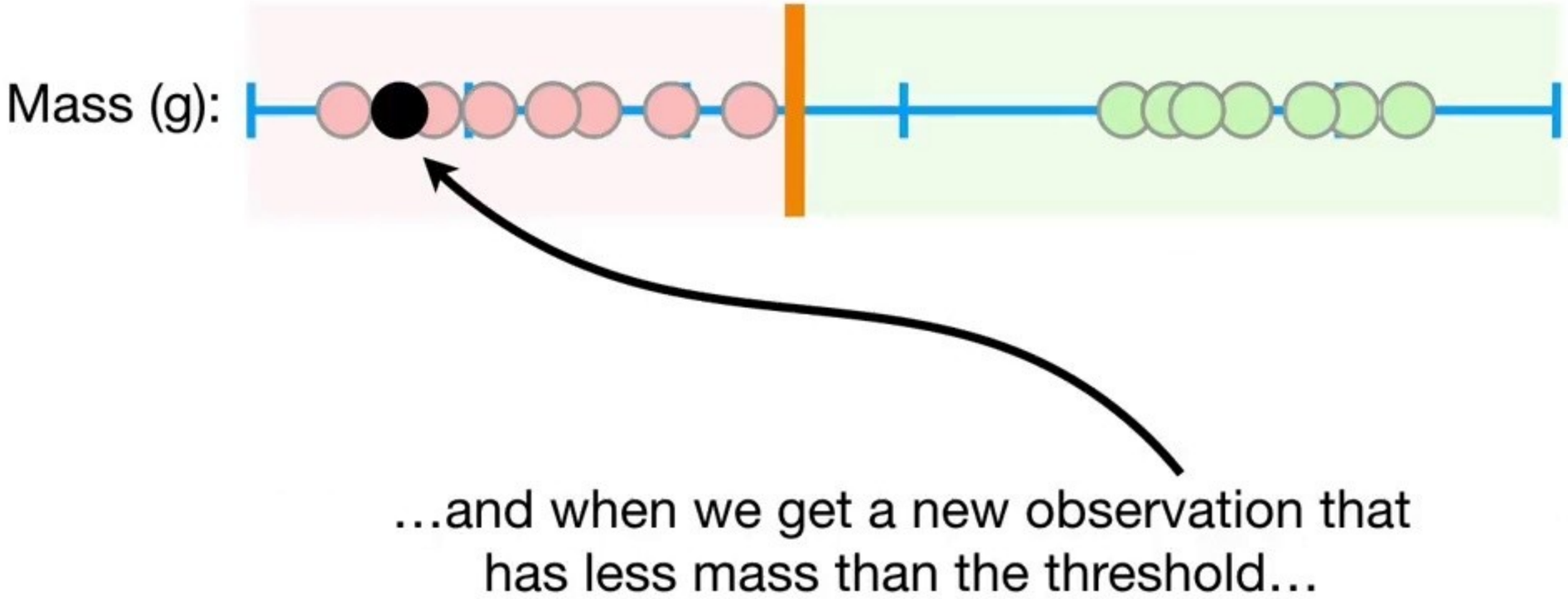


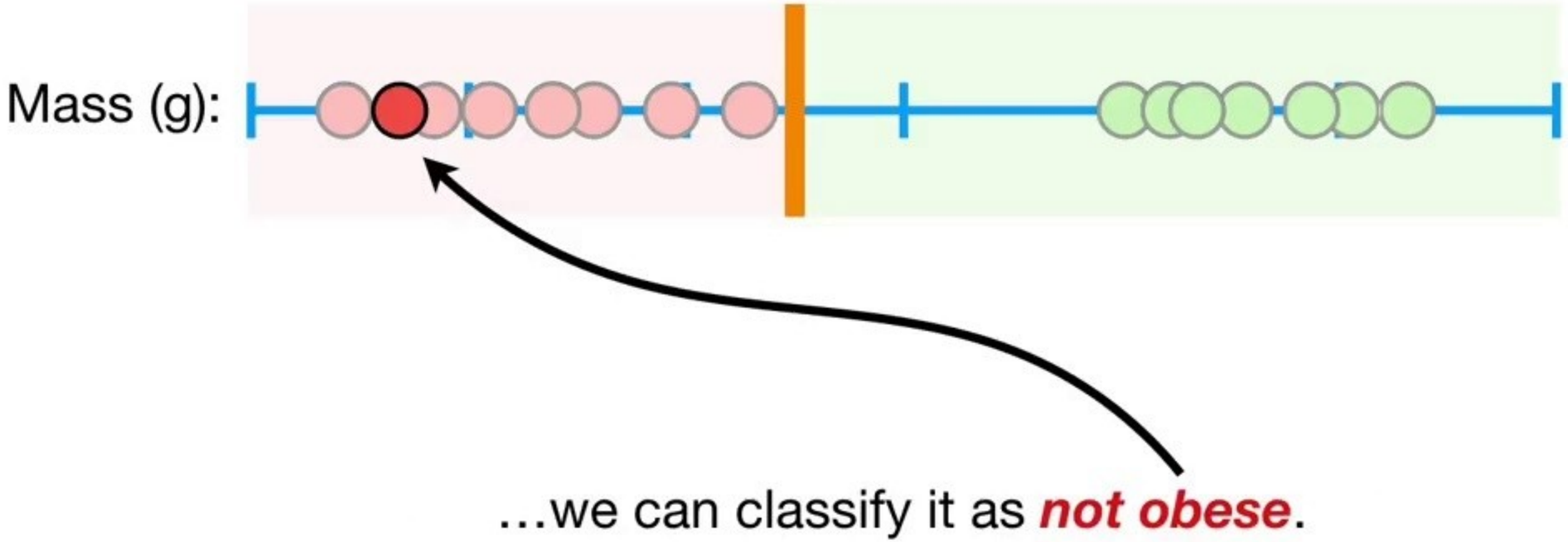
The **red dots** represent mice are ***not obese***…

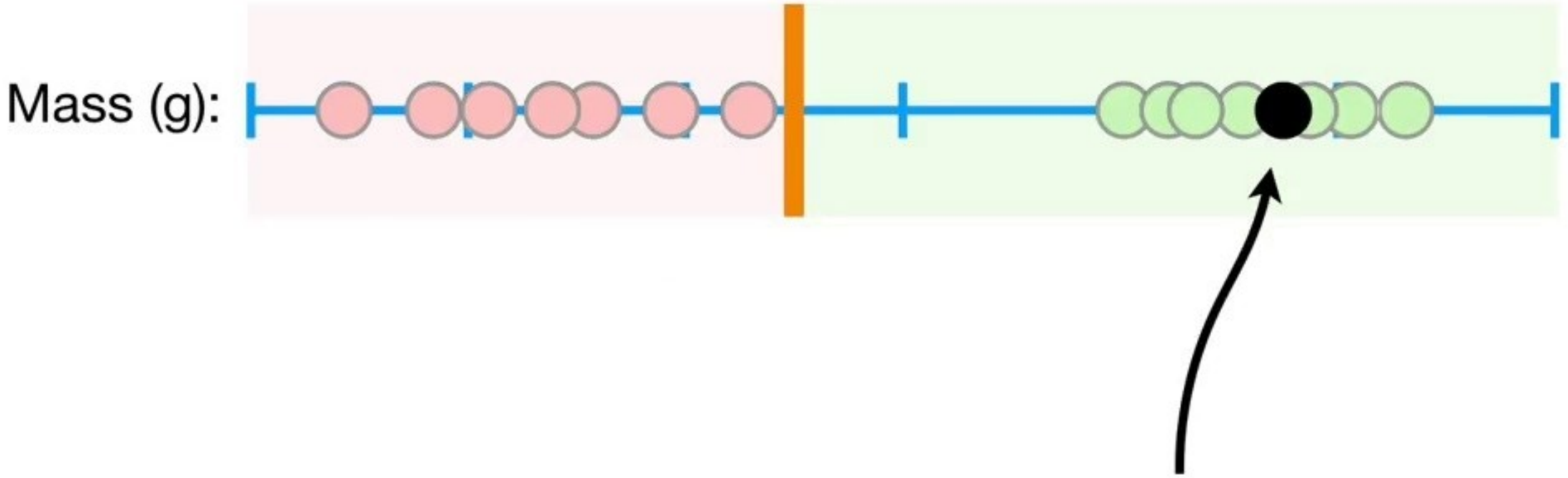


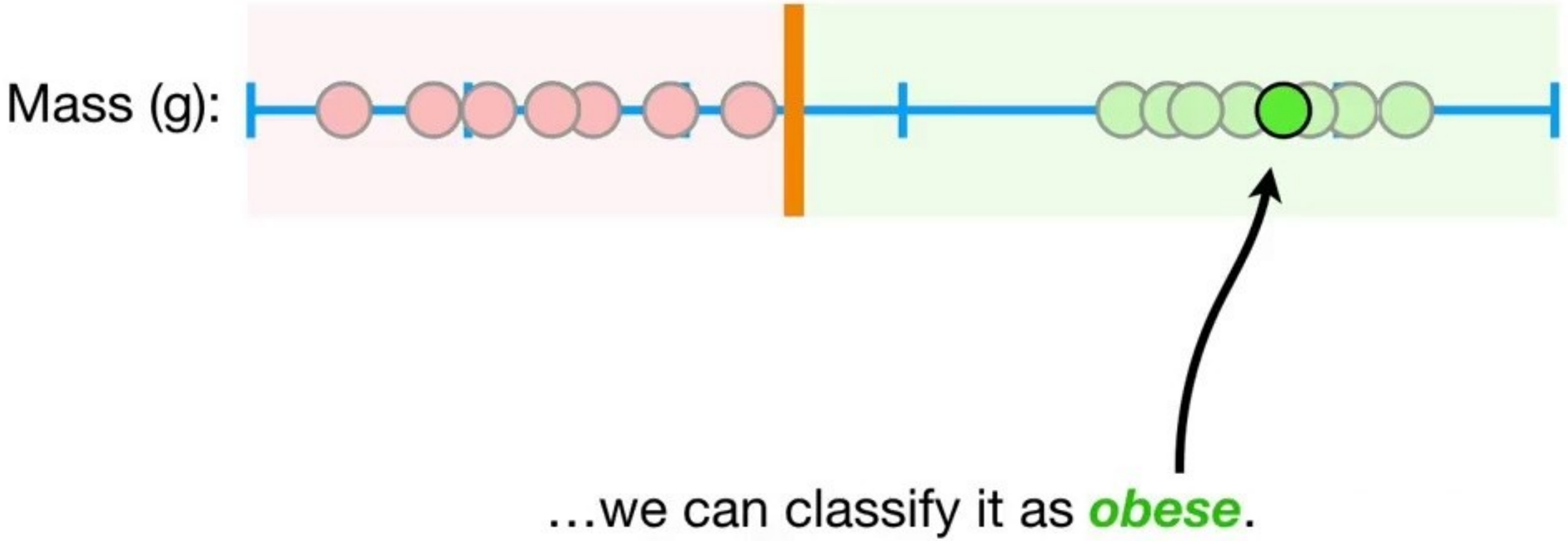
…and the **green dots** represent mice are ***obese***.

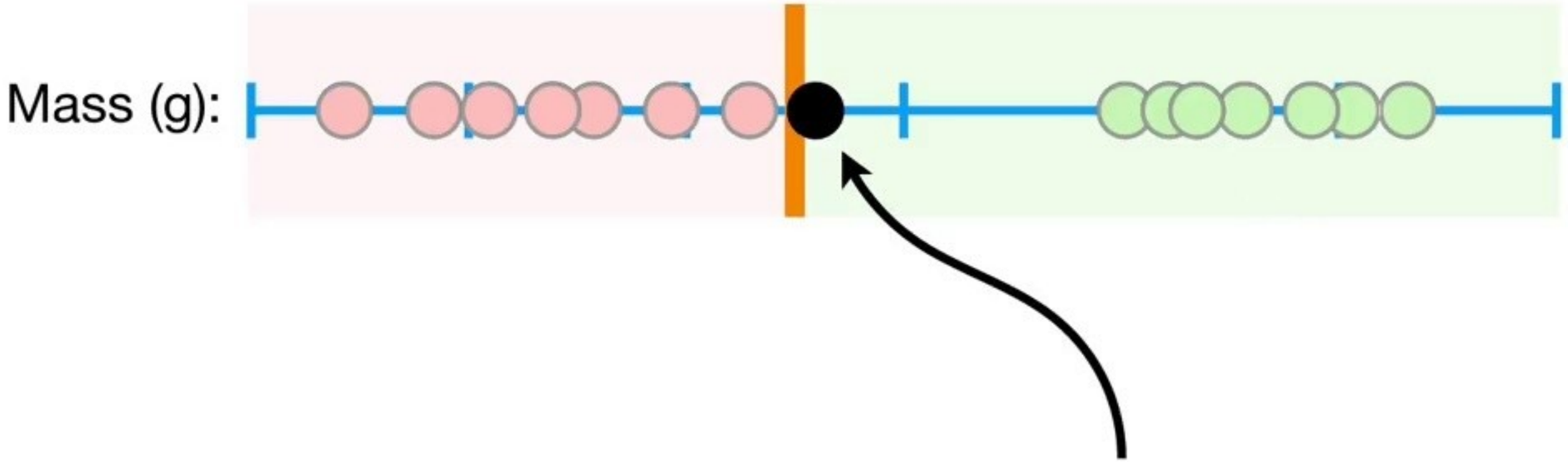

Mass (g):
Based on these observations, we can pick a threshold…

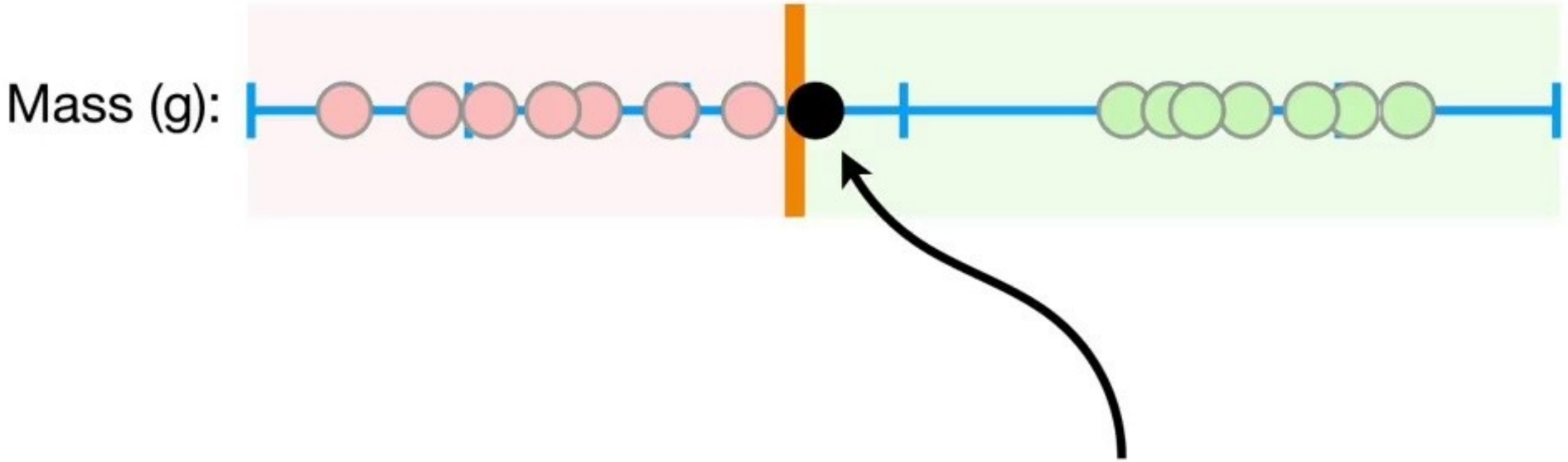

Mass (g):
…and when we get a new observation that
has less mass than the threshold…


Mass (g):
…we can classify it as not obese.

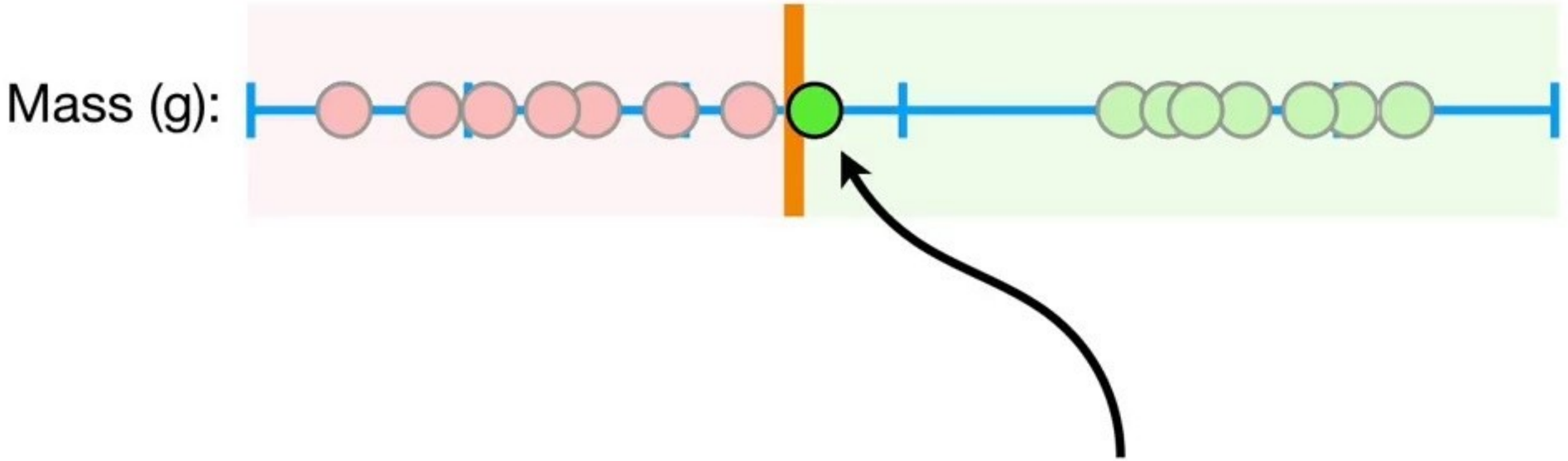

Mass (g):
And when we get a new observation with more mass than the threshold…


Mass (g):
…we can classify it as obese.

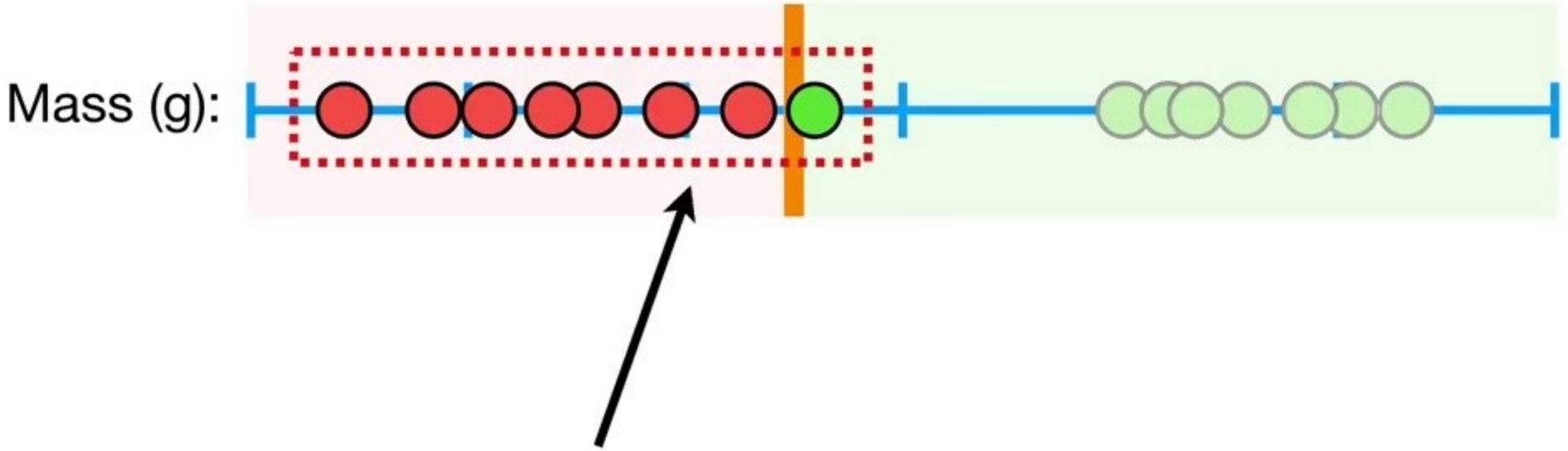

Mass (g):
However, what if get a new observation here?



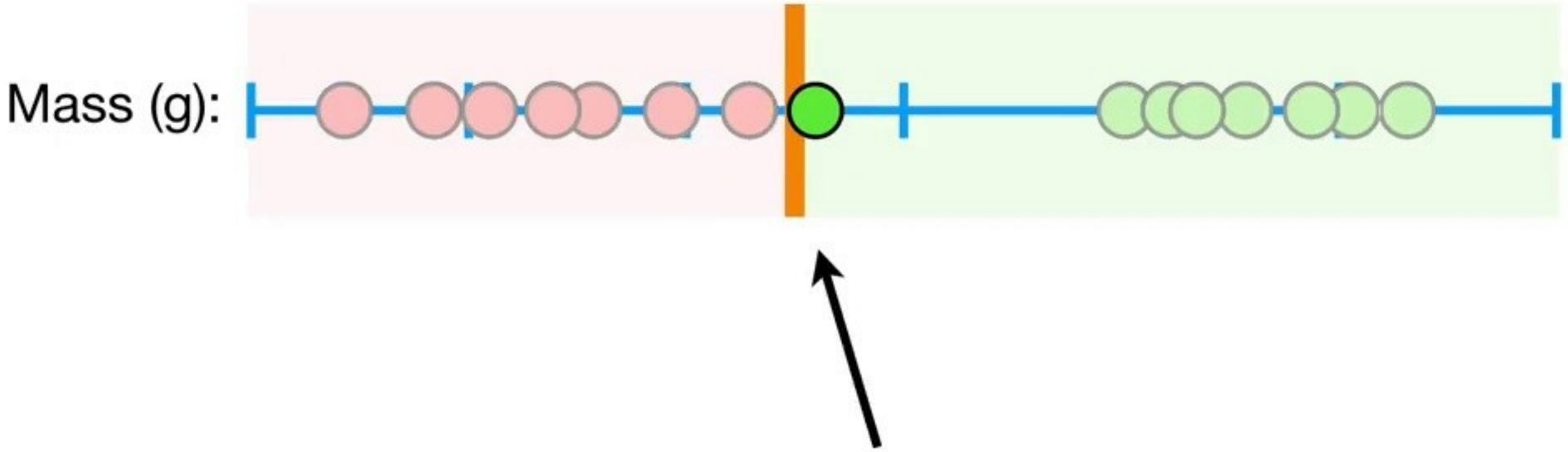
Because this observation has more mass than the threshold, we classify it as ***obese***.

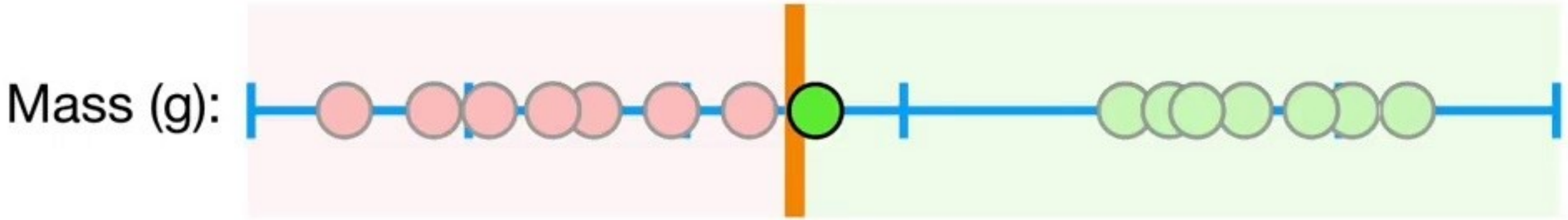


Because this observation has more mass than the threshold, we classify it as ***obese***.

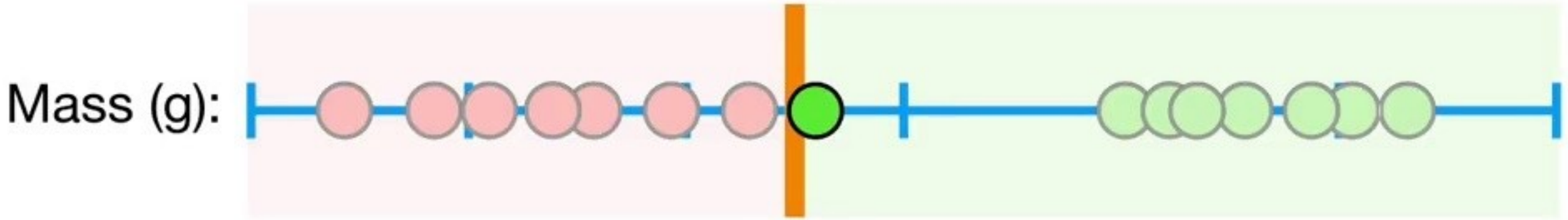


But that doesn’t make sense, because it is much closer to the observations that are ***not obese***.

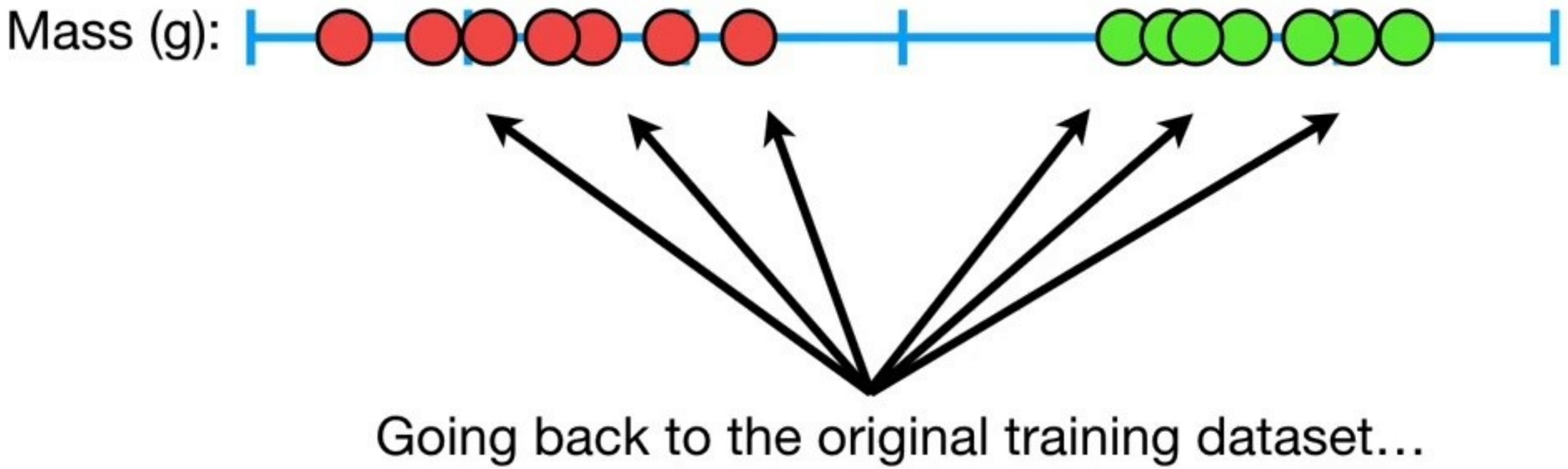

Mass (g):
So this threshold is pretty lame.

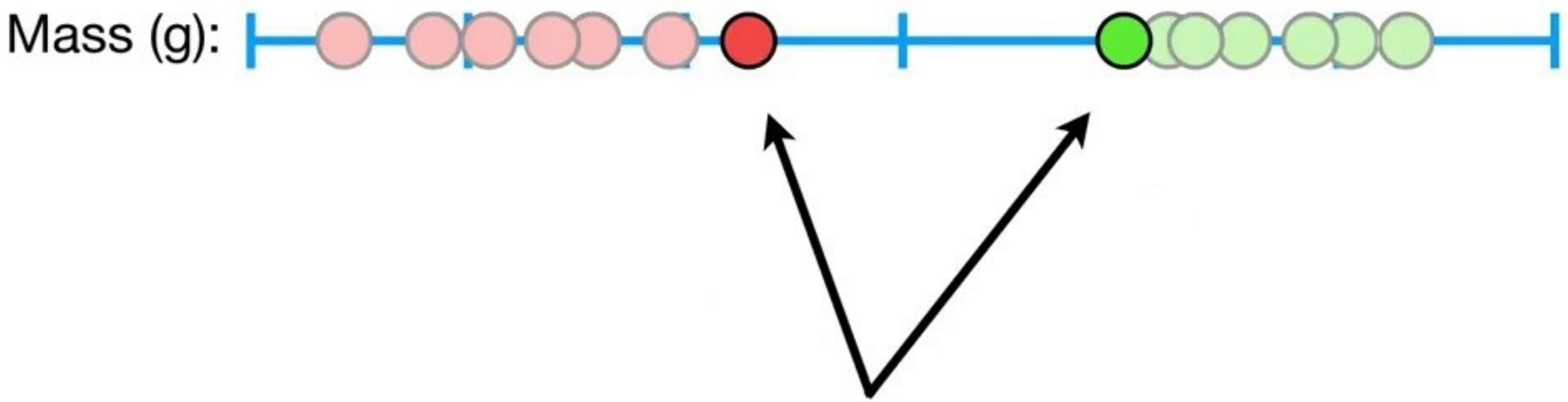


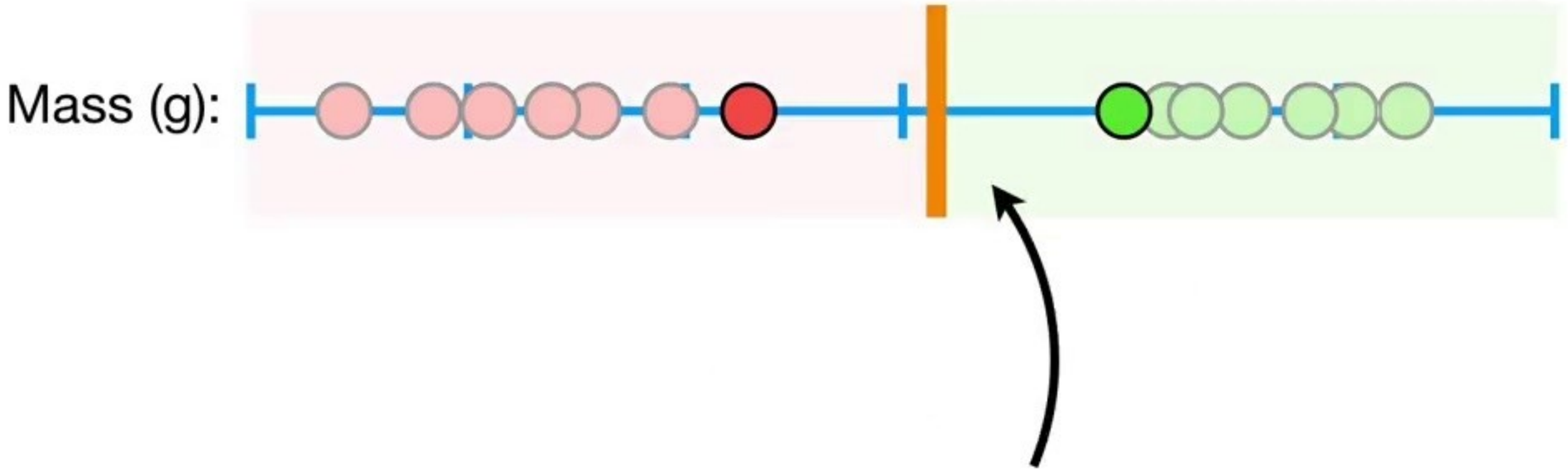
Can we do better?

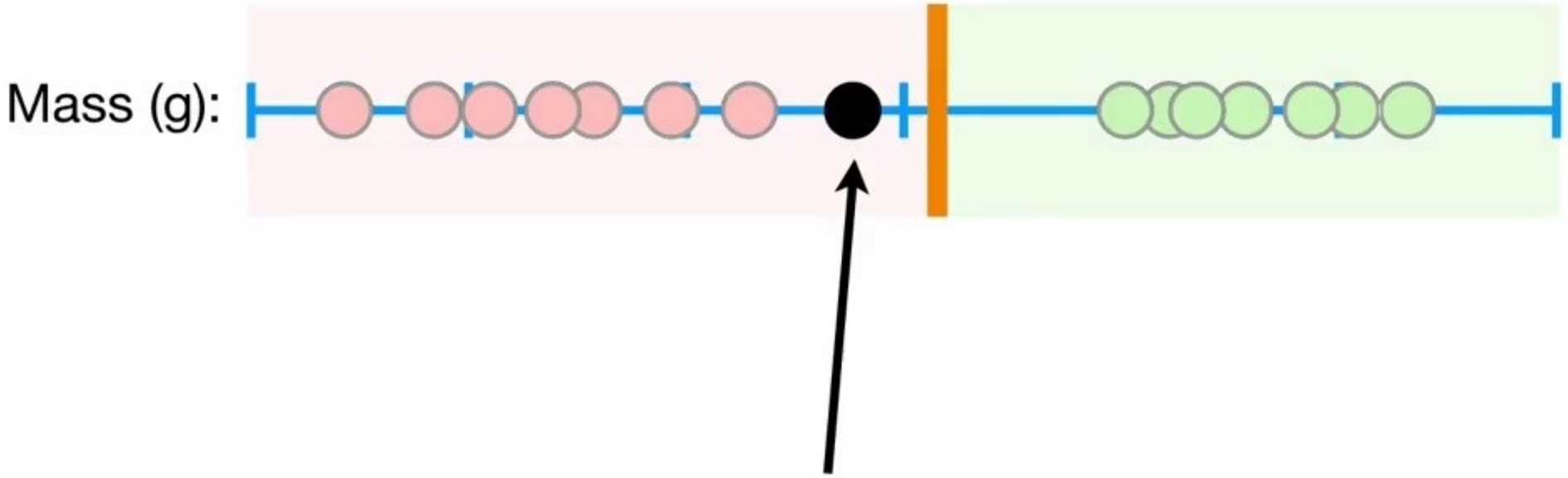


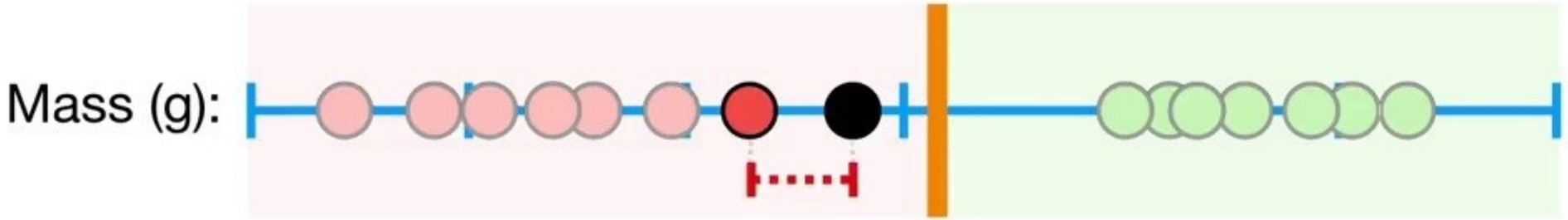
Yes!


Mass (g):
Going back to the original training dataset…

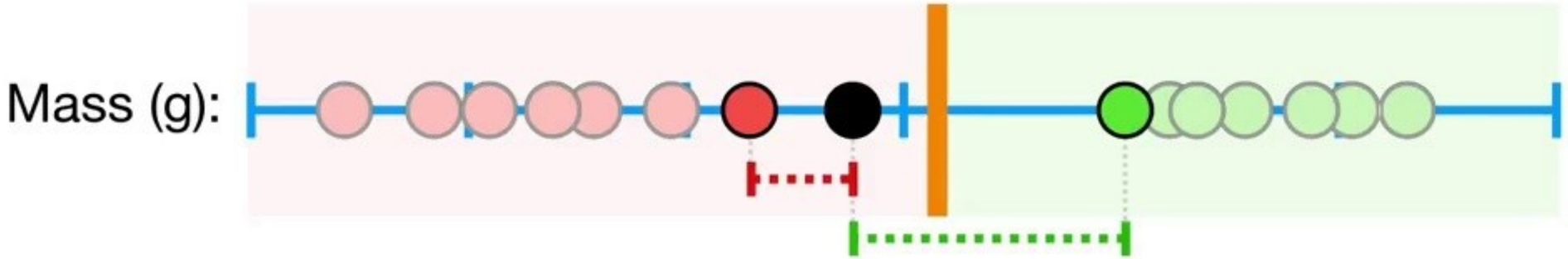

Mass (g):
…we can focus on the observations on
the edges of each cluster…


Mass (g):
…and use the midpoint between
them as the threshold.

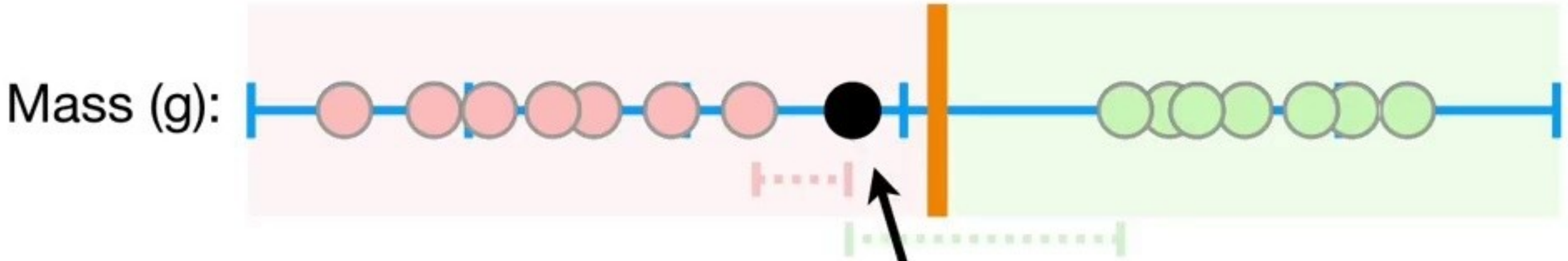

Mass (g):
Now, when a new observation falls
on the left side of the threshold…



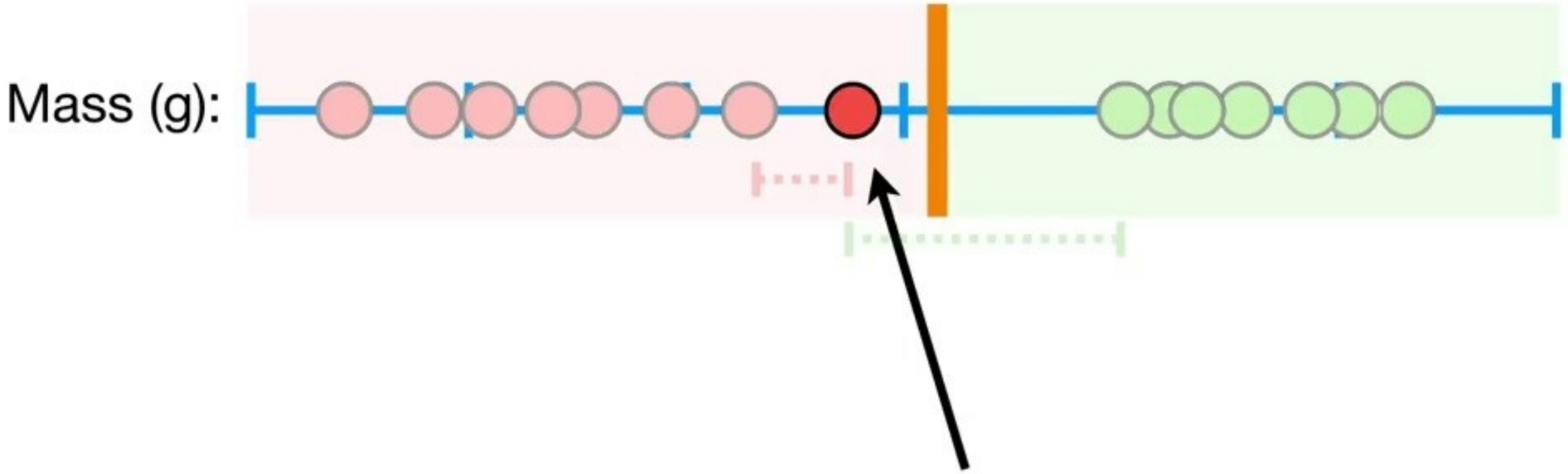
…it will be closer to the
observations that are ***not obese***…

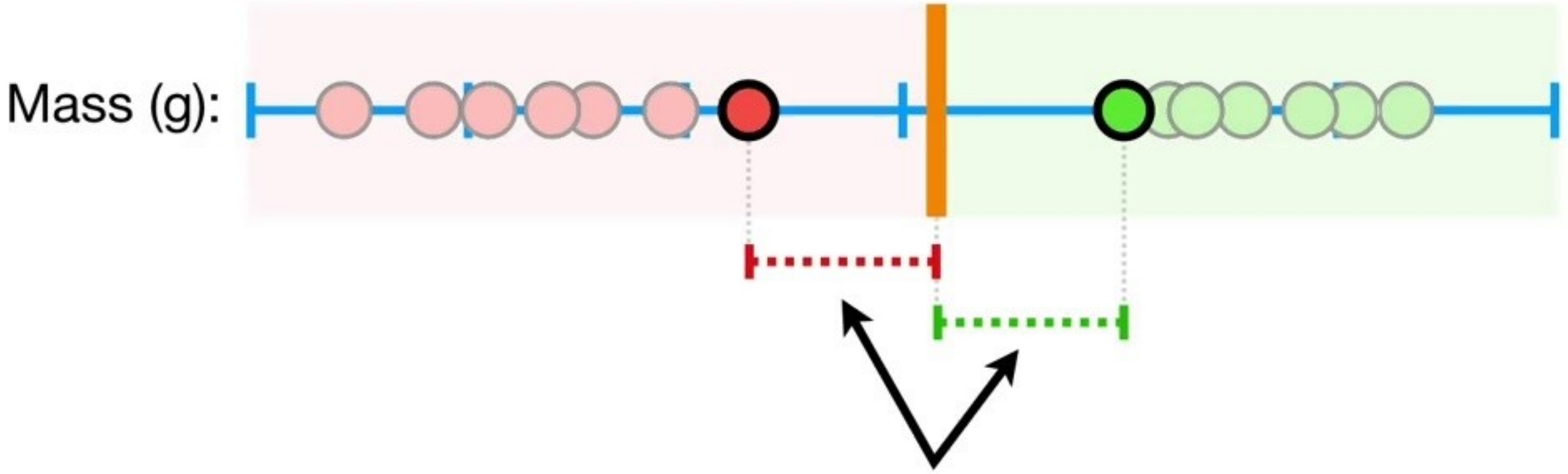


…than it is to the ***obese*** observations.

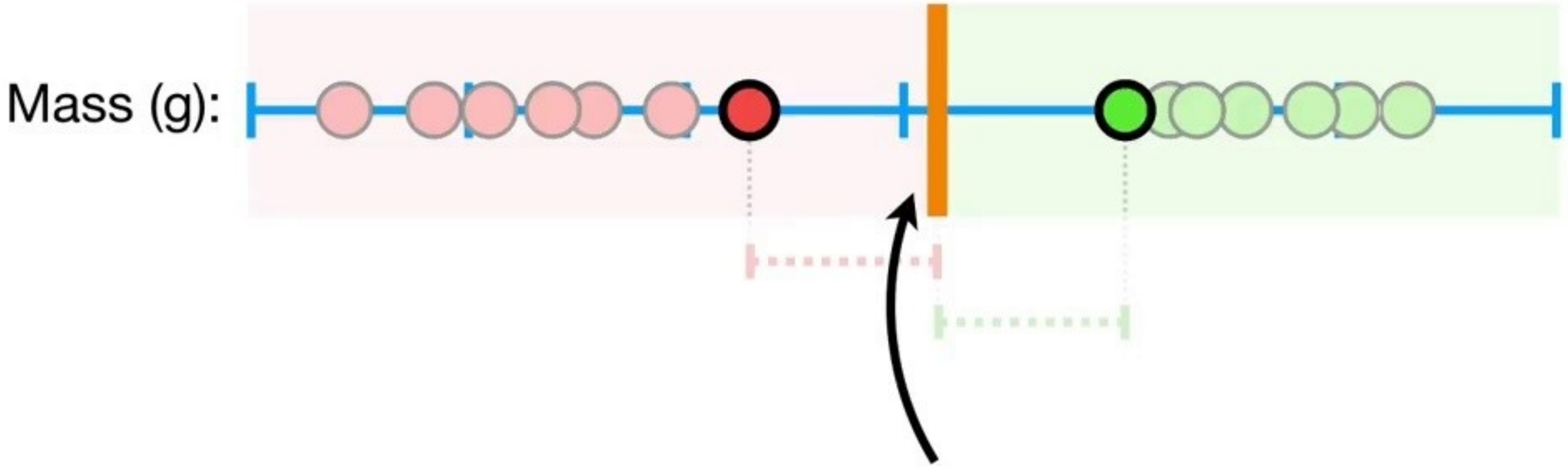


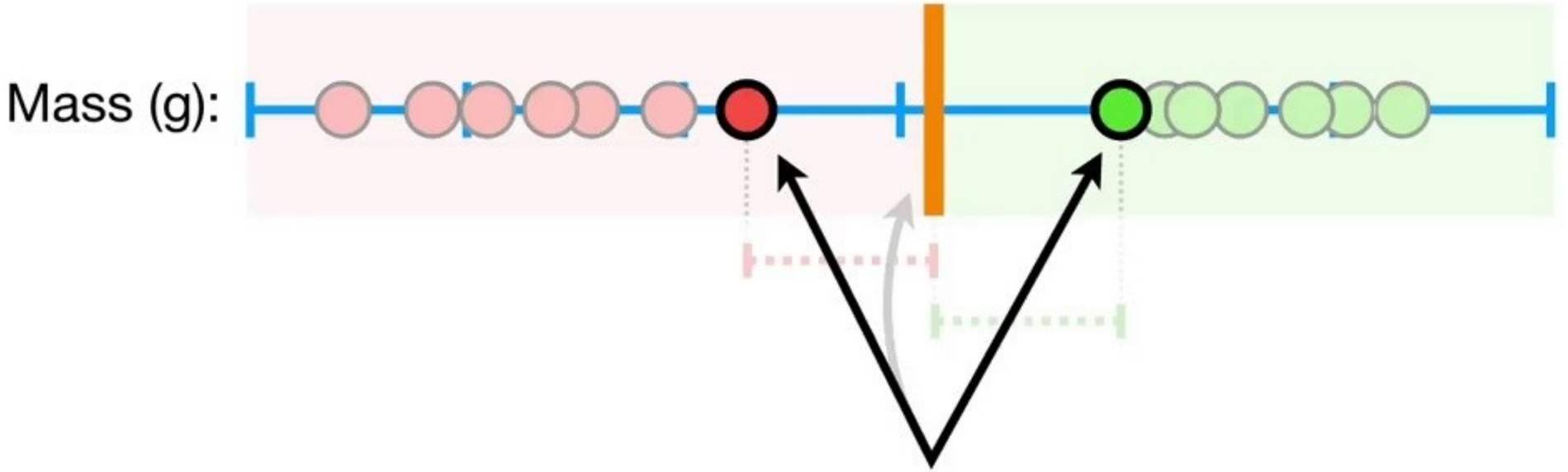
So it makes sense to classify this new observation as ***not obese***.


Mass (g):
So it makes sense to classify this new observation as **not obese**.

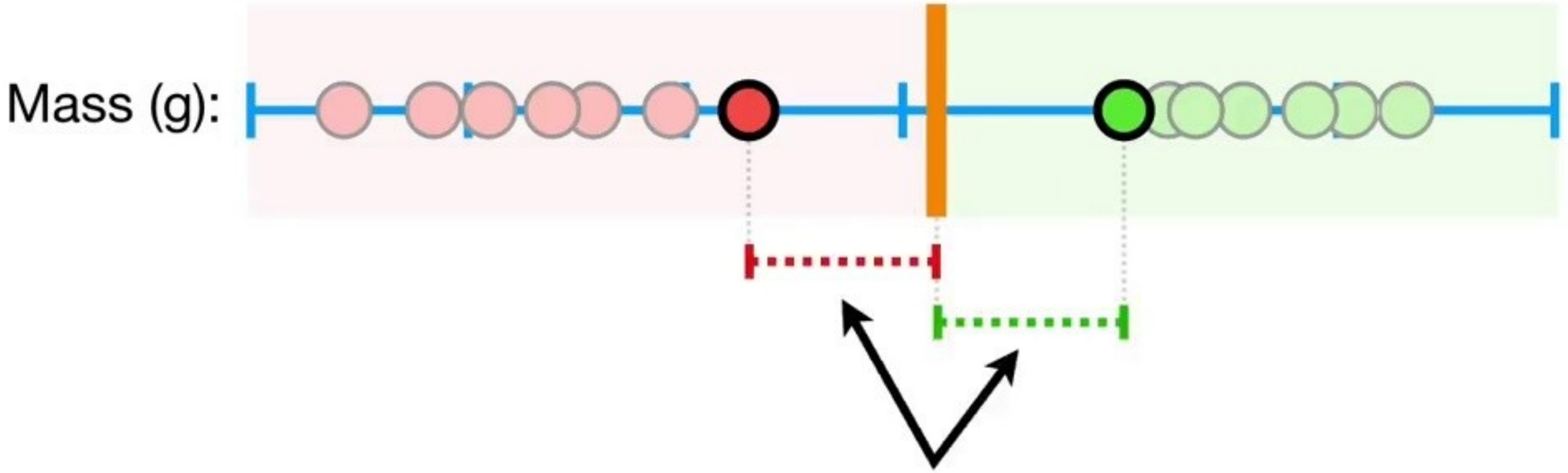


The shortest distance between the observations and the threshold is called the **margin**.

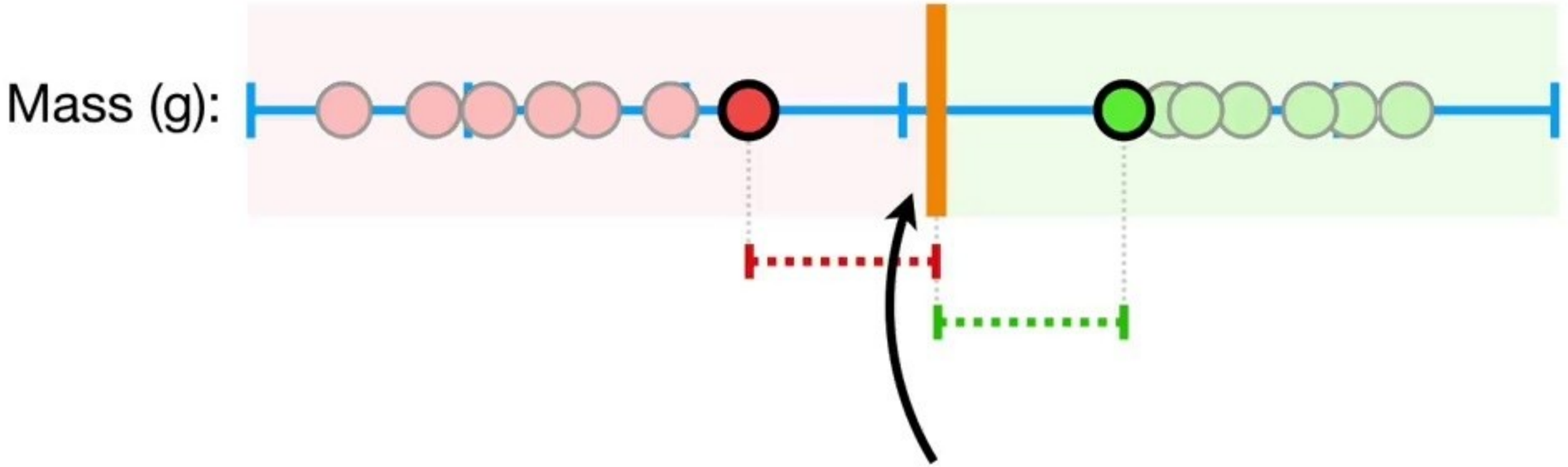

Mass (g):
Since we put the threshold halfway between these two observations…



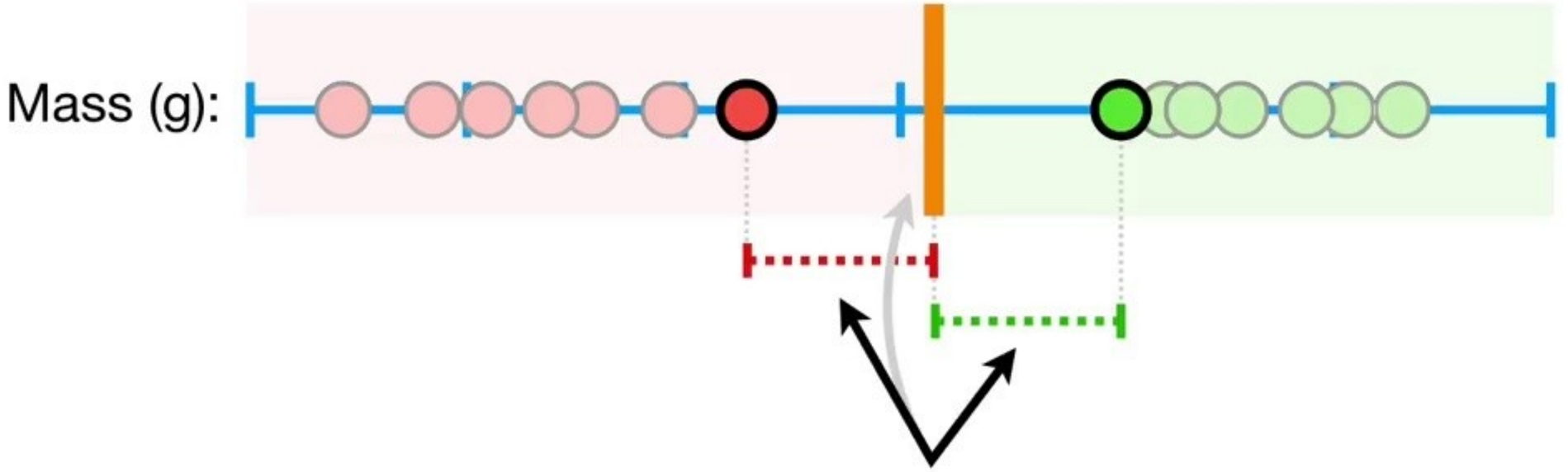
Since we put the threshold halfway between these two observations…



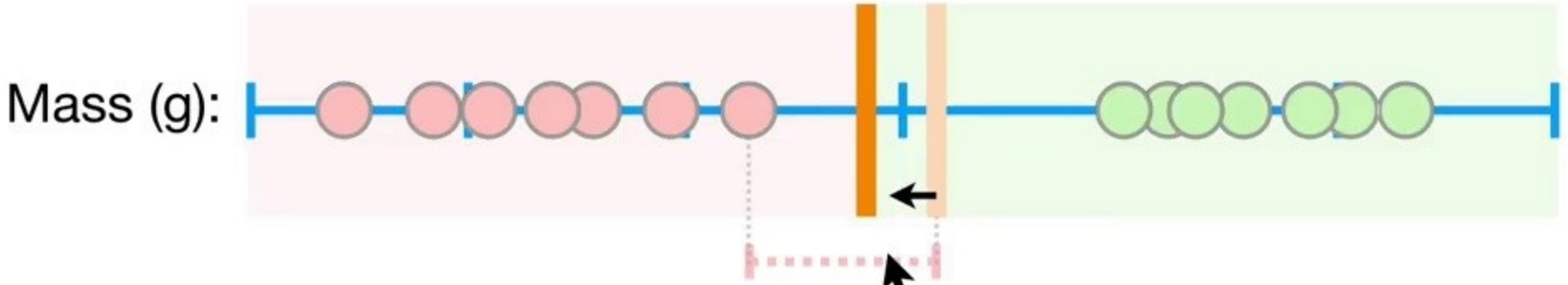
…the distances between the observations and the threshold are the same and both reflect the **margin**.



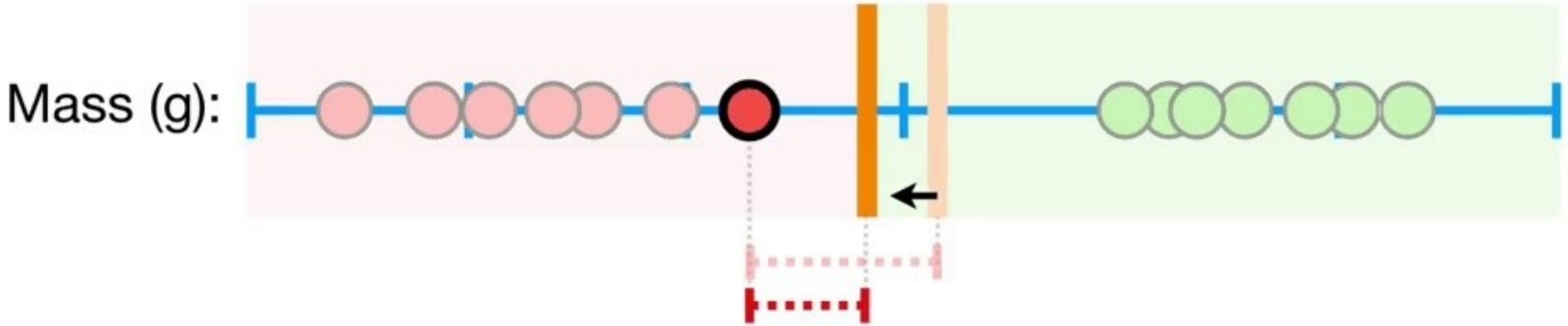
When the threshold is halfway between the two observations, the **margin** is as large as it can be.



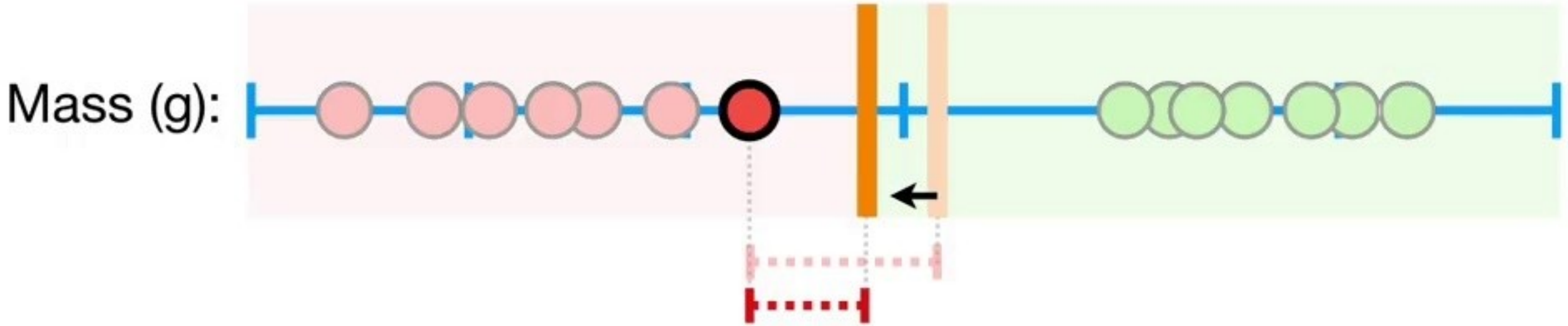
When the threshold is halfway between the two observations, the **margin** is as large as it can be.



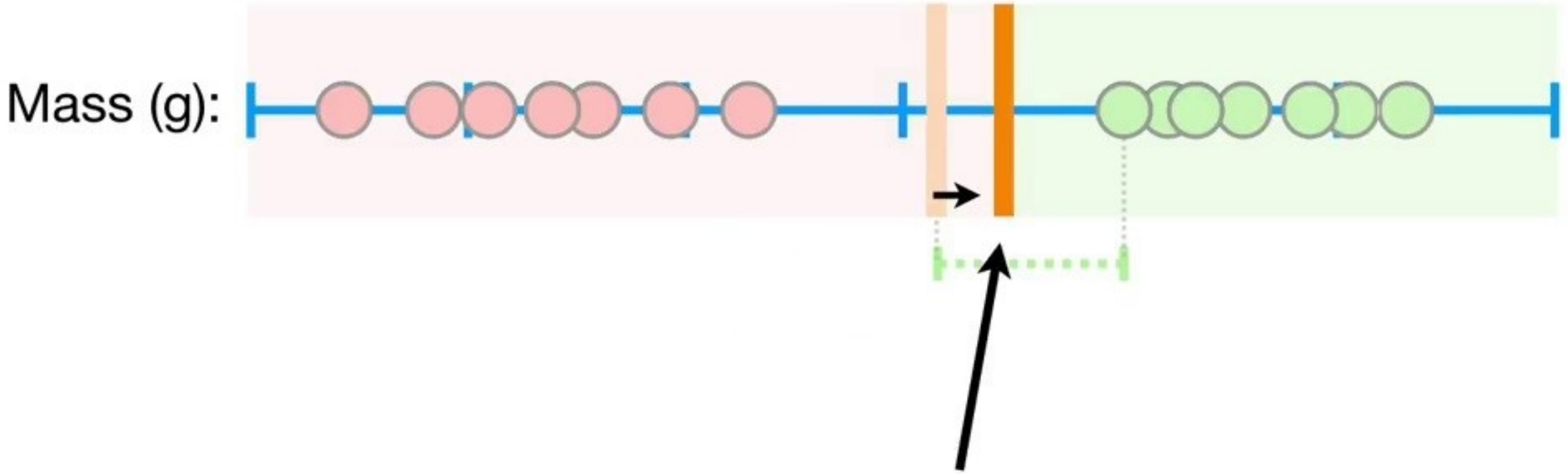
For example, if we moved the threshold to the left a little bit…

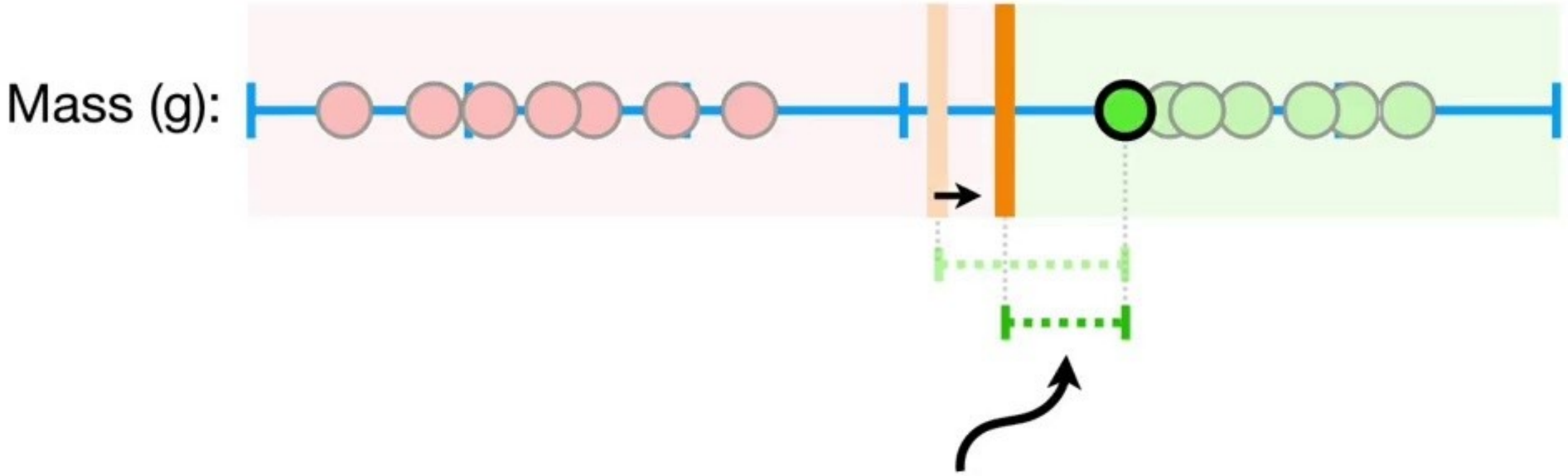


…then the distance between the threshold and the observation that is ***not obese*** would be smaller…

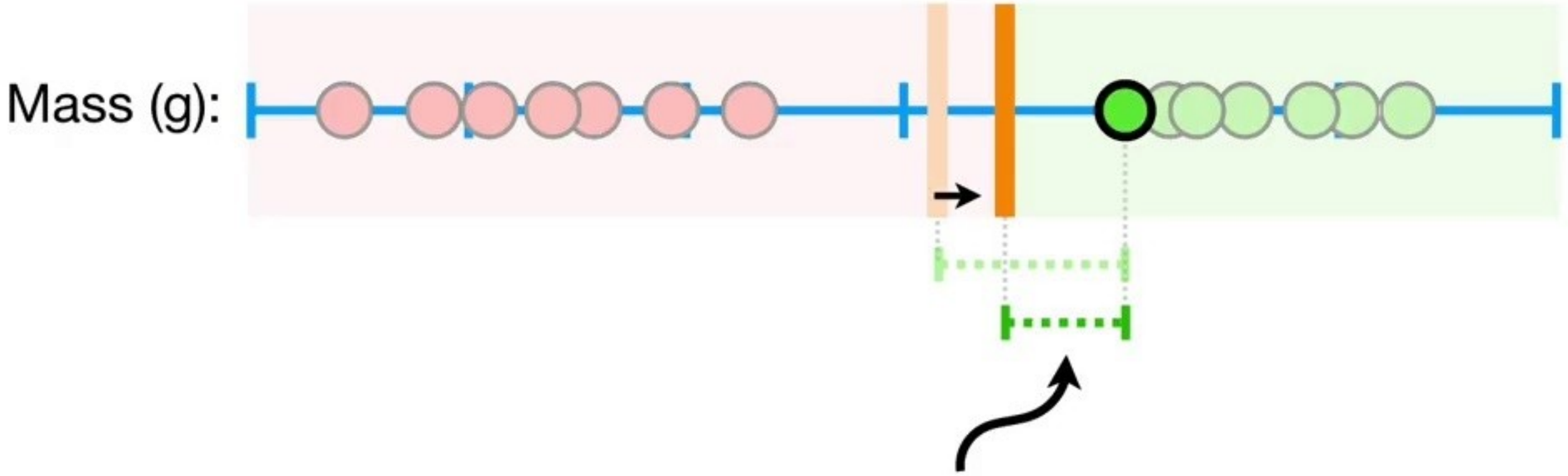


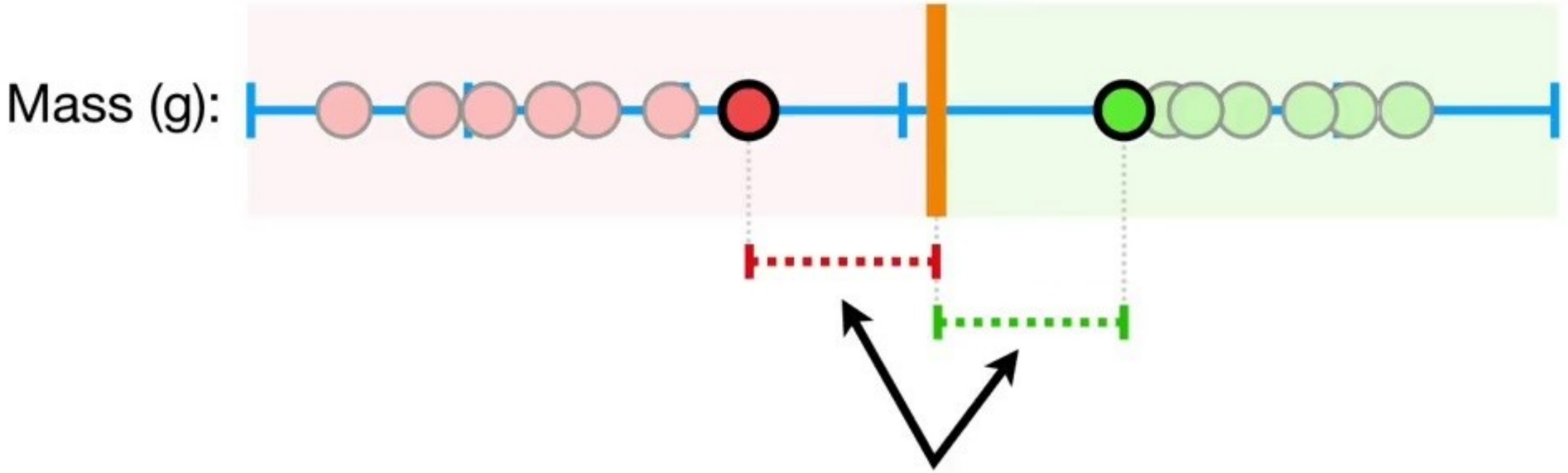
…and thus, the **margin** would be smaller than it was before.


Mass (g):
And if we moved the threshold to
the right a little bit…

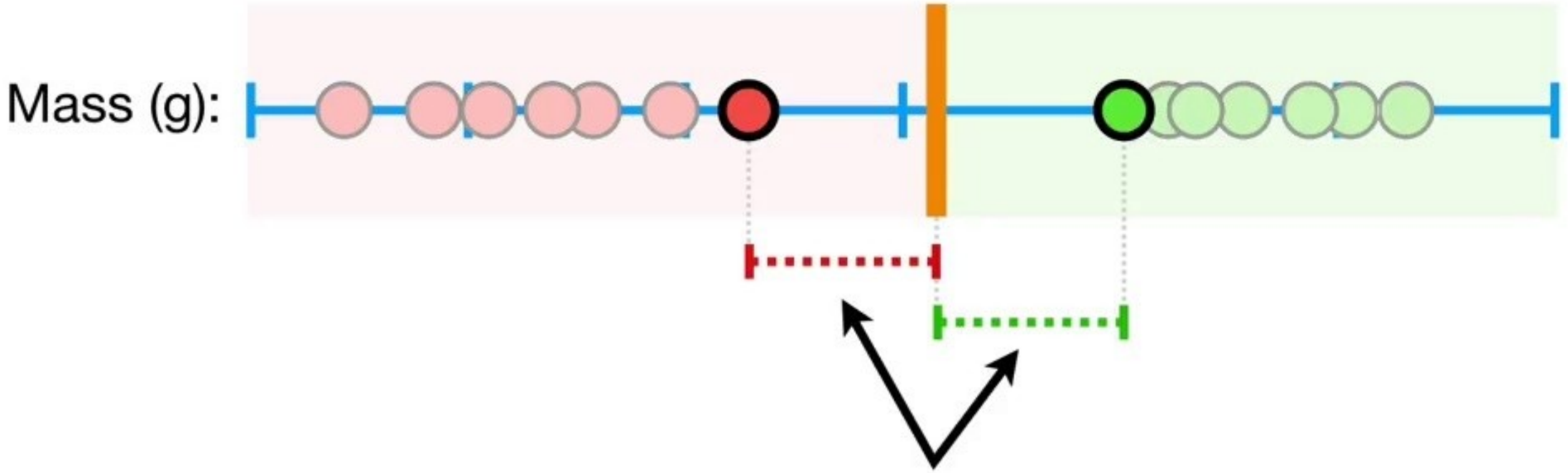


…then the distance between the ***obese*** observation and the threshold would get smaller…


Mass (g):
…and again, the **margin**
would be smaller.

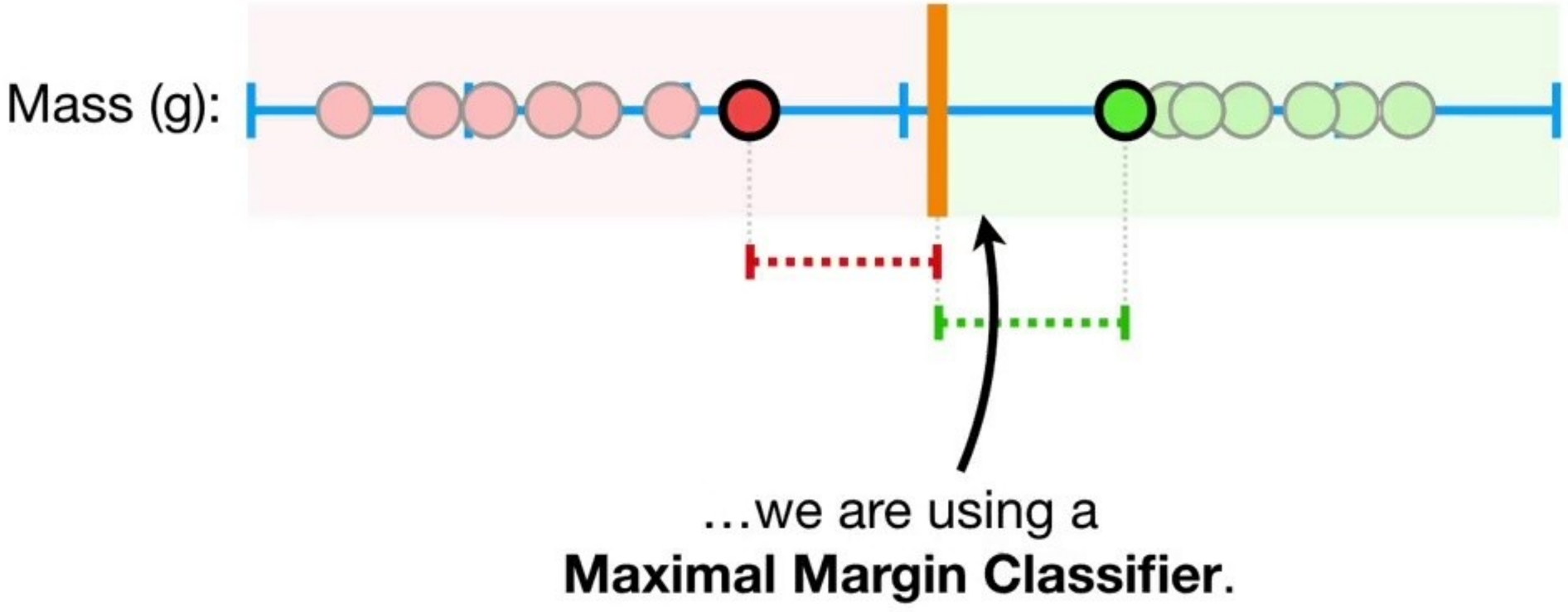


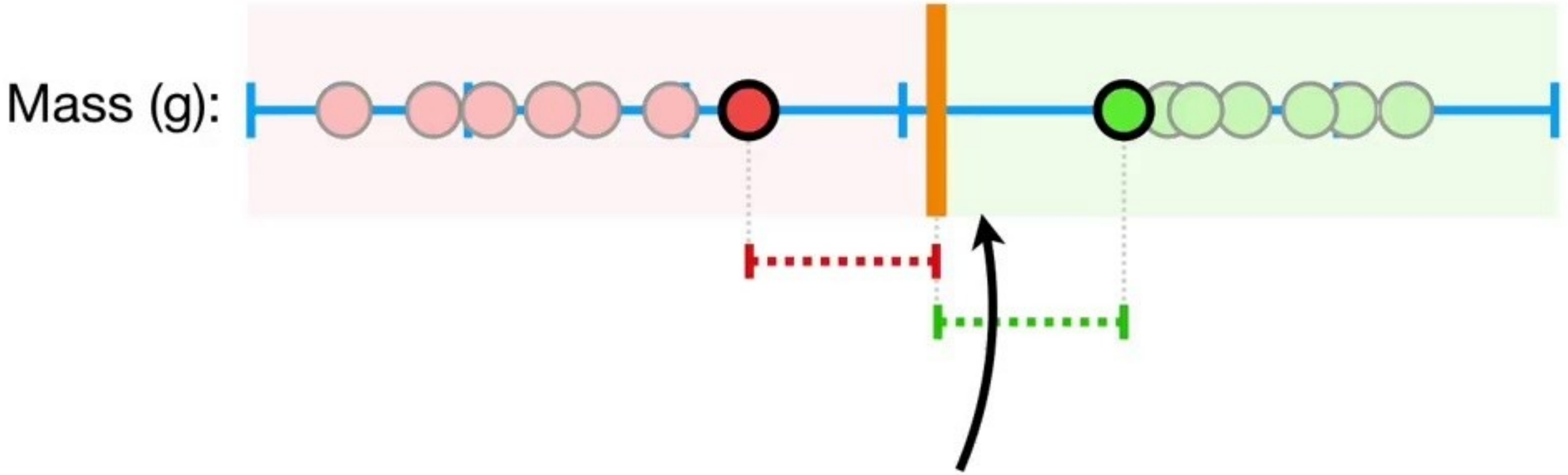
When we use the threshold that gives us the largest **margin** to make classifications…



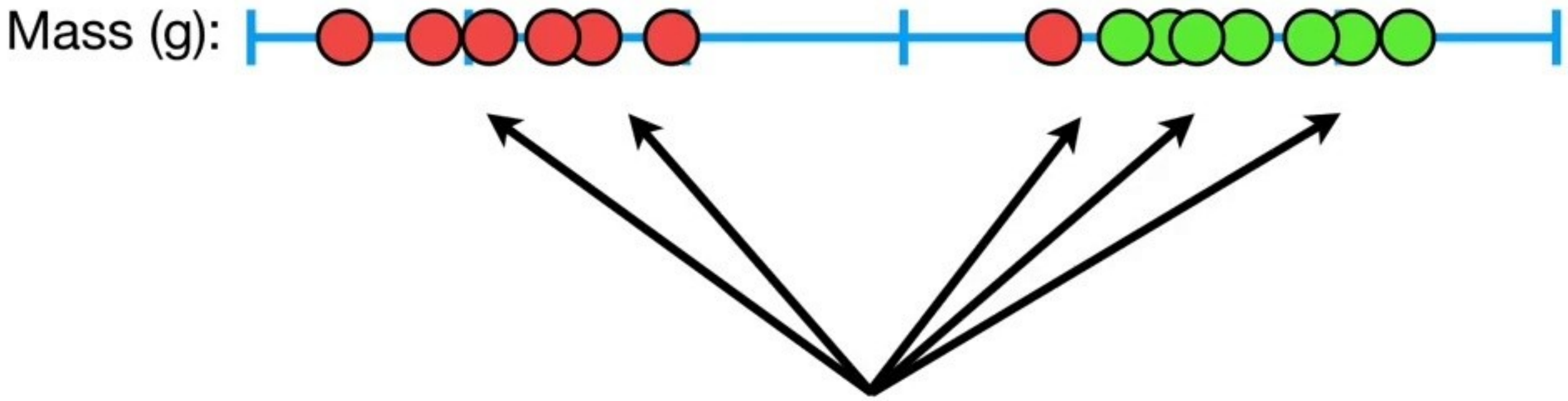
When we use the threshold that gives us the largest **margin** to make classifications…

(terminology alert!)

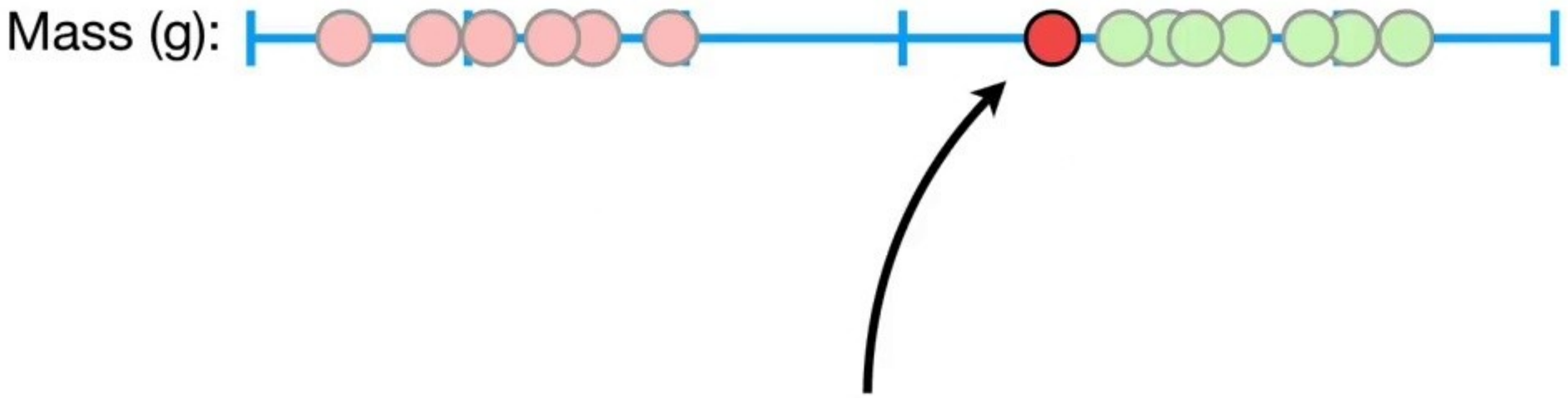

Mass (g):
…we are using a
Maximal Margin Classifier.

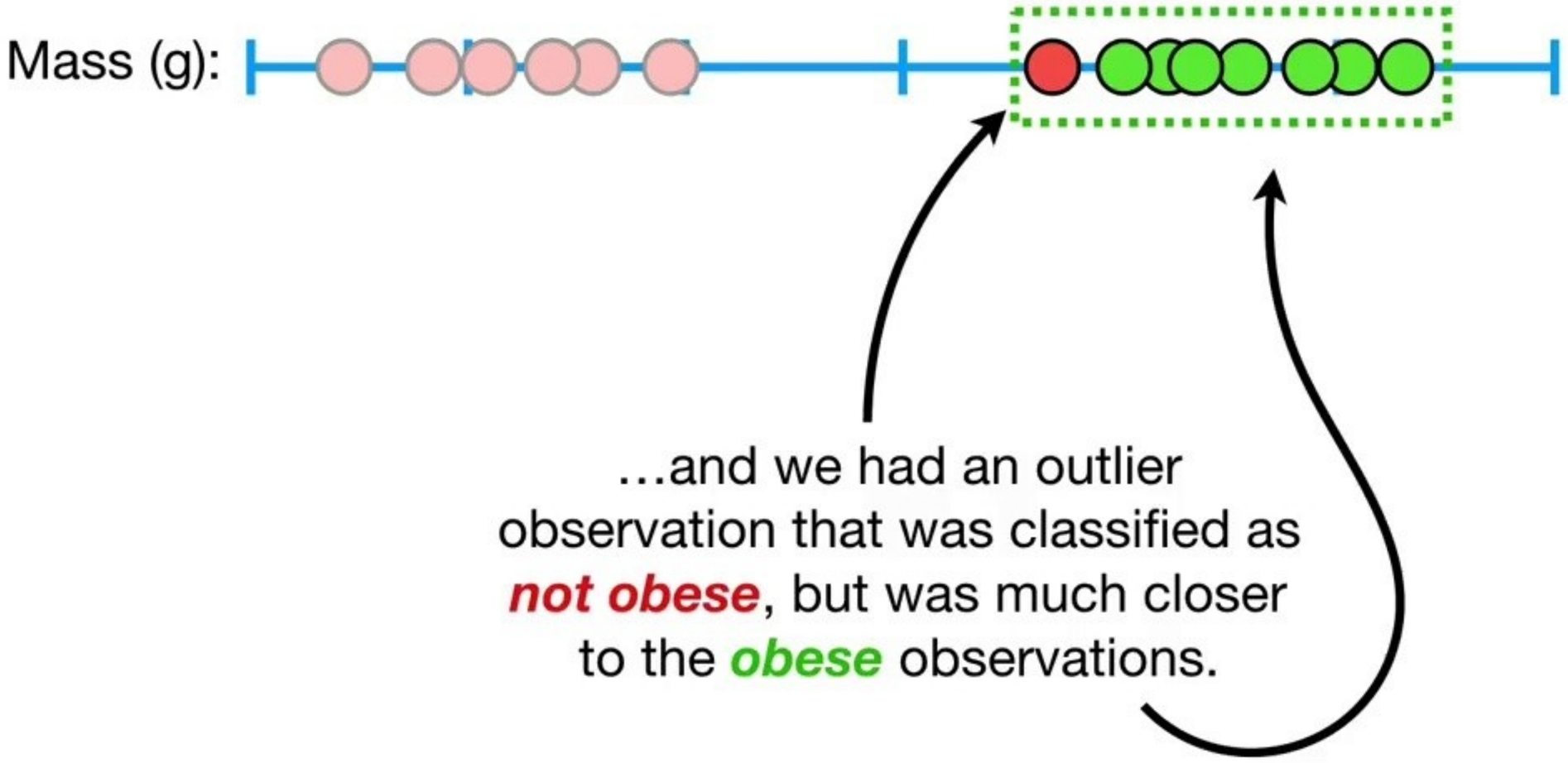


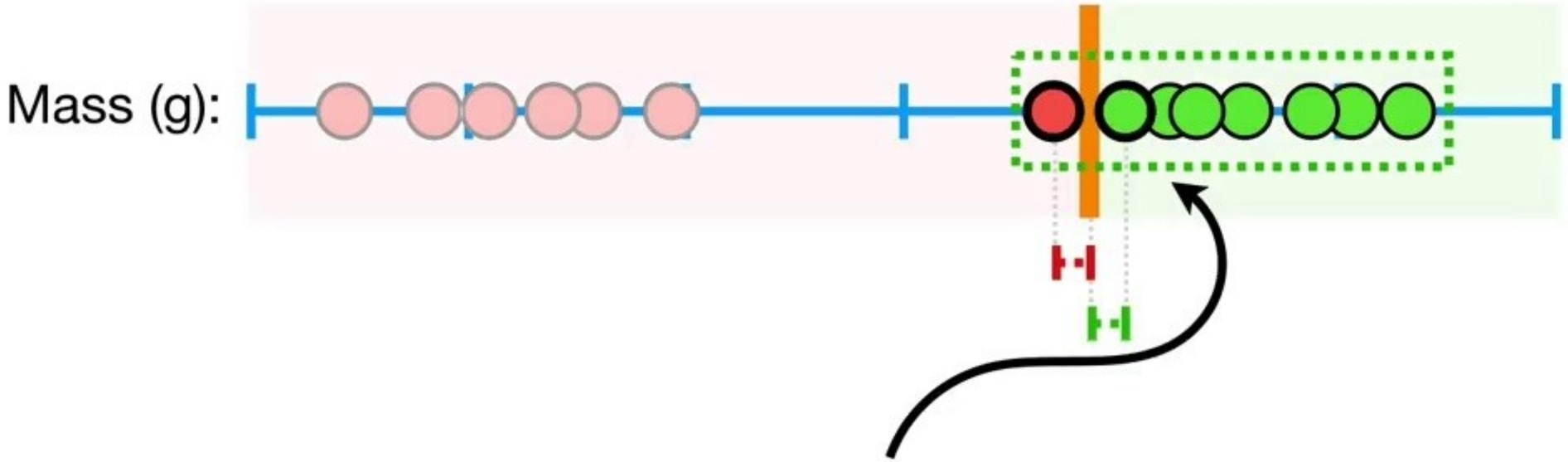
Maximal Margin Classifiers
seem pretty cool…



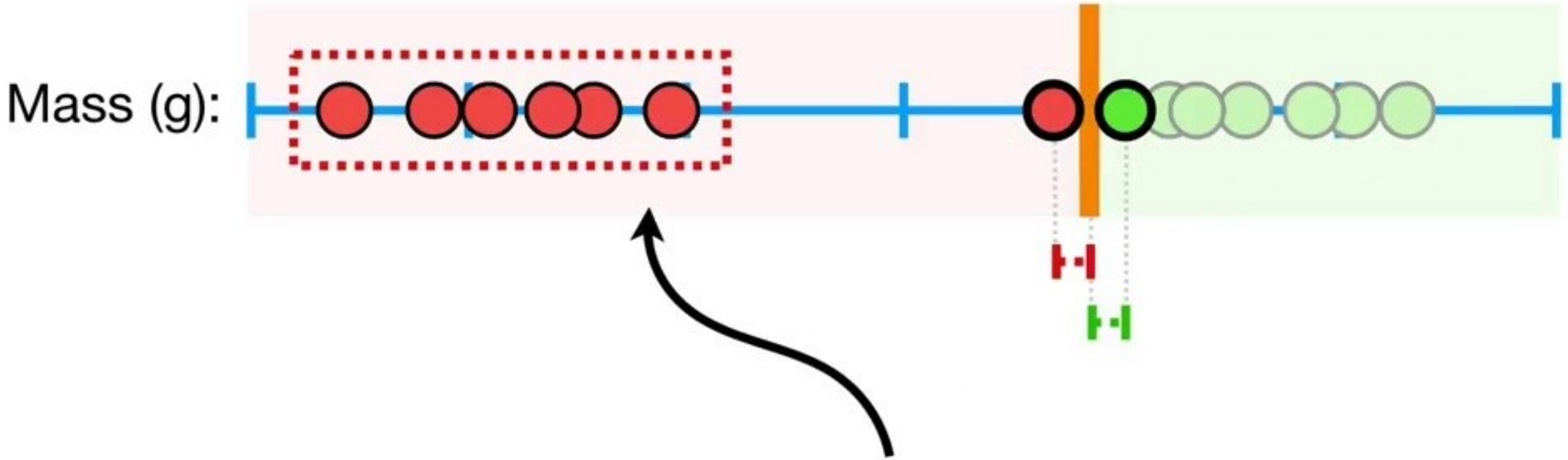
…but what if our training data looked like this….


Mass (g):
…and we had an outlier observation that was classified as not obese, but was much closer to the obese observations.

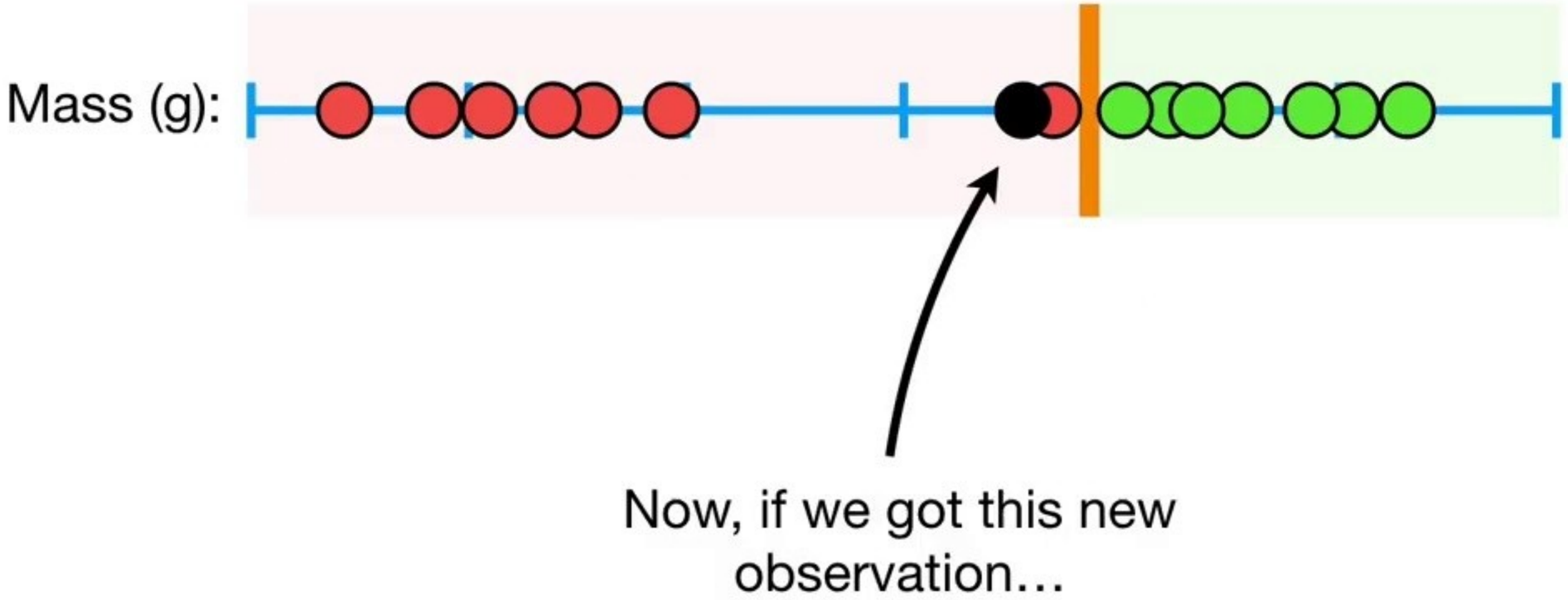

Mass (g):
…and we had an outlier observation that was classified as not obese, but was much closer to the obese observations.

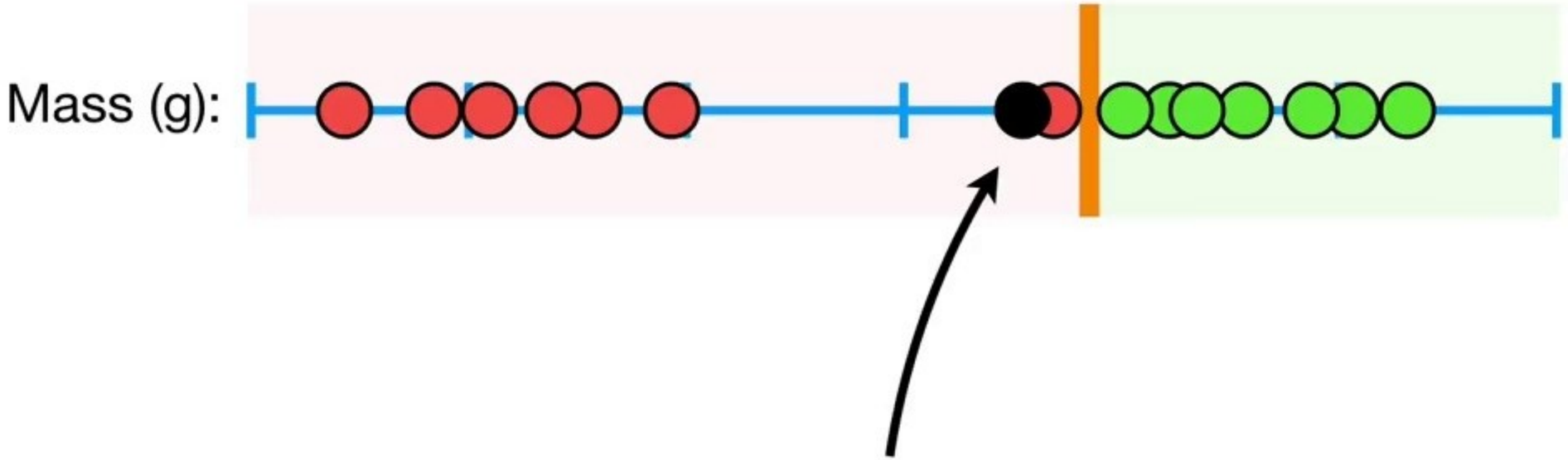


In this case, the **Maximum Margin Classifier** would be super close to the ***obese*** observations…

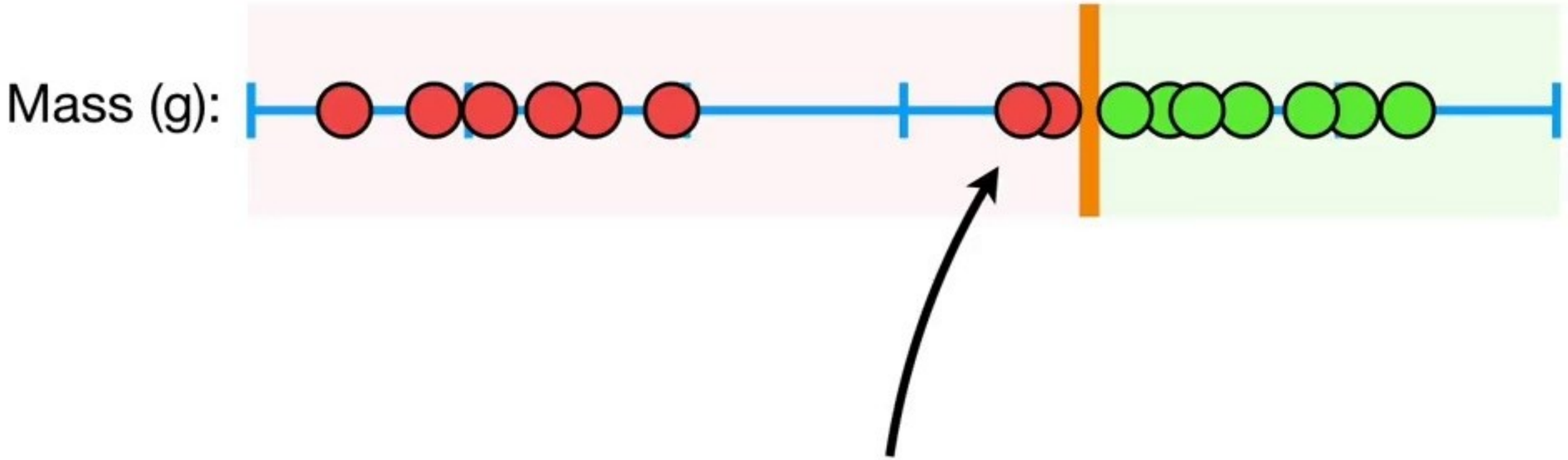


…and really far from the majority of the observations that are **not obese**.

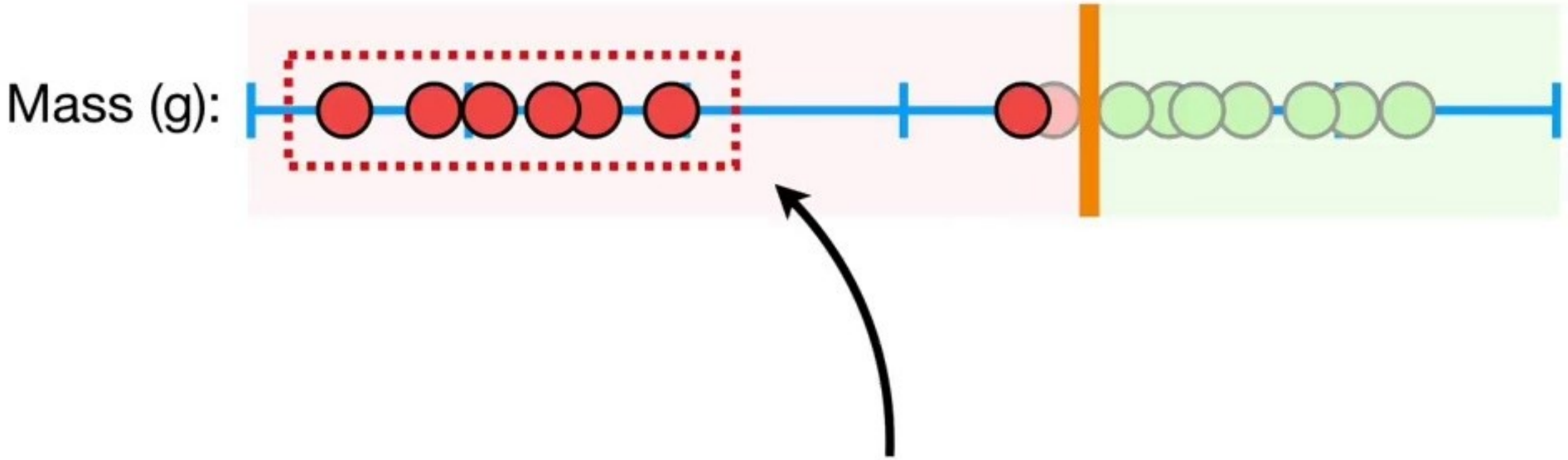

Mass (g):
Now, if we got this new observation…

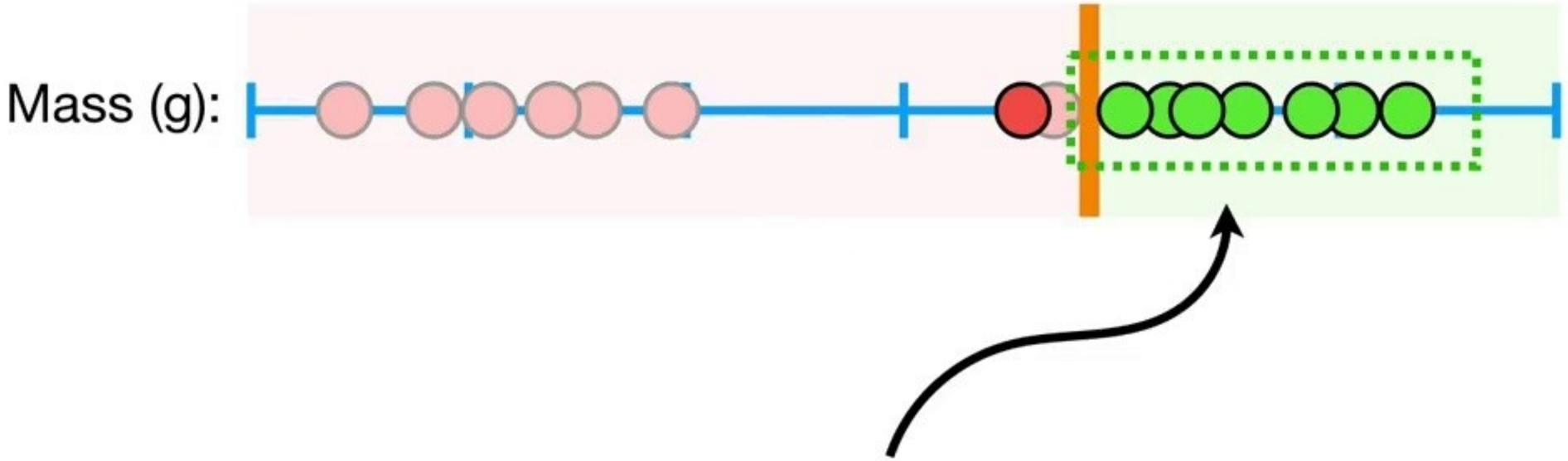


…we would classify it as ***not obese***, even though most of the ***not obese*** observations are much further away than the ***obese*** observations.

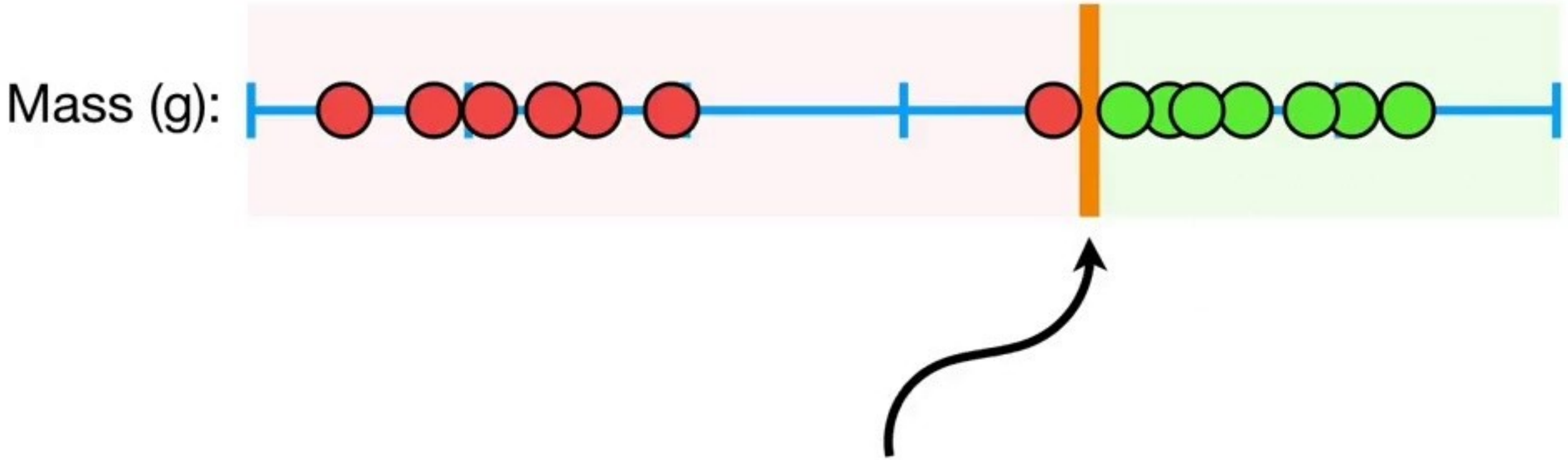


…we would classify it as ***not obese***, even though most of the ***not obese*** observations are much further away than the ***obese*** observations.

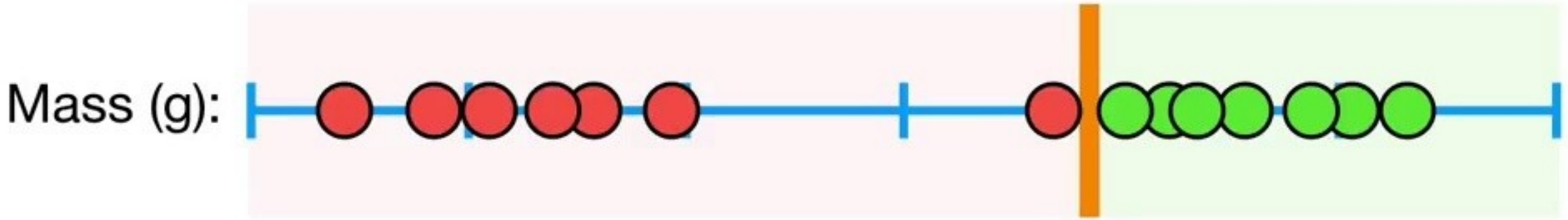

Mass (g):
…we would classify it as not obese, even though most of the not obese observations are much further away than the obese observations.



…we would classify it as ***not obese***, even though most of the ***not obese*** observations are much further away than the ***obese*** observations.



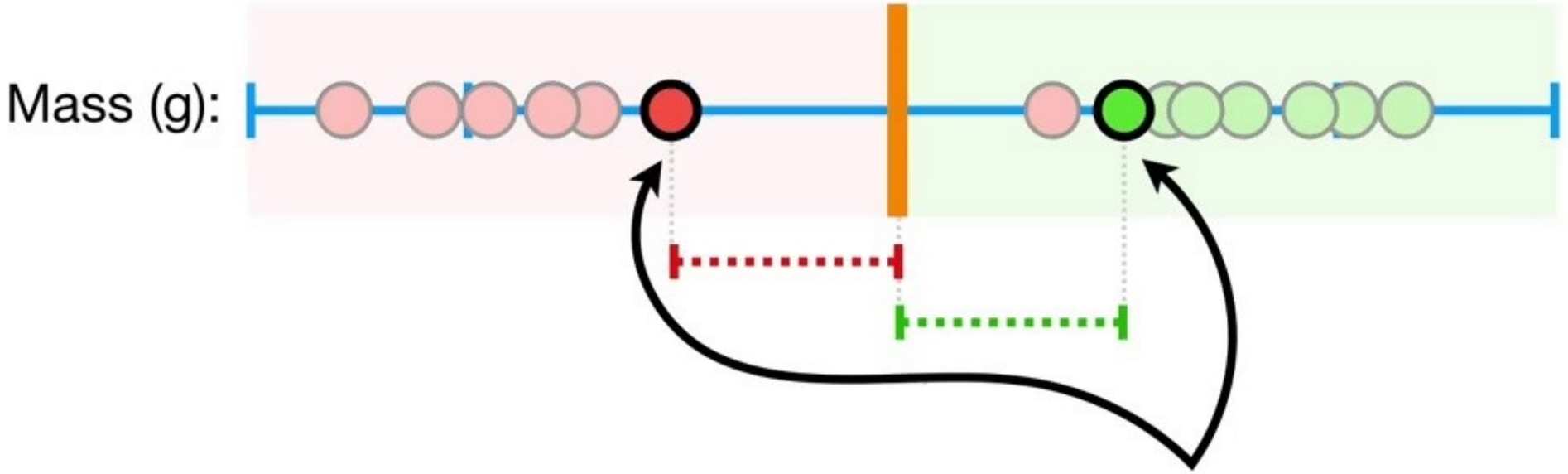
So **Maximal Margin Classifiers** are *super sensitive to outliers* in the training data and that makes them pretty lame.



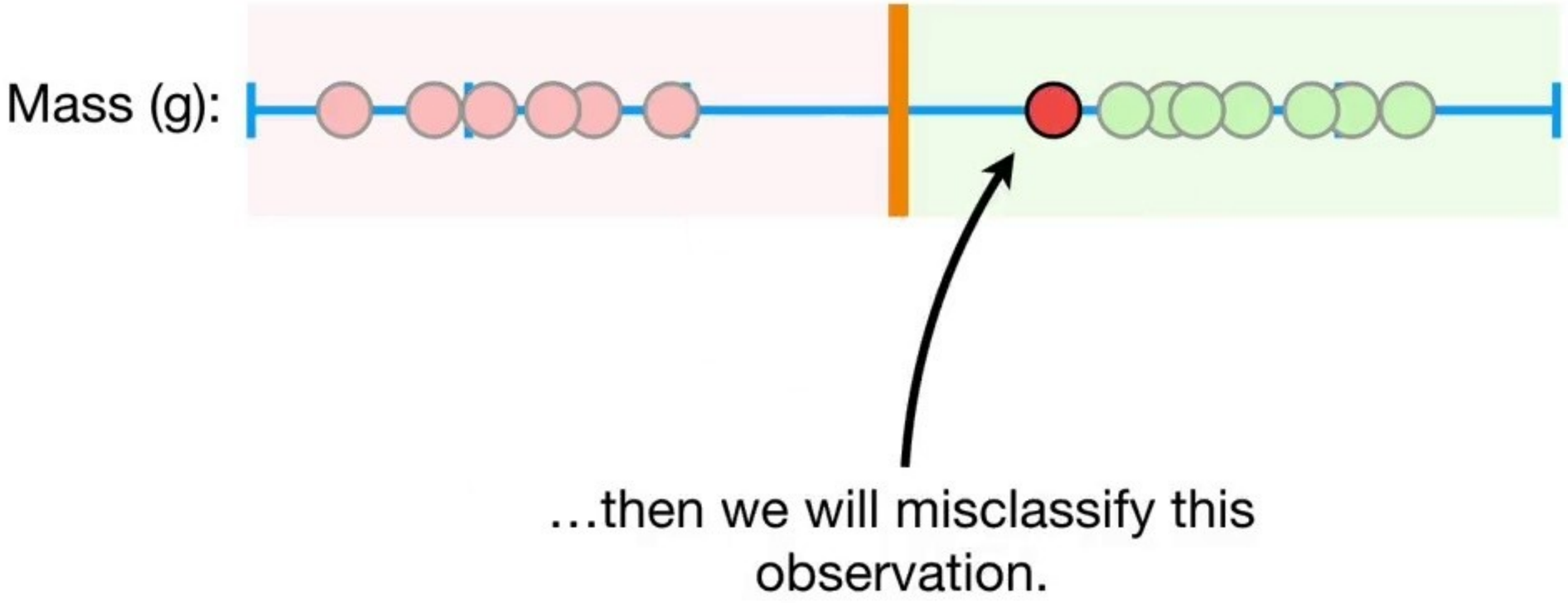
Can we do better?

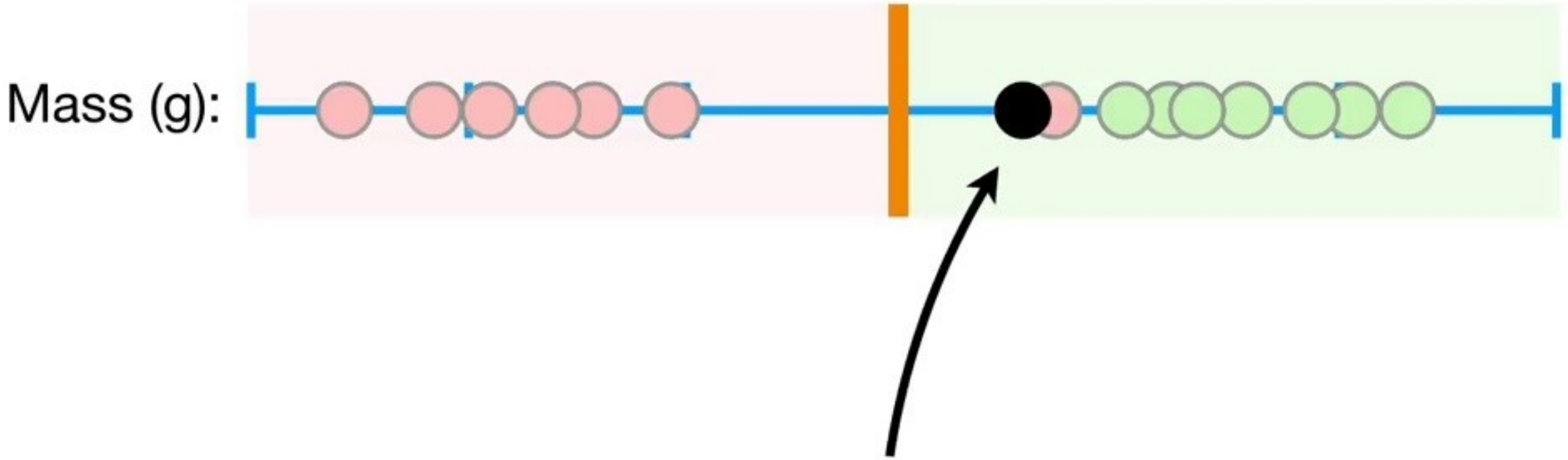
YES!!!

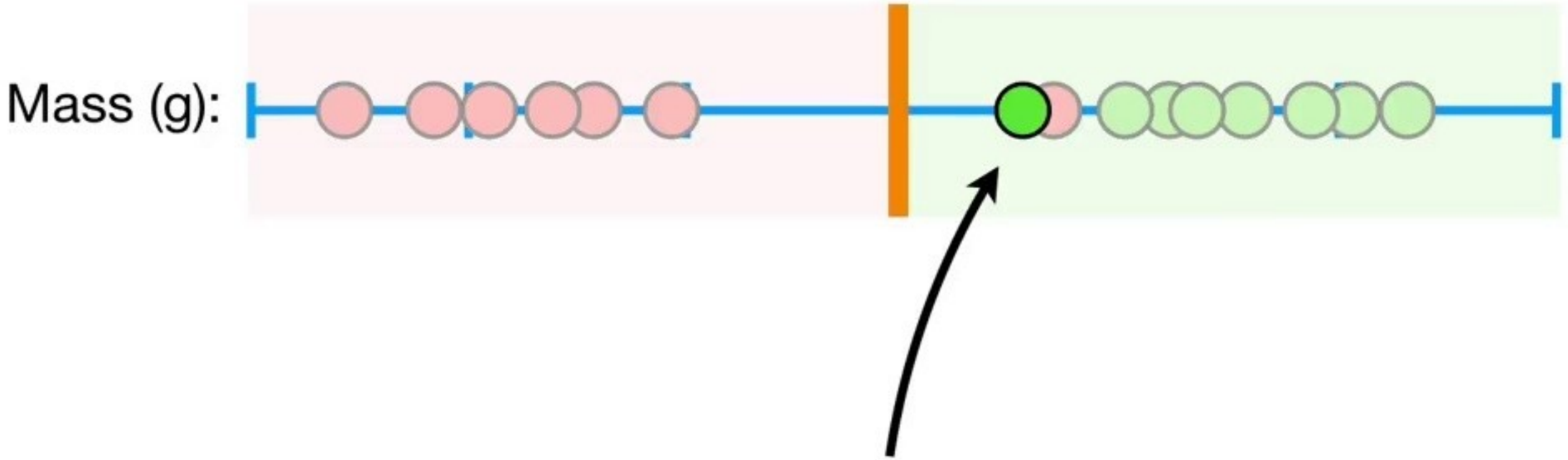
To make a threshold that is not so sensitive to outliers we must **allow misclassifications**.

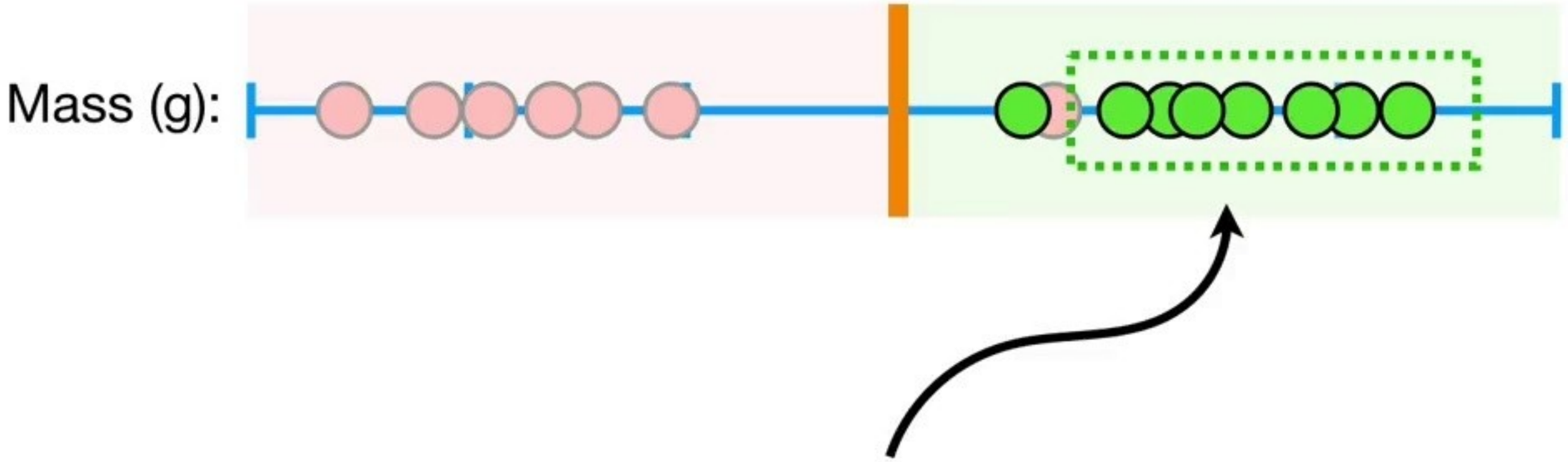


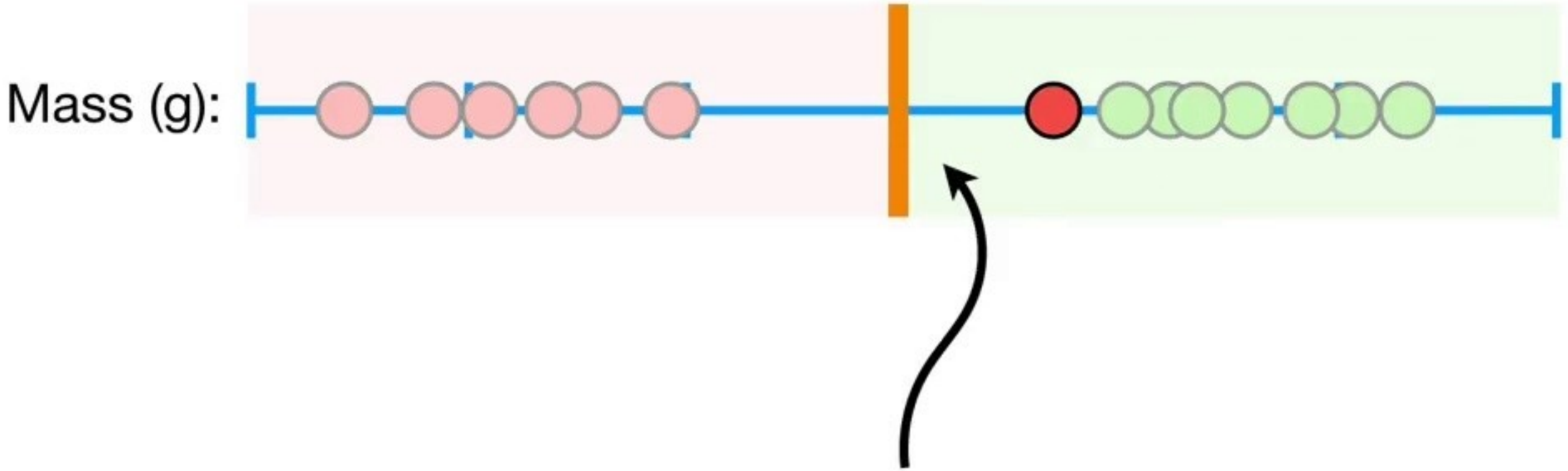
For example, if we put the threshold halfway between these two observations…


Mass (g):
…then we will misclassify this observation.

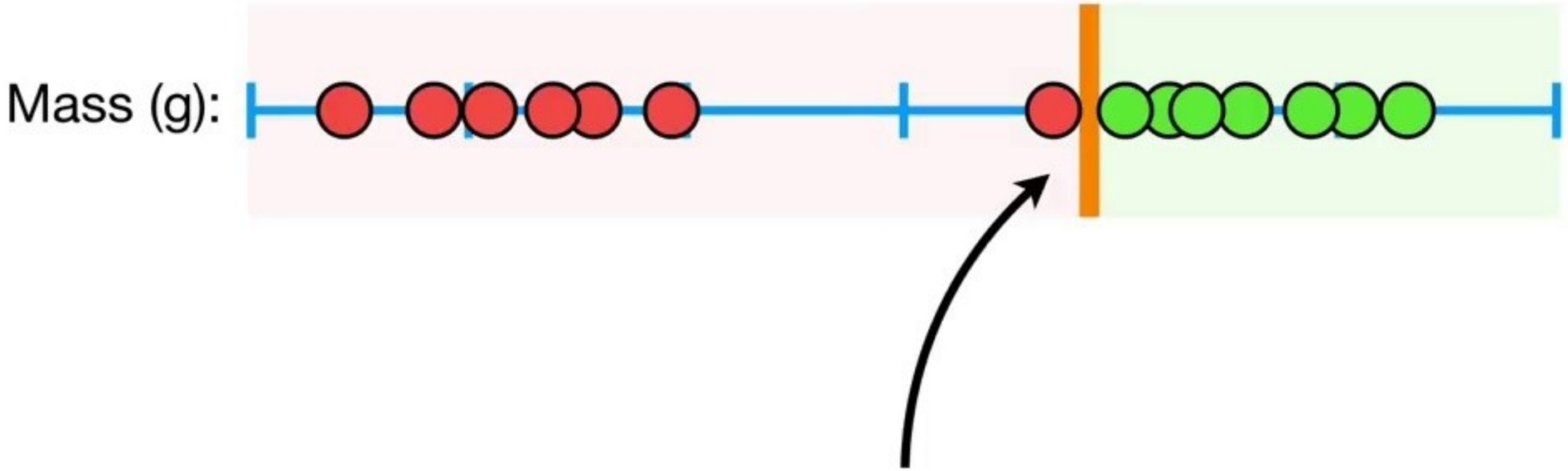

Mass (g):
However, now when we get a
new observation here…


Mass (g):
…we will classify it as *obese*…

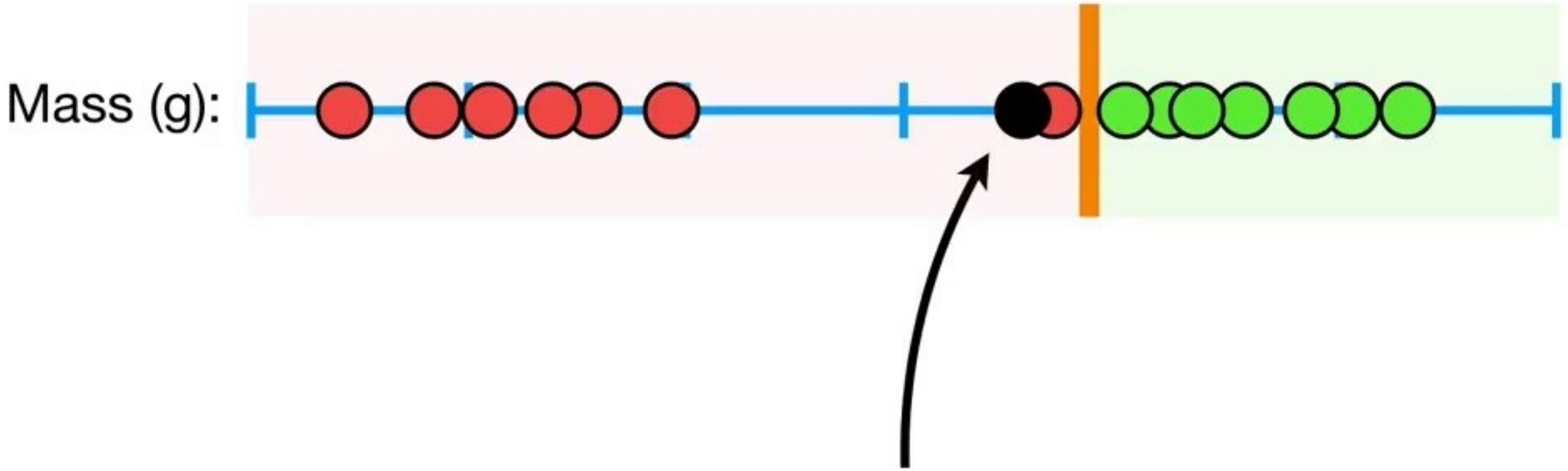

Mass (g):
…and that makes sense
because it is closer to most of
the obese observations.

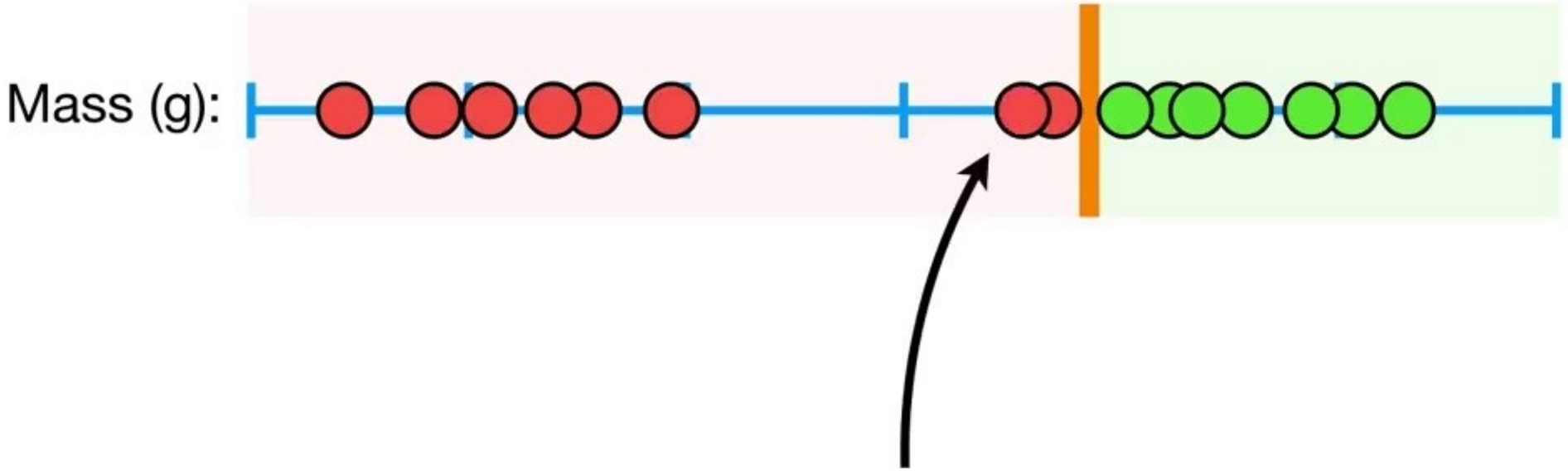


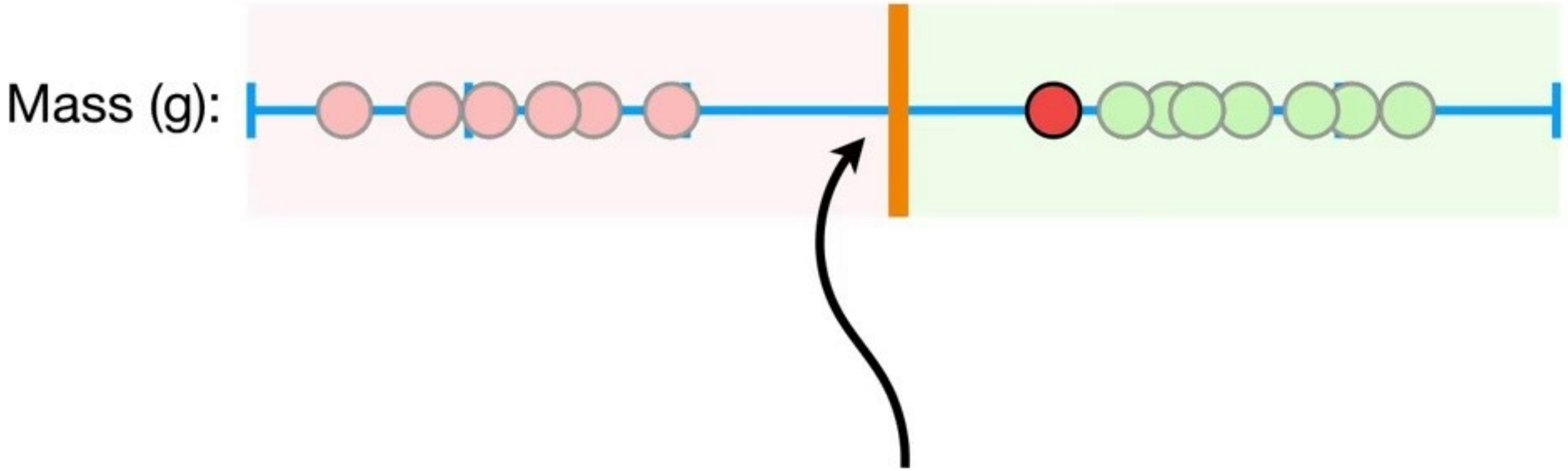
Choosing a threshold that allows misclassifications is an example of the **Bias/Variance Tradeoff** that plagues all of machine learning.



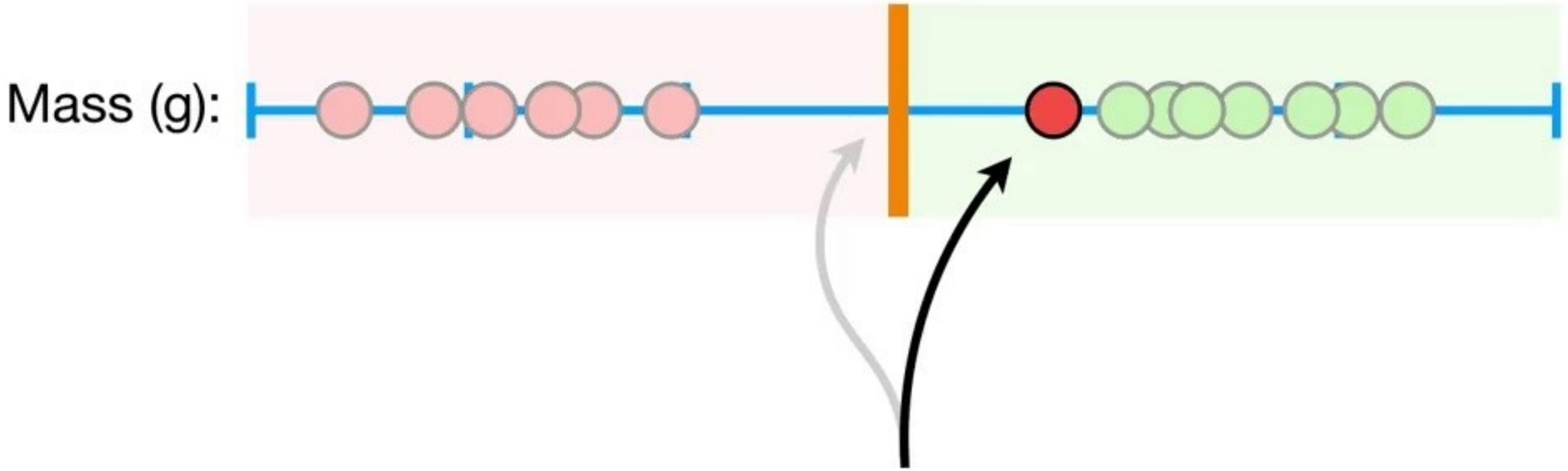
In other words, before we allowed misclassifications, we picked a threshold that was very sensitive to the training data (low bias)…


Mass (g):
…and it performed poorly when
we got new data (high variance).

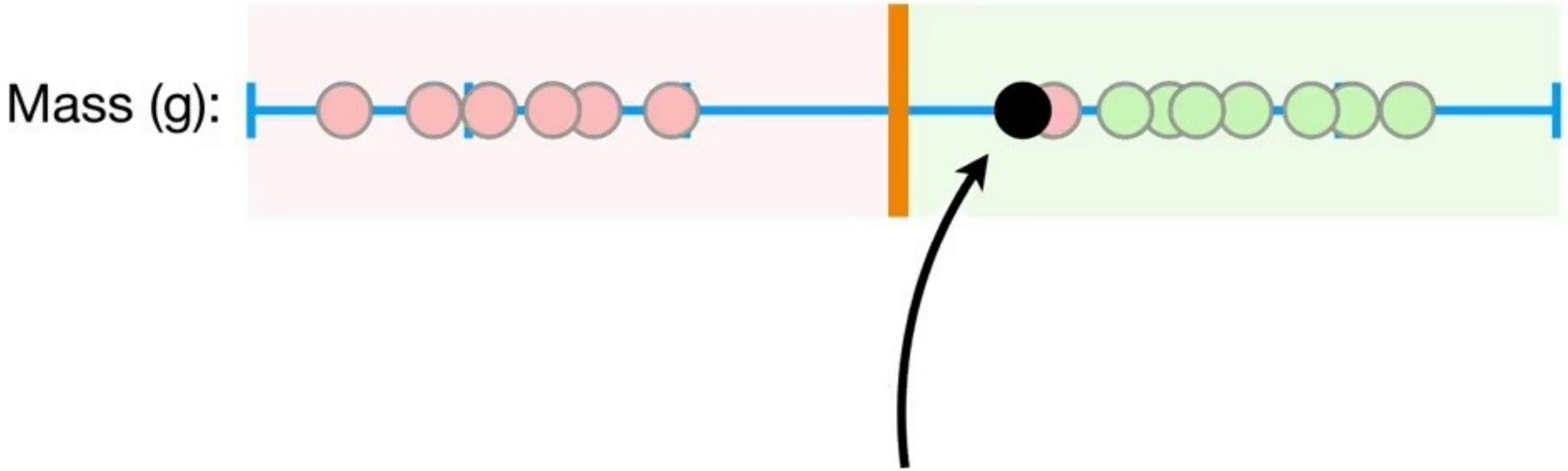

Mass (g):
…and it performed poorly when
we got new data (high variance).

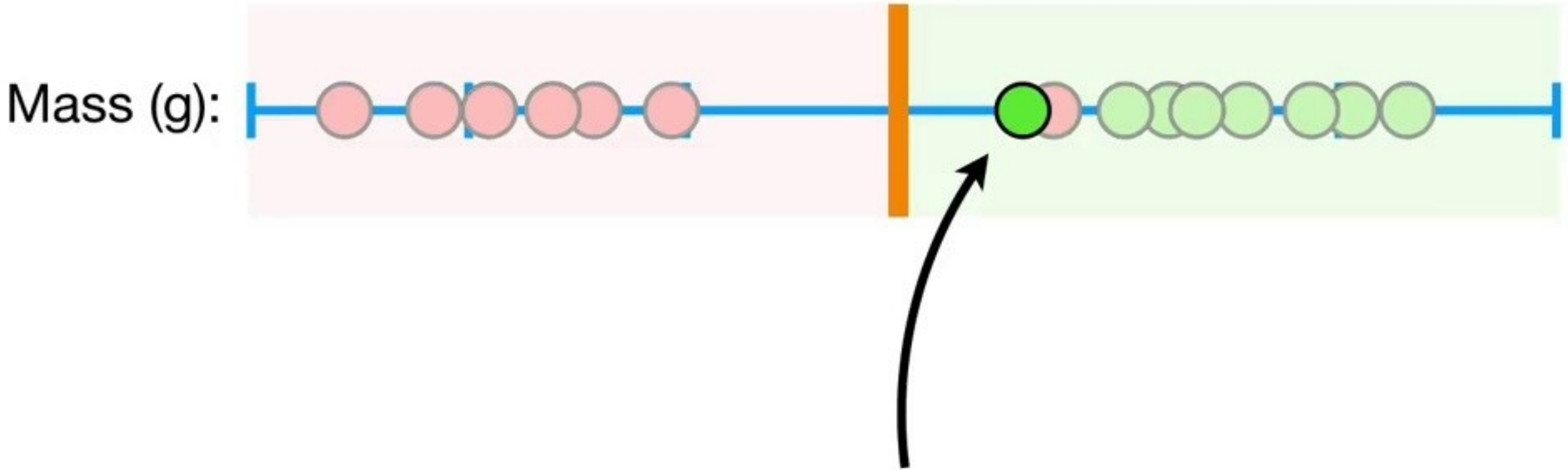


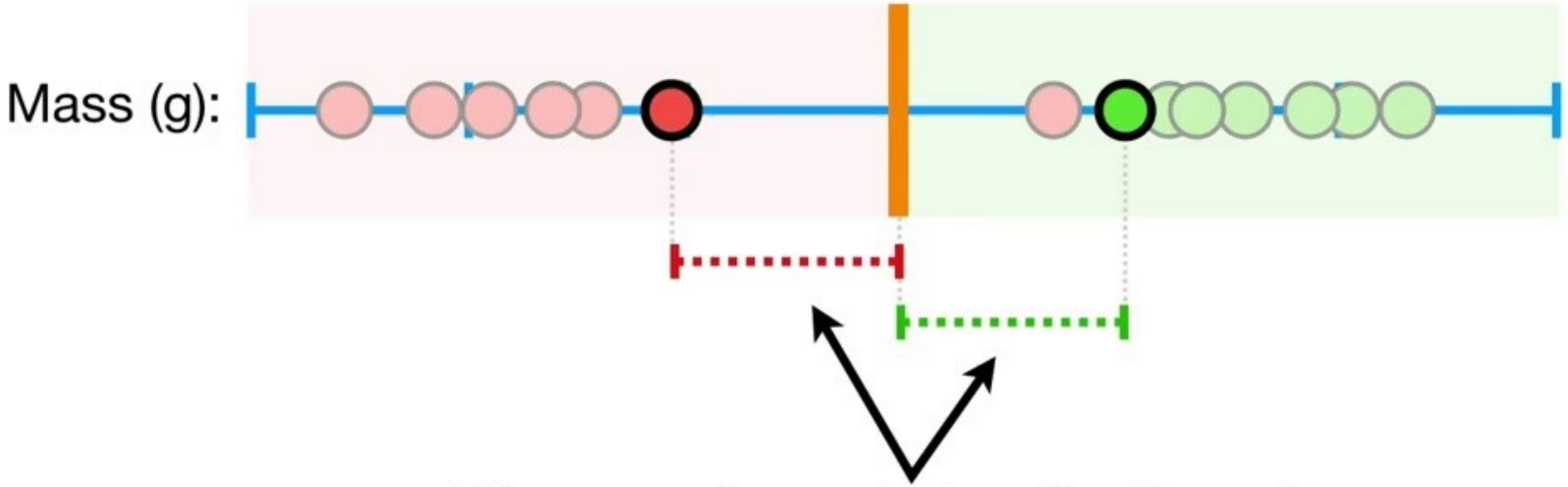
In contrast, when we picked a threshold that was less sensitive to the training data and allowed misclassifications (higher bias)…



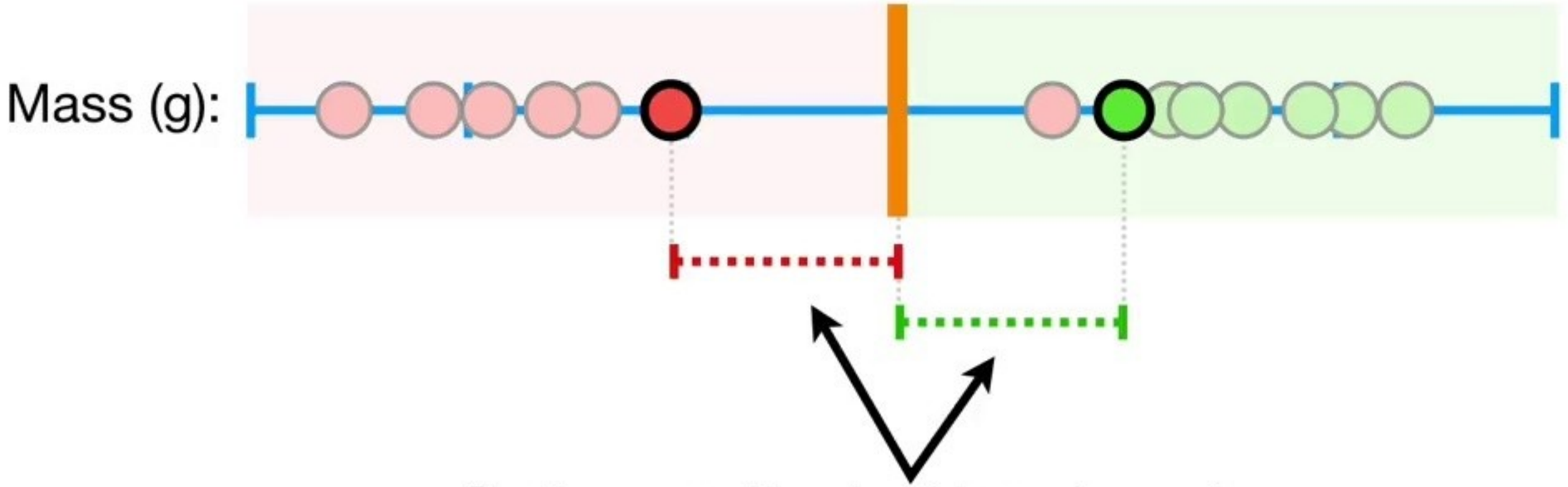
In contrast, when we picked a threshold that was less sensitive to the training data and allowed misclassifications (higher bias)…


Mass (g):
…it performed better when we got
new data (low variance).

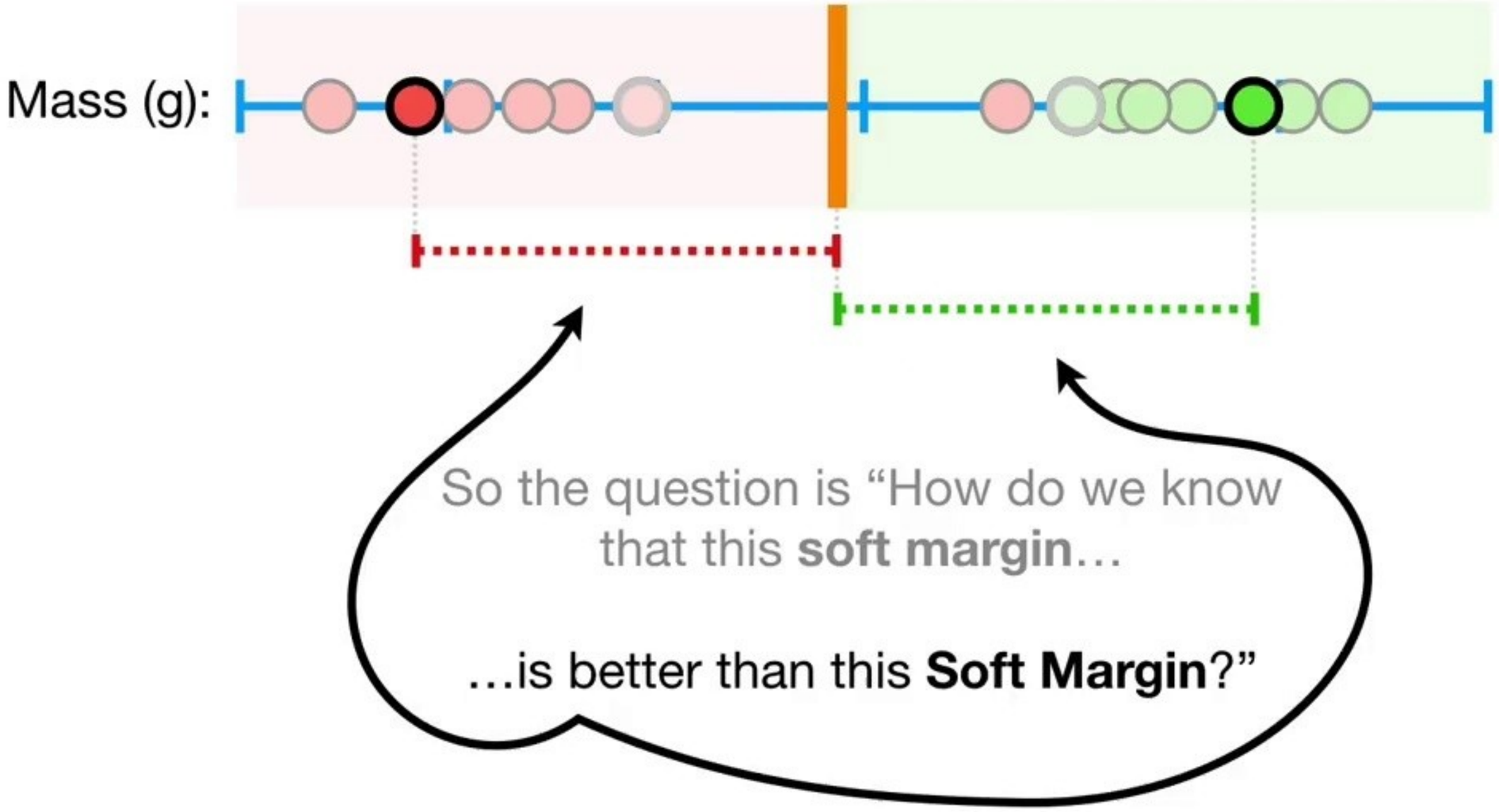

Mass (g):
…it performed better when we got
new data (low variance).

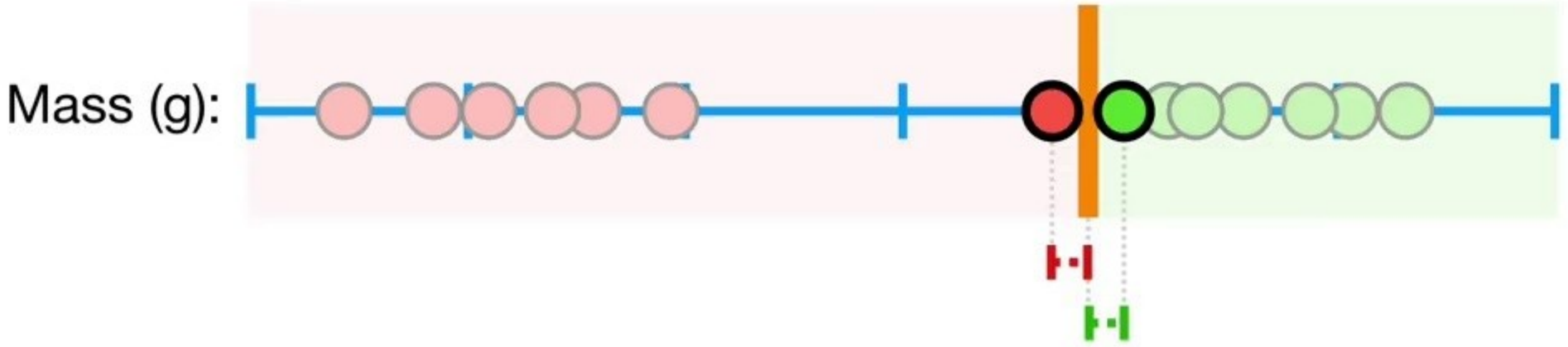


When we allow misclassifications, the distance between the observations and the threshold is called a **Soft Margin**.

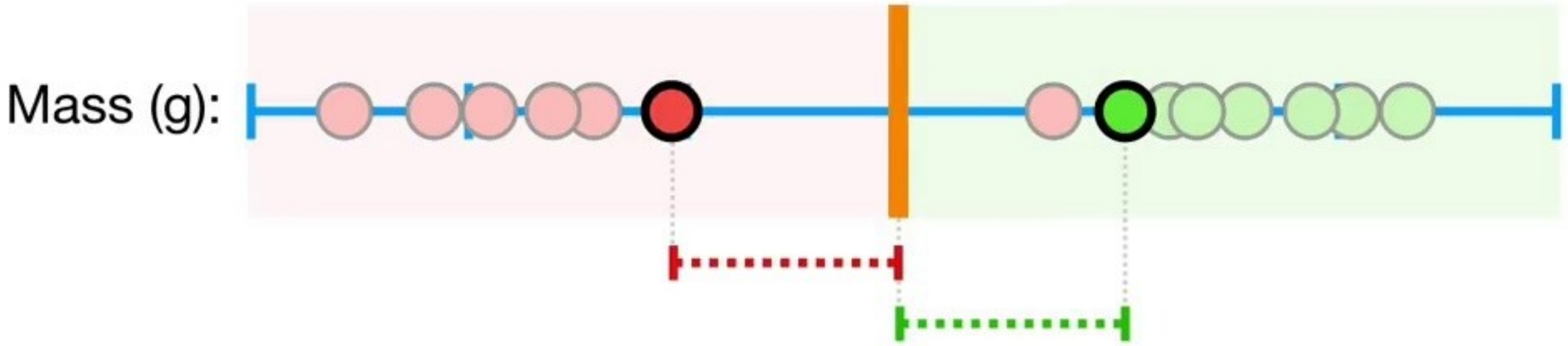


So the question is “How do we know that this **soft margin**…


Mass (g):
So the question is “How do we know that this **soft margin**…
…is better than this **Soft Margin**?”



The answer is simple: We use **Cross Validation** to determine how many misclassifications and observations to allow inside of the **Soft Margin** to get the best classification.



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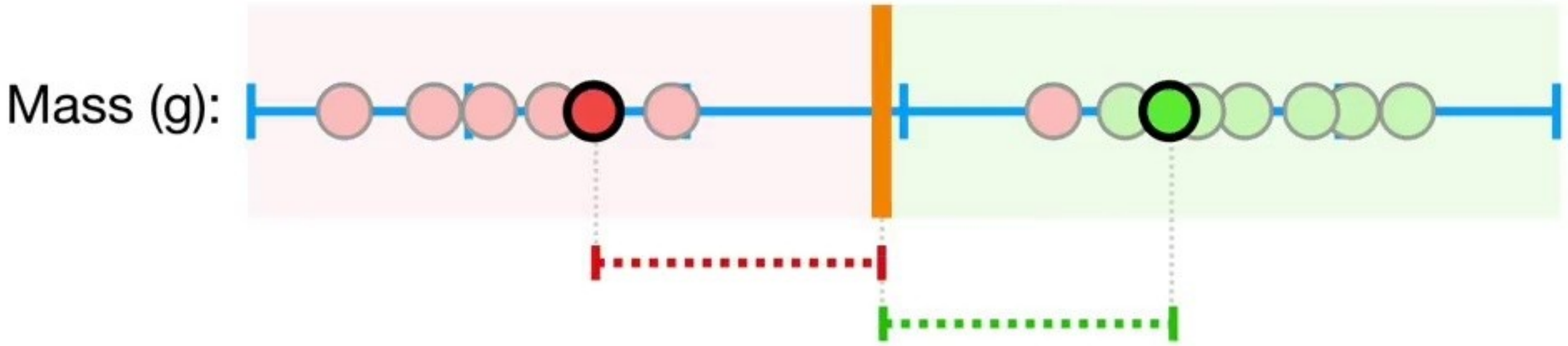

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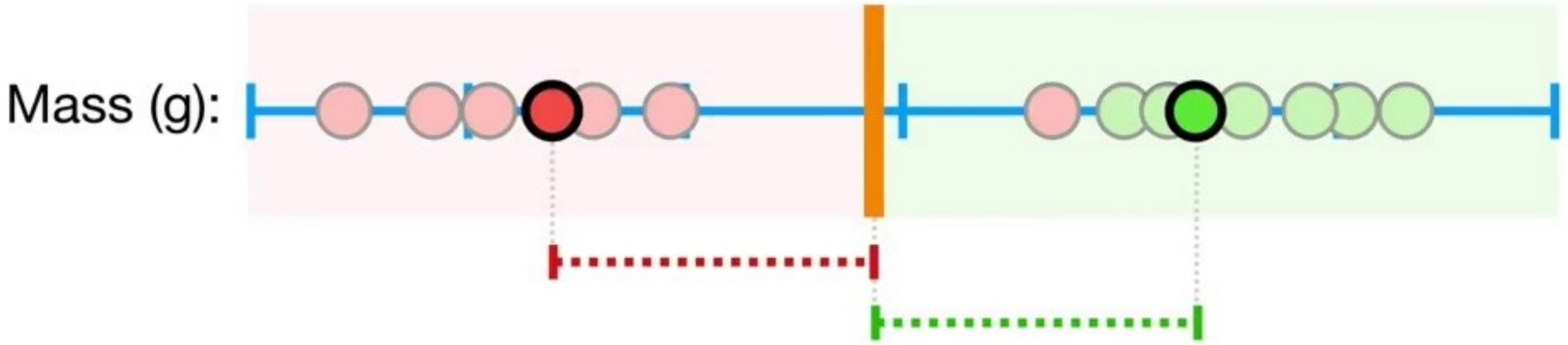

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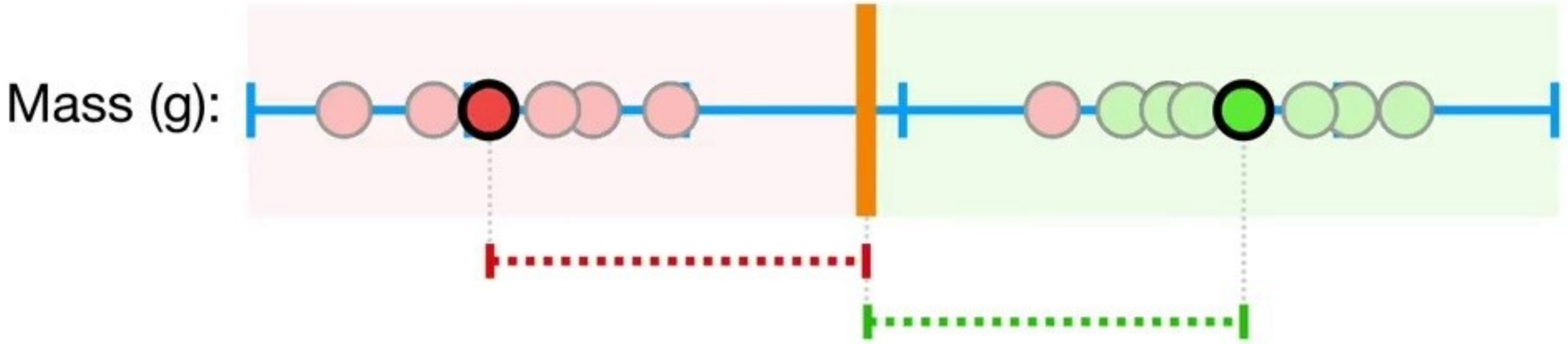

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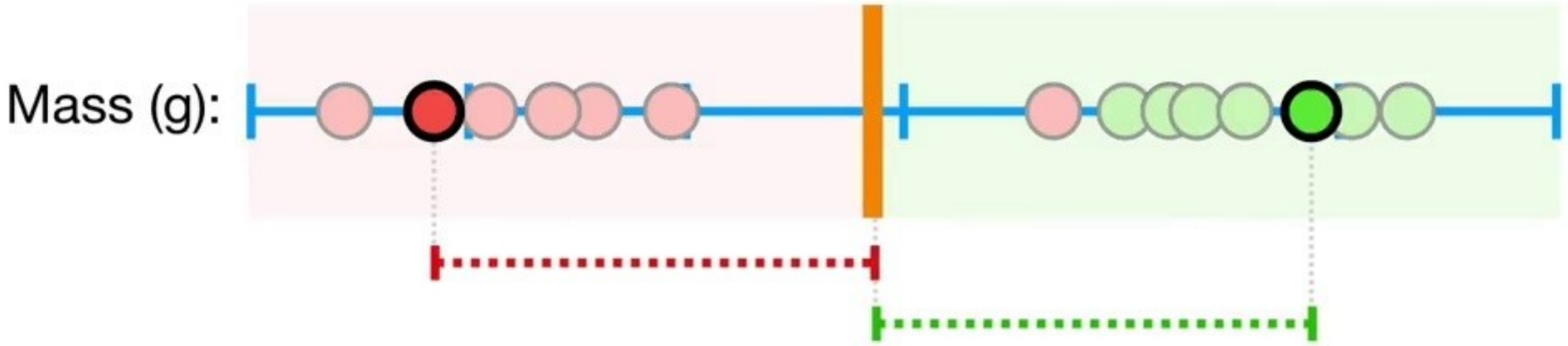
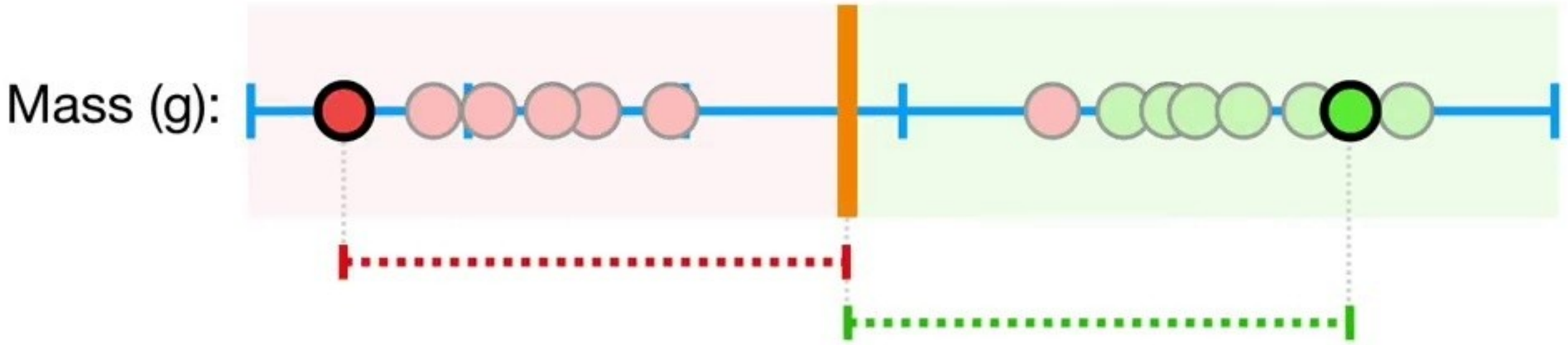
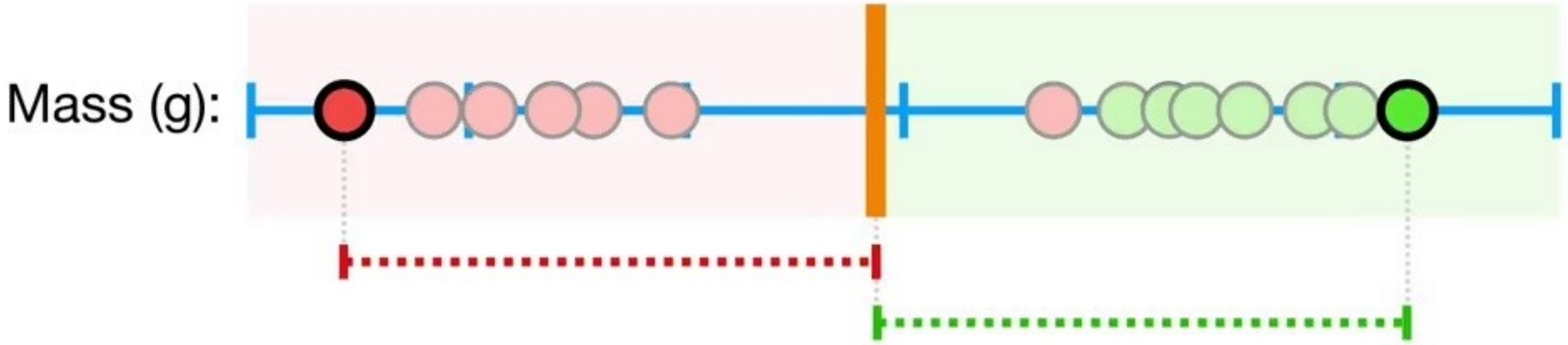


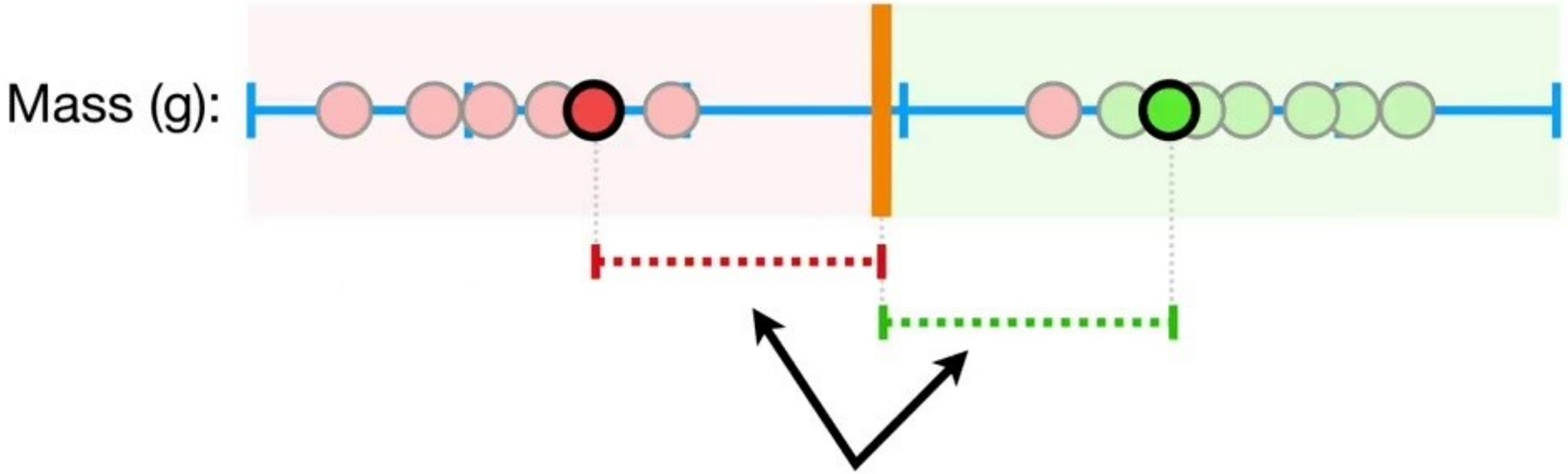
The answer is simple: We use **Cross Validation** to determine how many misclassifications and observations to allow inside of the **Soft Margin** to get the best classification.



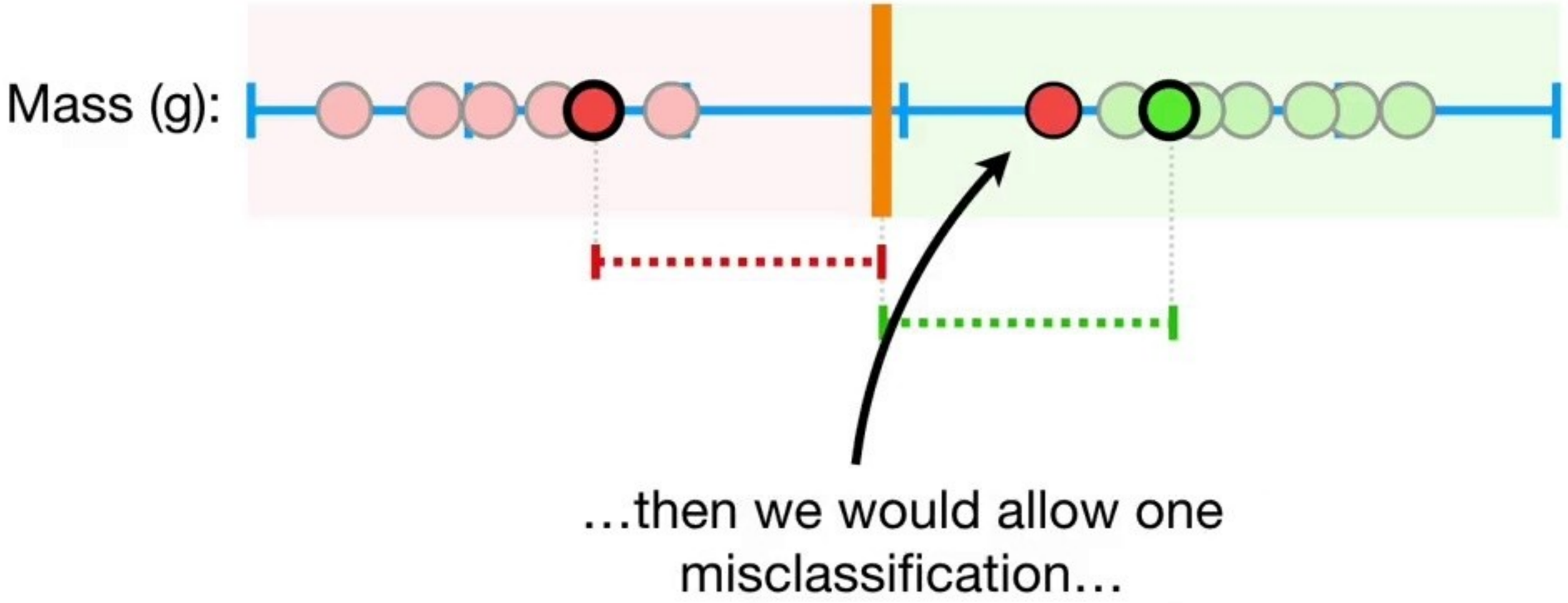
The answer is simple: We use **Cross Validation** to determine how many misclassifications and observations to allow inside of the **Soft Margin** to get the best classification.

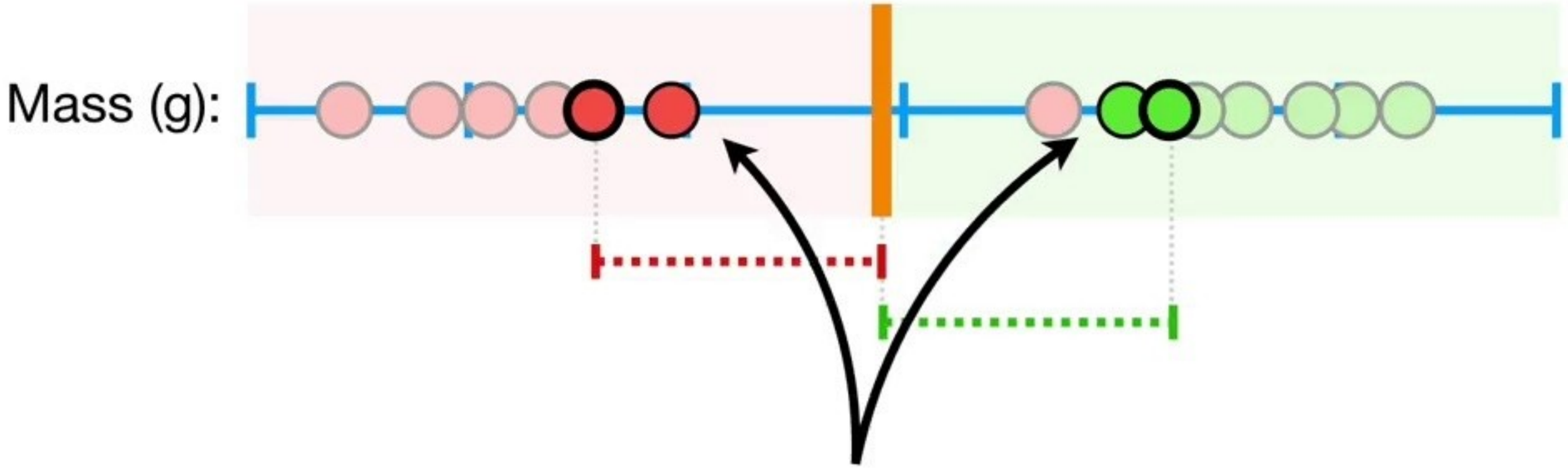


The answer is simple: We use **Cross Validation** to determine how many misclassifications and observations to allow inside of the **Soft Margin** to get the best classification.

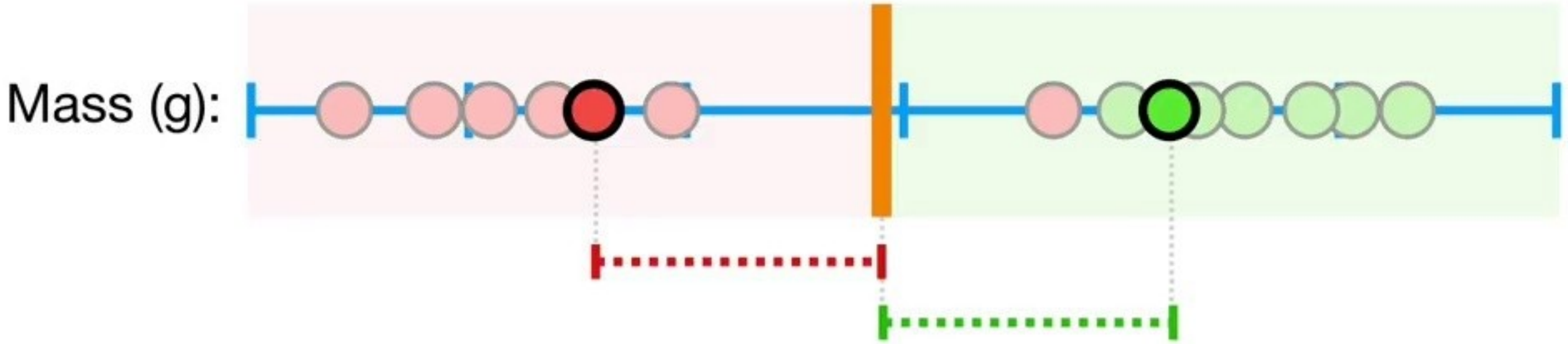


For example, if **Cross Validation** determined that this was the best **Soft Margin**…

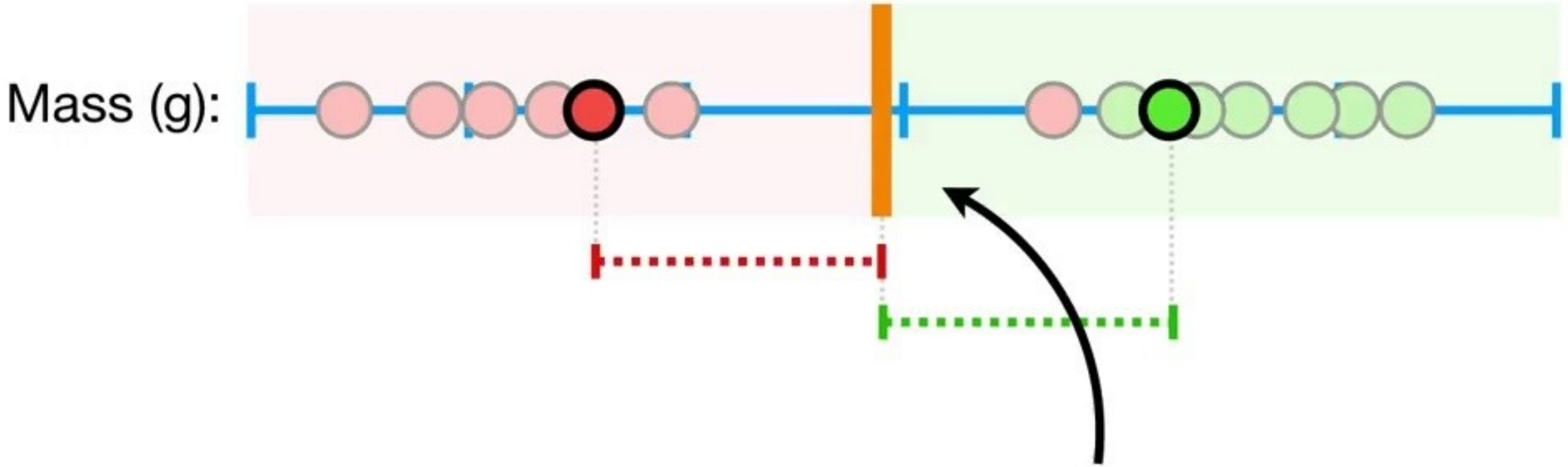

Mass (g):
…then we would allow one misclassification…



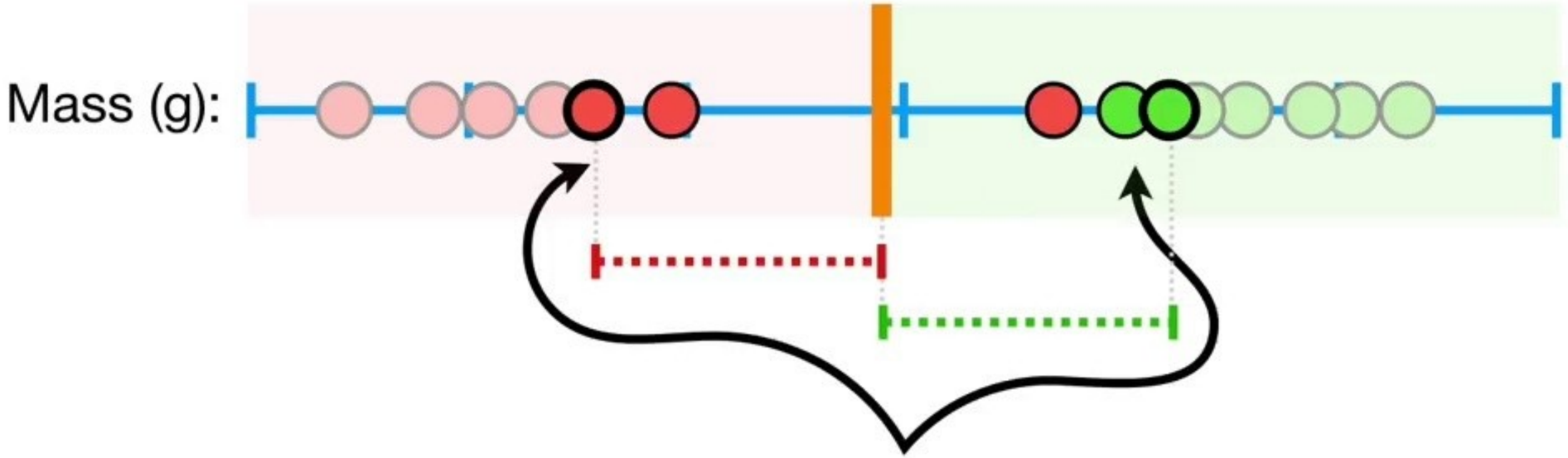
…and two observations, that are correctly classified, to be within the **Soft Margin**.



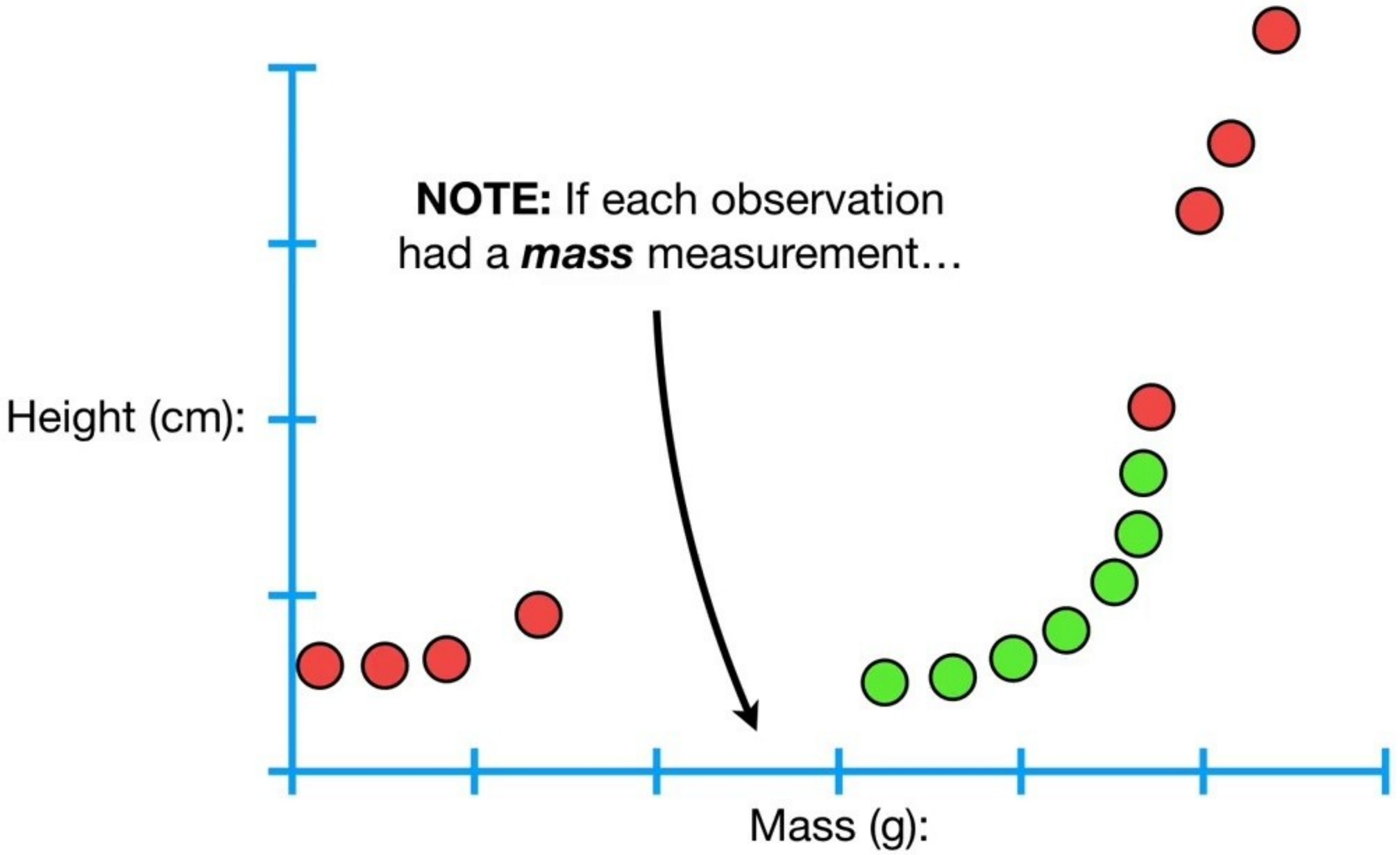
When we use a **Soft Margin** to determine the location of a threshold…

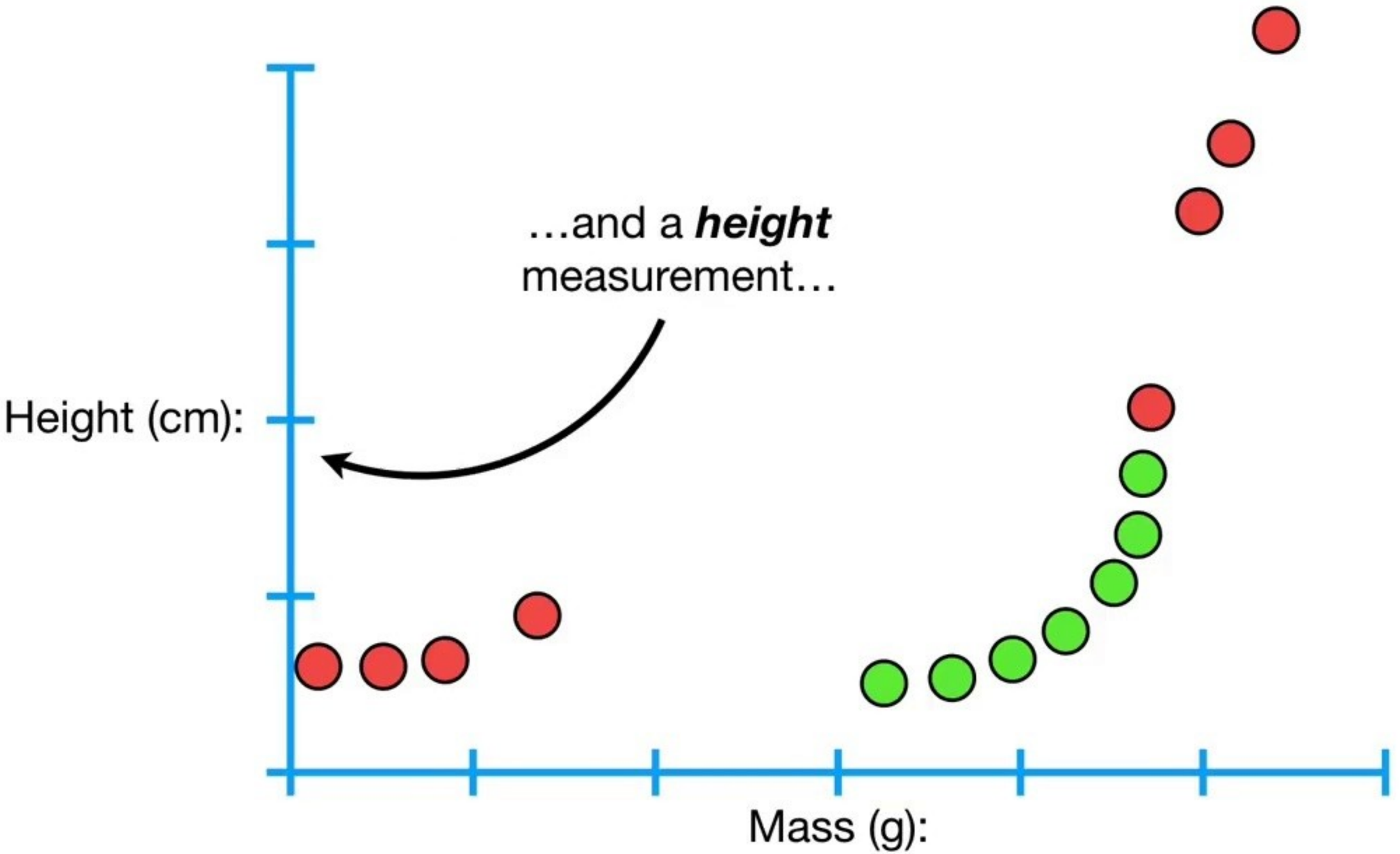


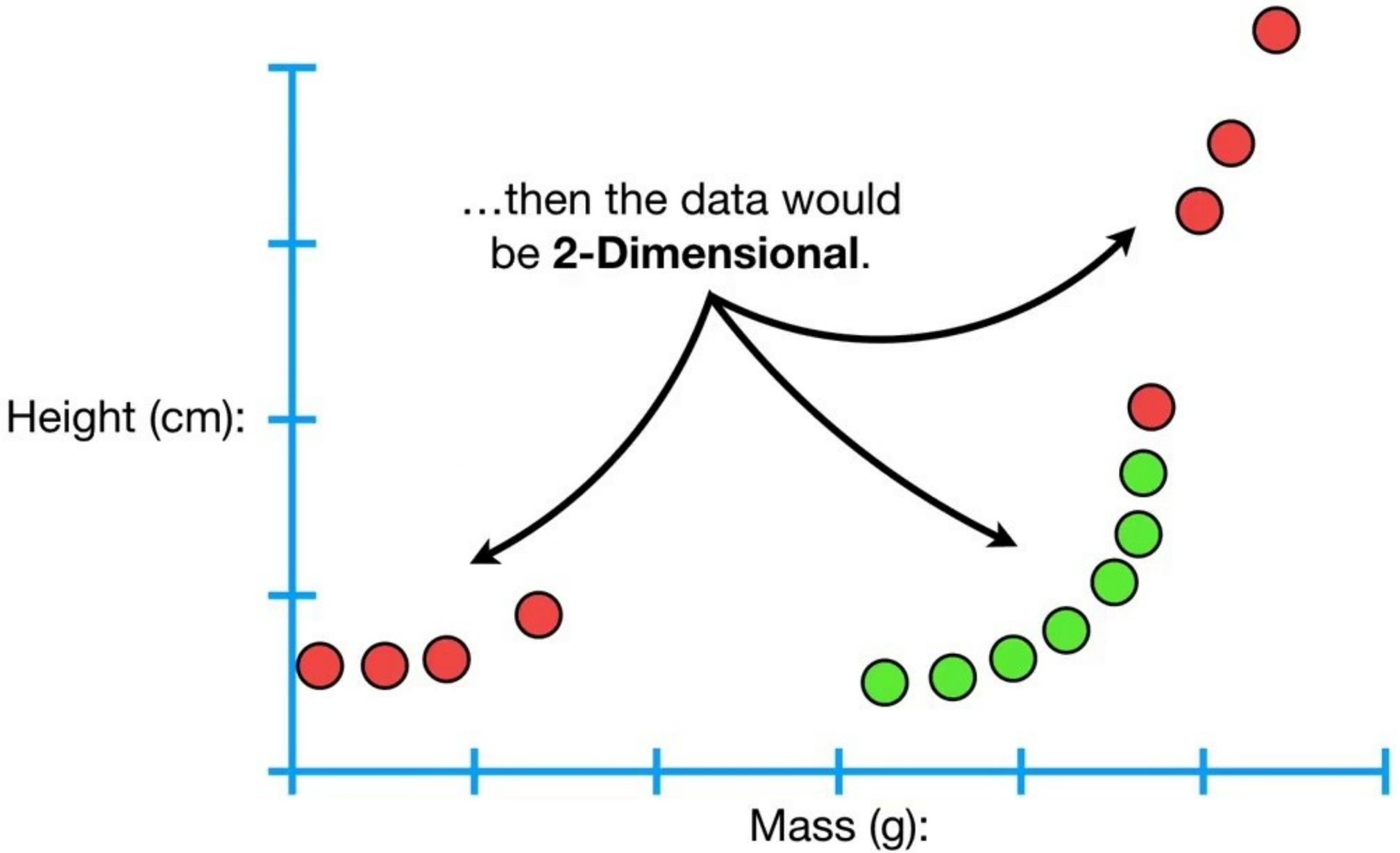
…then we are using a **Soft Margin Classifier** aka a **Support Vector Classifier** to classify observations.

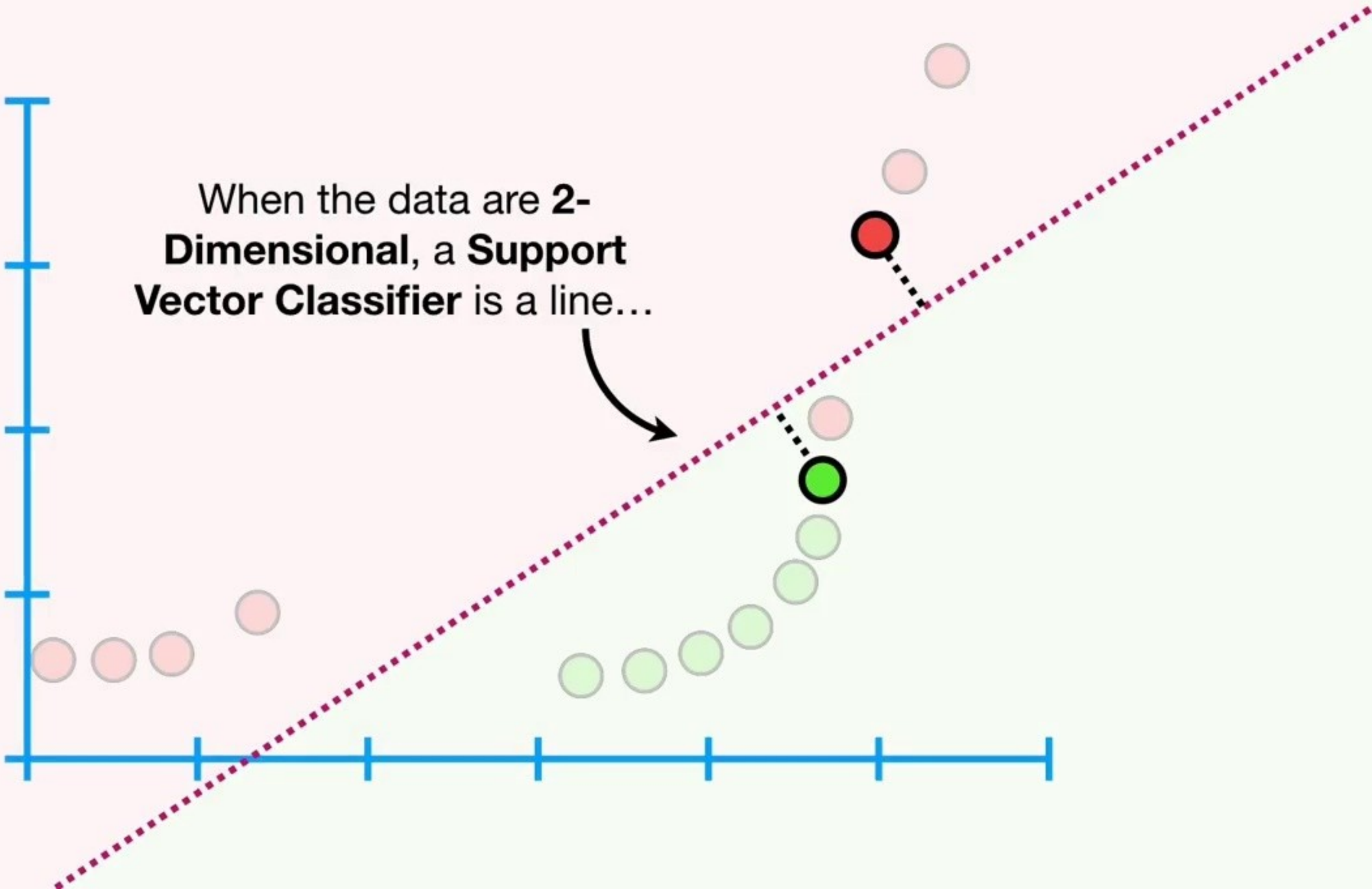


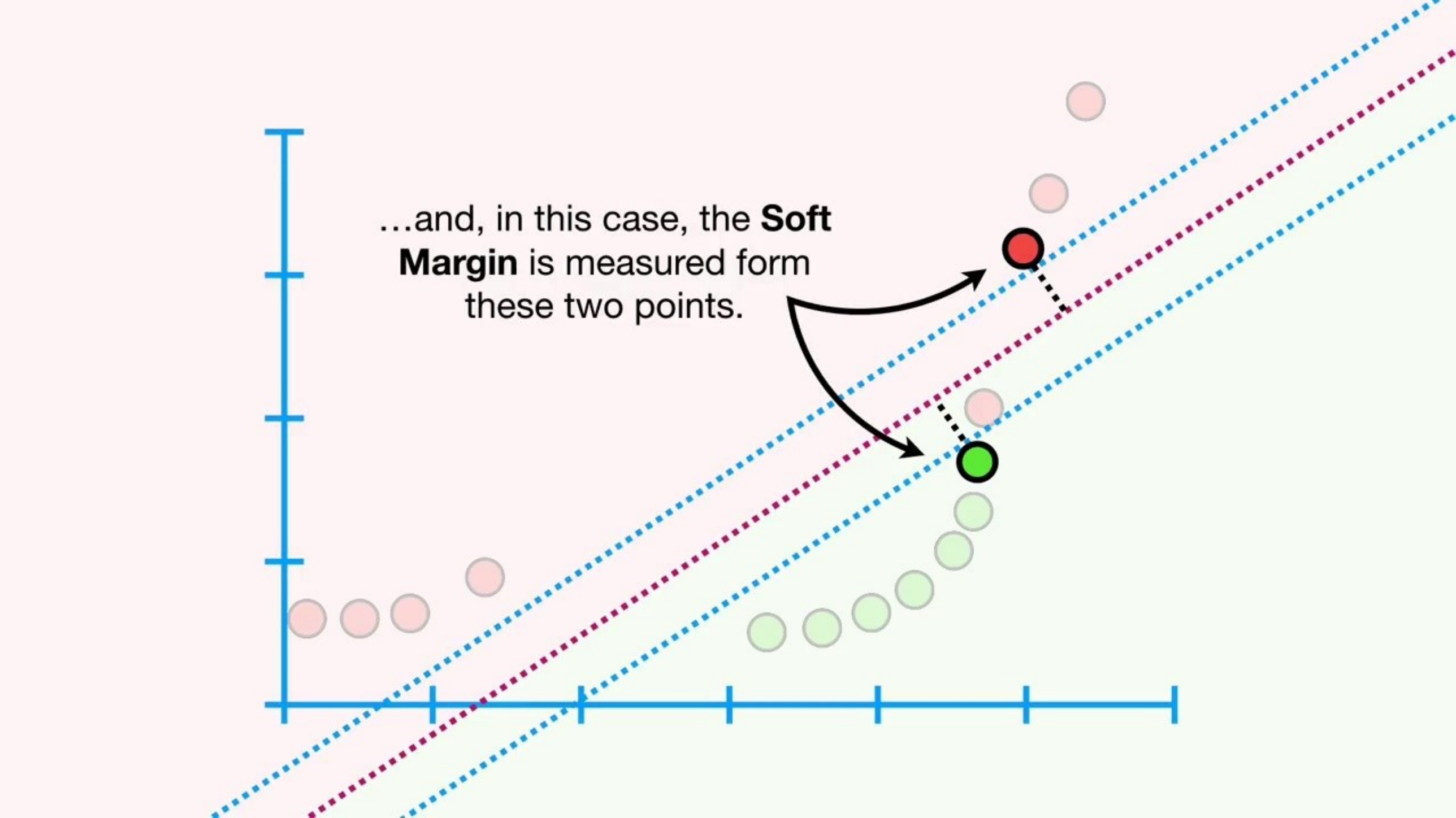
The name **Support Vector Classifier** comes from the fact that the observations on the edge *and within* the **Soft Margin** are called **Support Vectors**.

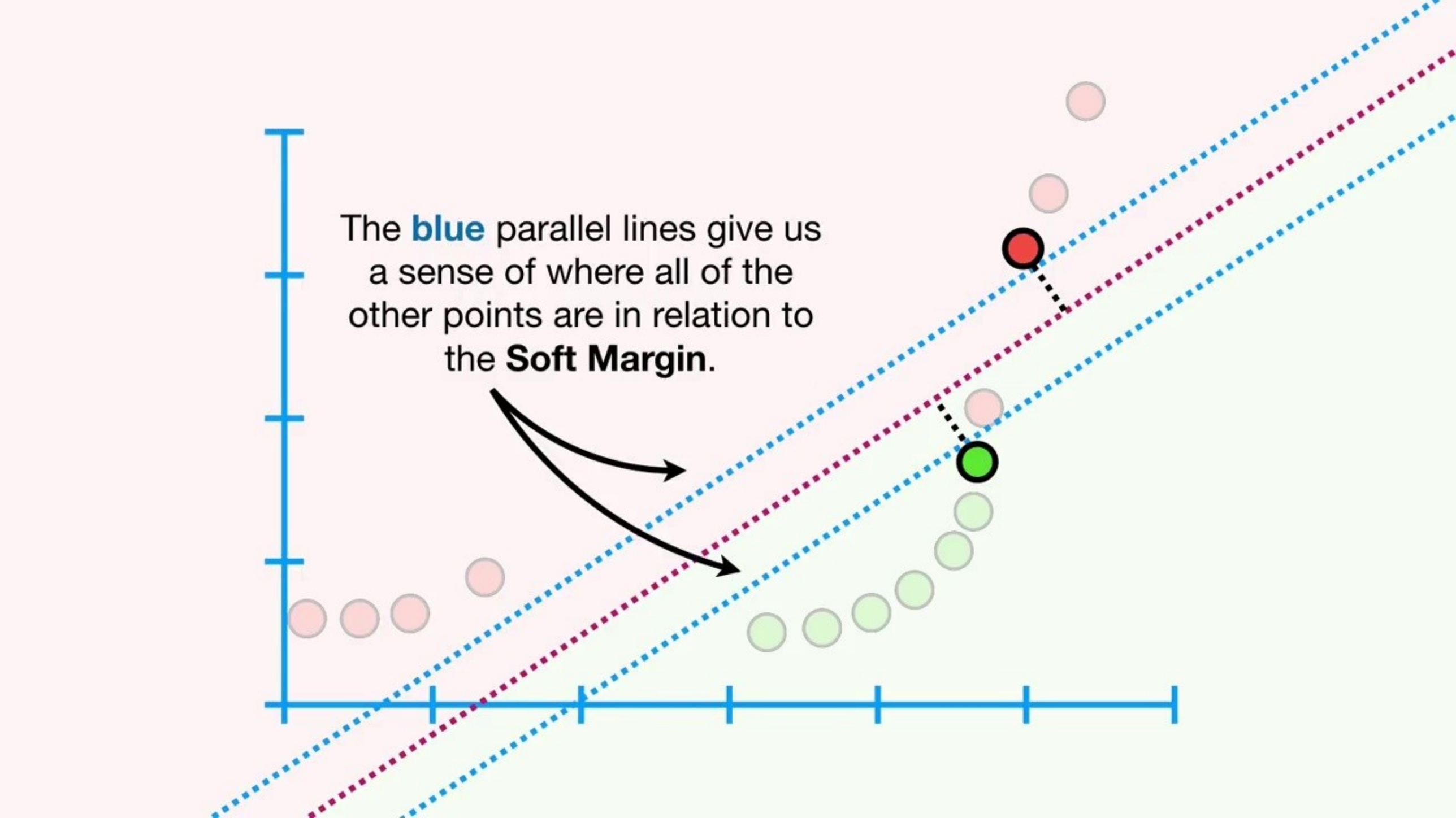

NOTE: If each observation had a ***mass*** measurement…
Height (cm):
Mass (g):

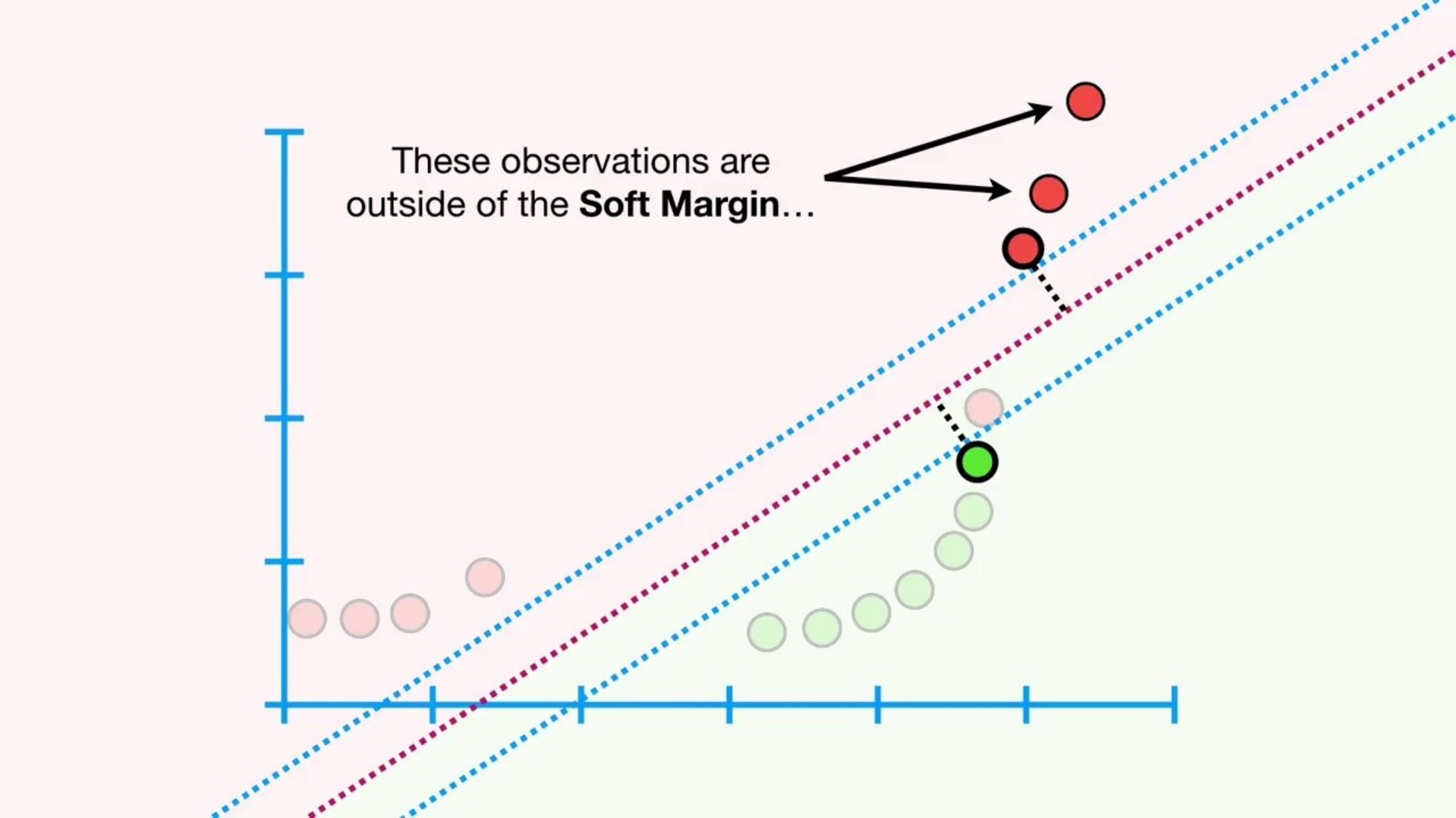

…and a *height* measurement…
Height (cm):
Mass (g):

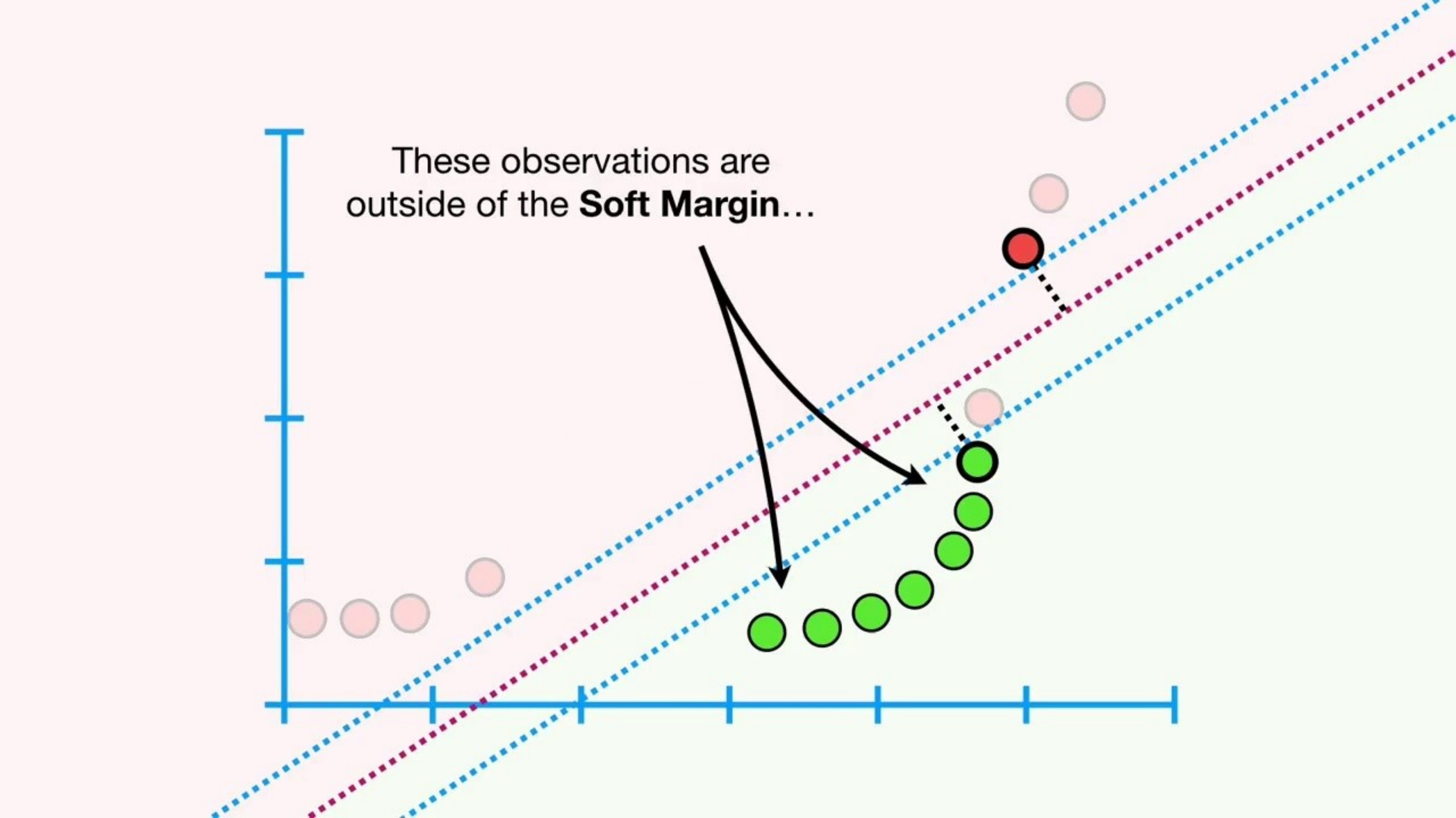

…then the data would
be **2-Dimensional**.
Height (cm):
Mass (g):

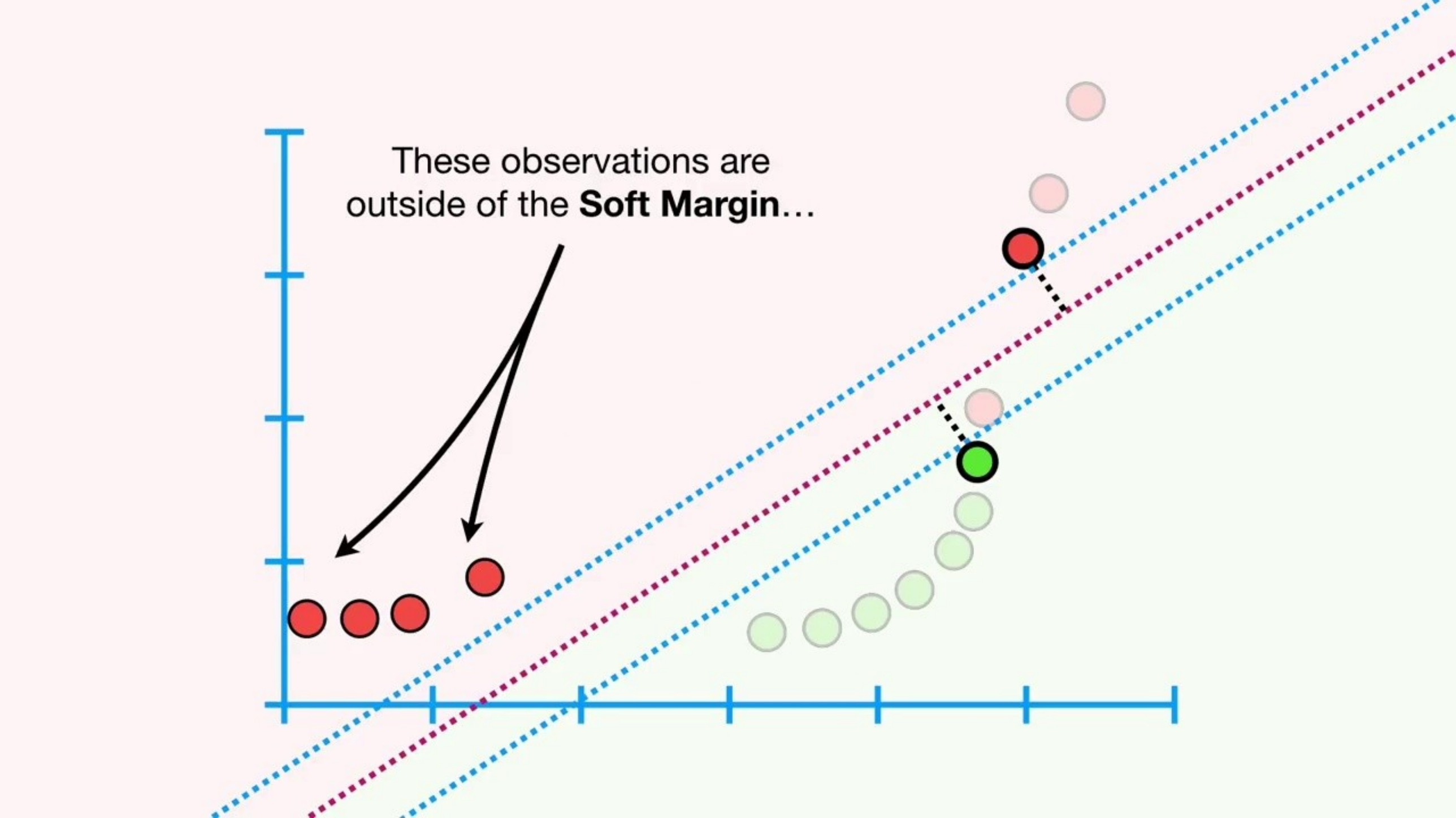

When the data are **2-Dimensional**, a **Support Vector Classifier** is a line…

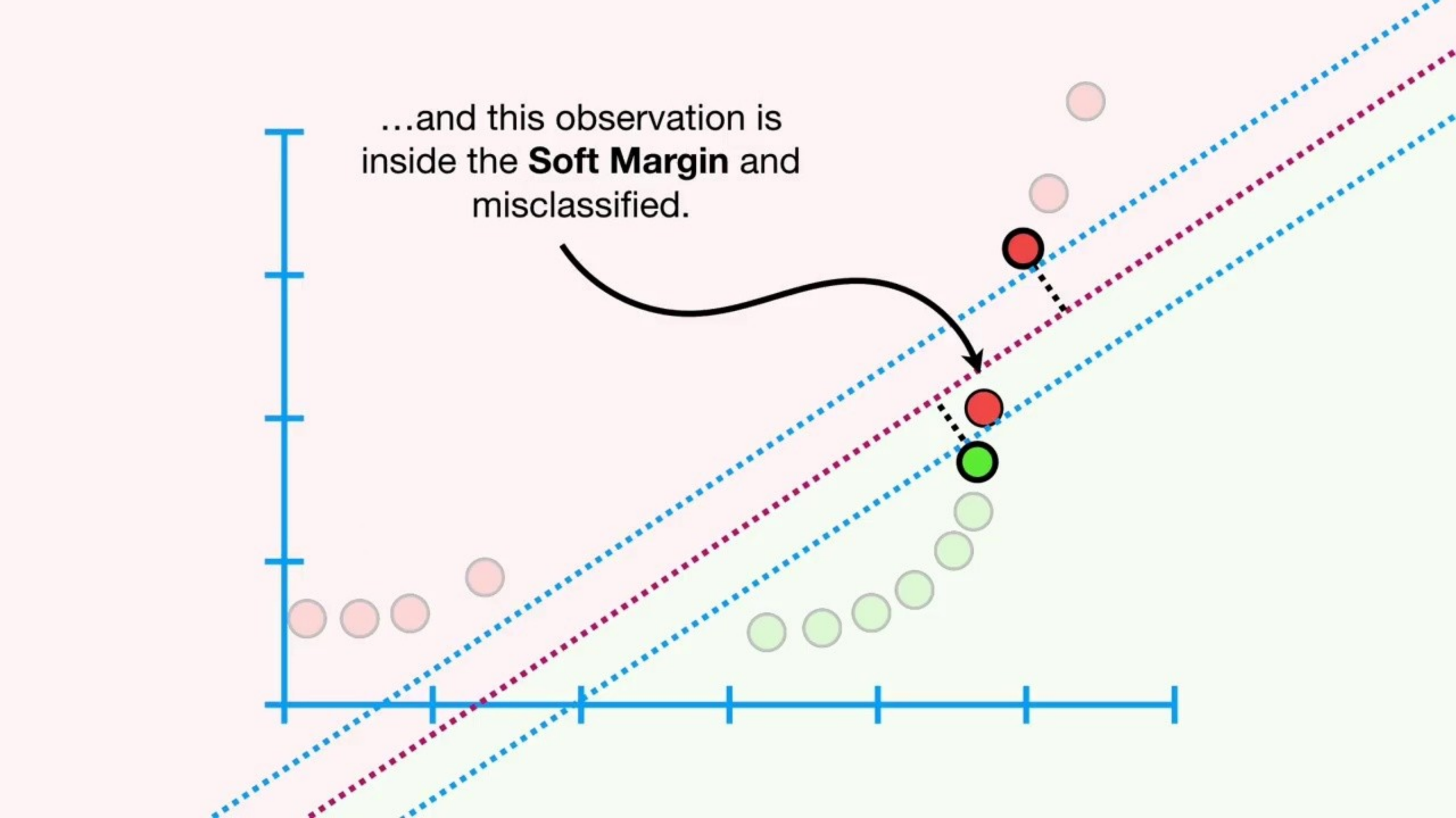

…and, in this case, the **Soft Margin** is measured form these two points.

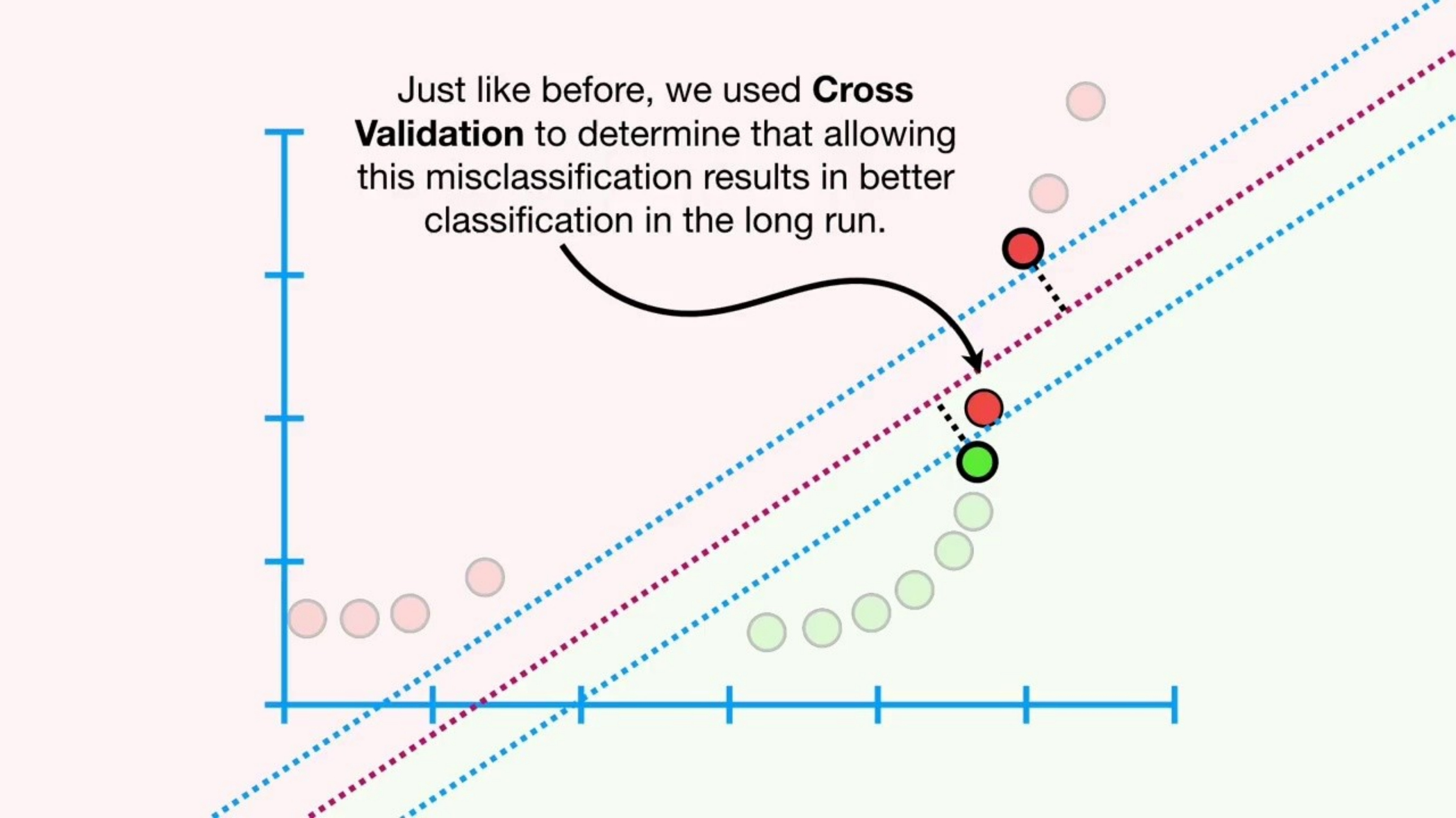

The blue parallel lines give us a sense of where all of the other points are in relation to the Soft Margin.

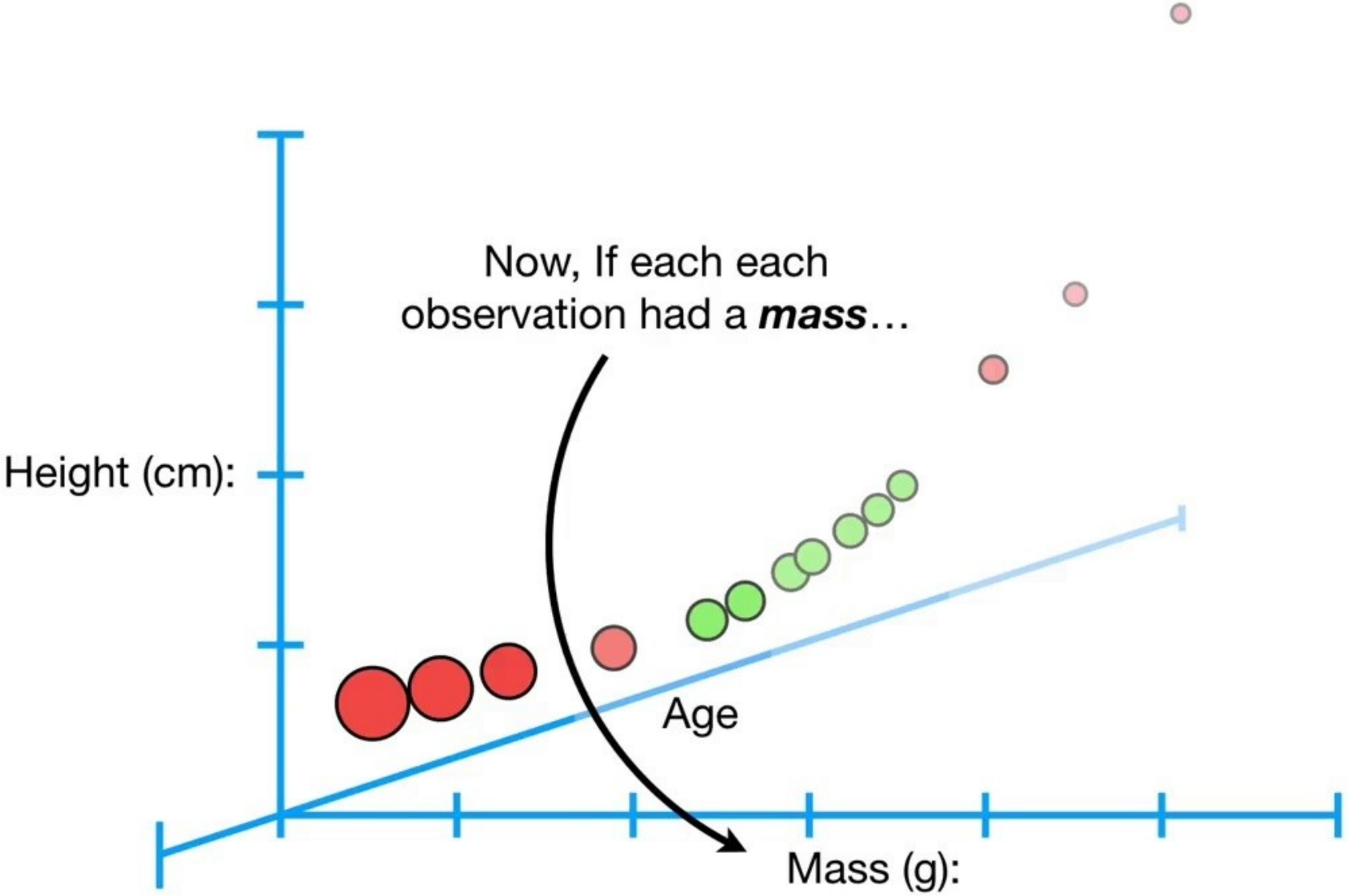

These observations are
outside of the **Soft Margin**…

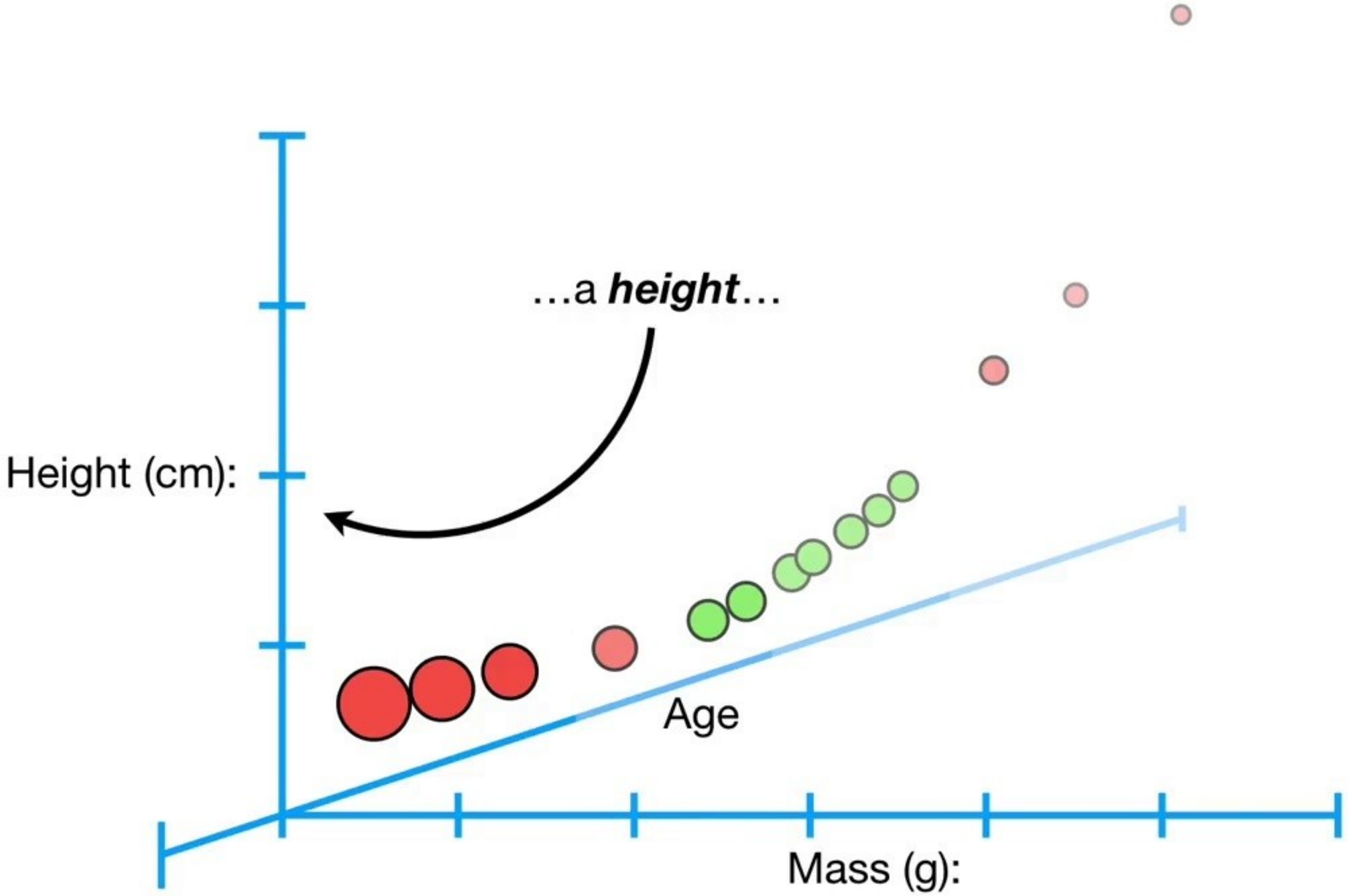

These observations are
outside of the **Soft Margin**…

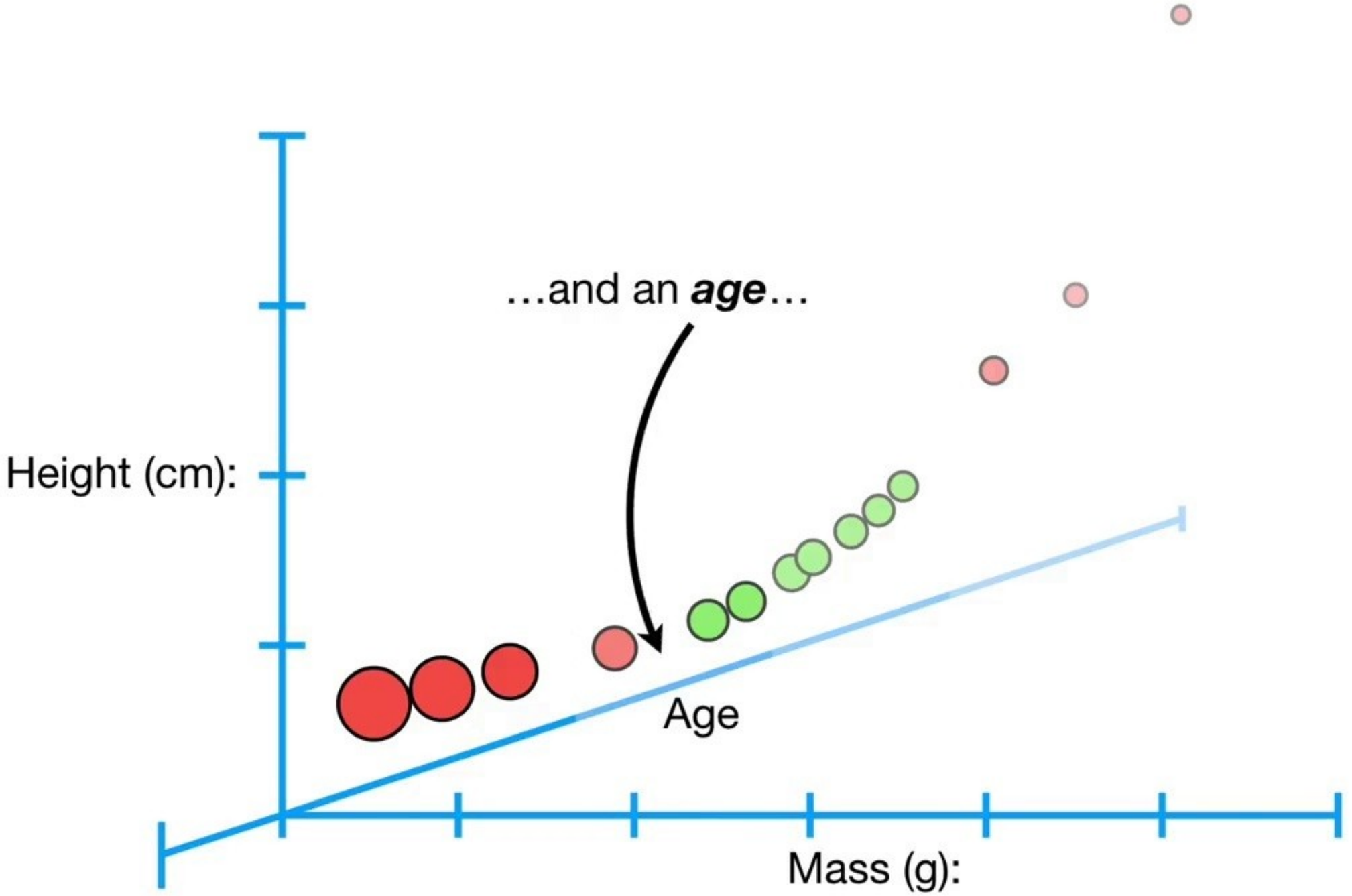

These observations are
outside of the **Soft Margin**…

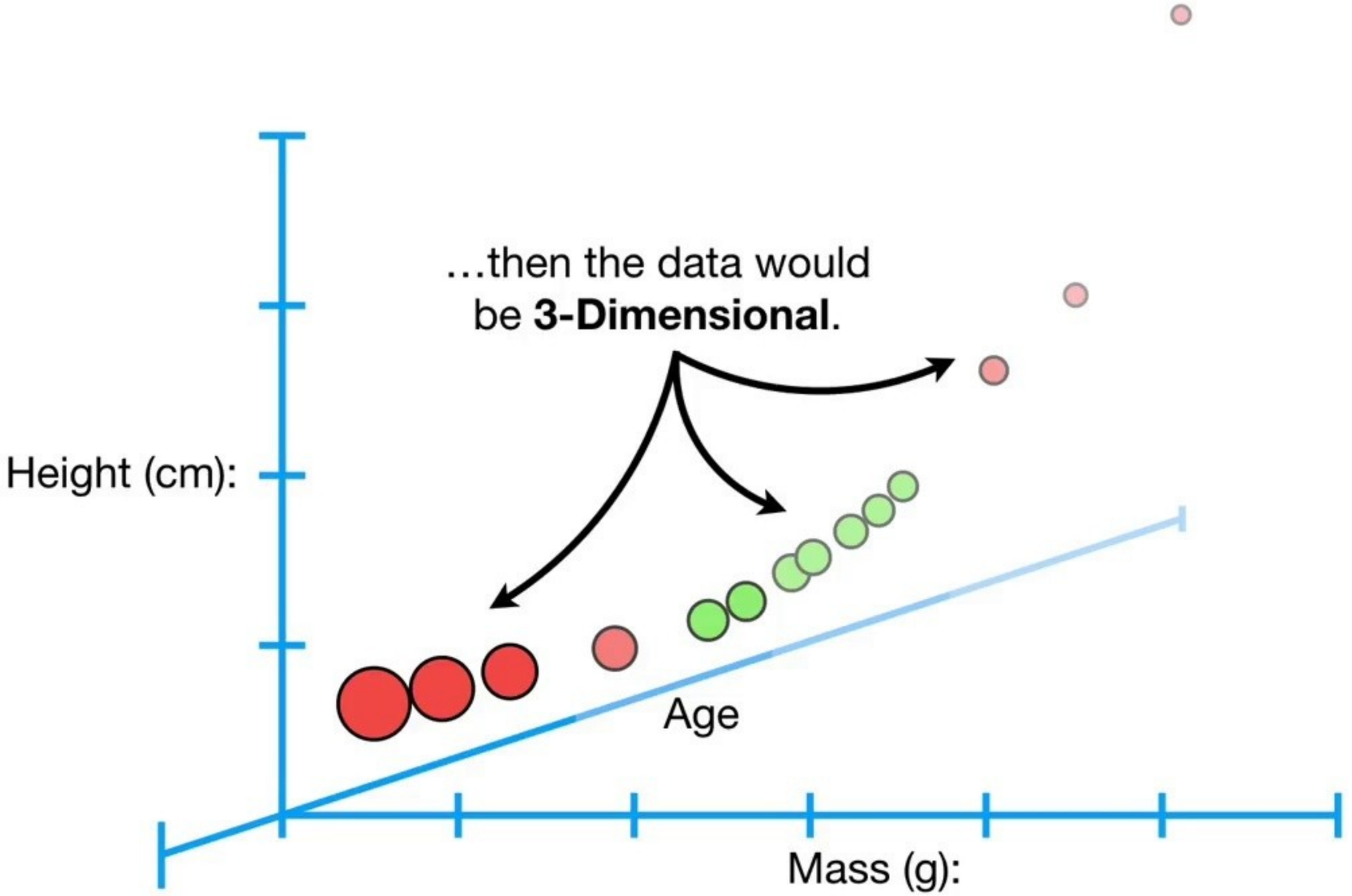

…and this observation is
inside the **Soft Margin** and
misclassified.

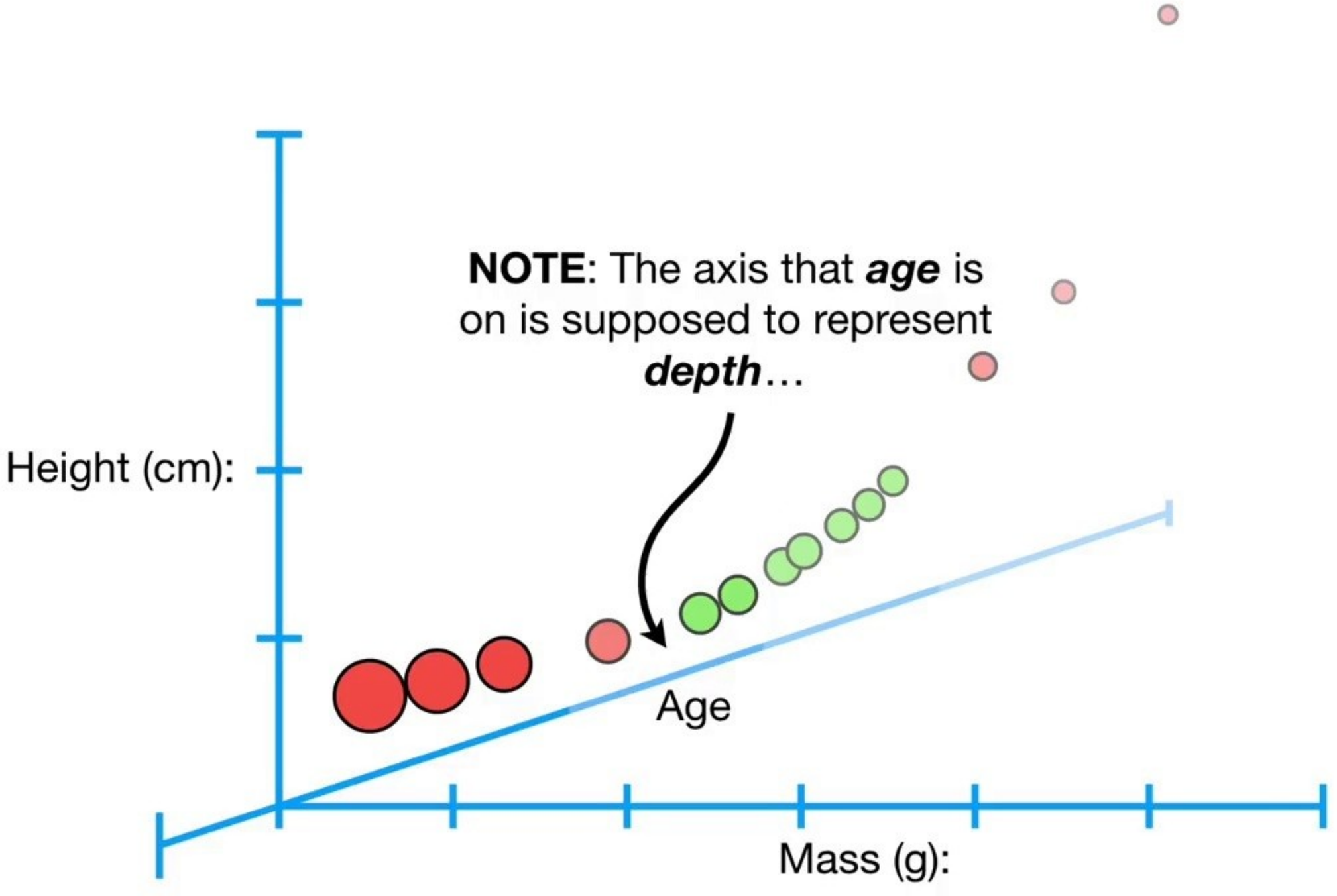

Just like before, we used **Cross Validation** to determine that allowing this misclassification results in better classification in the long run.

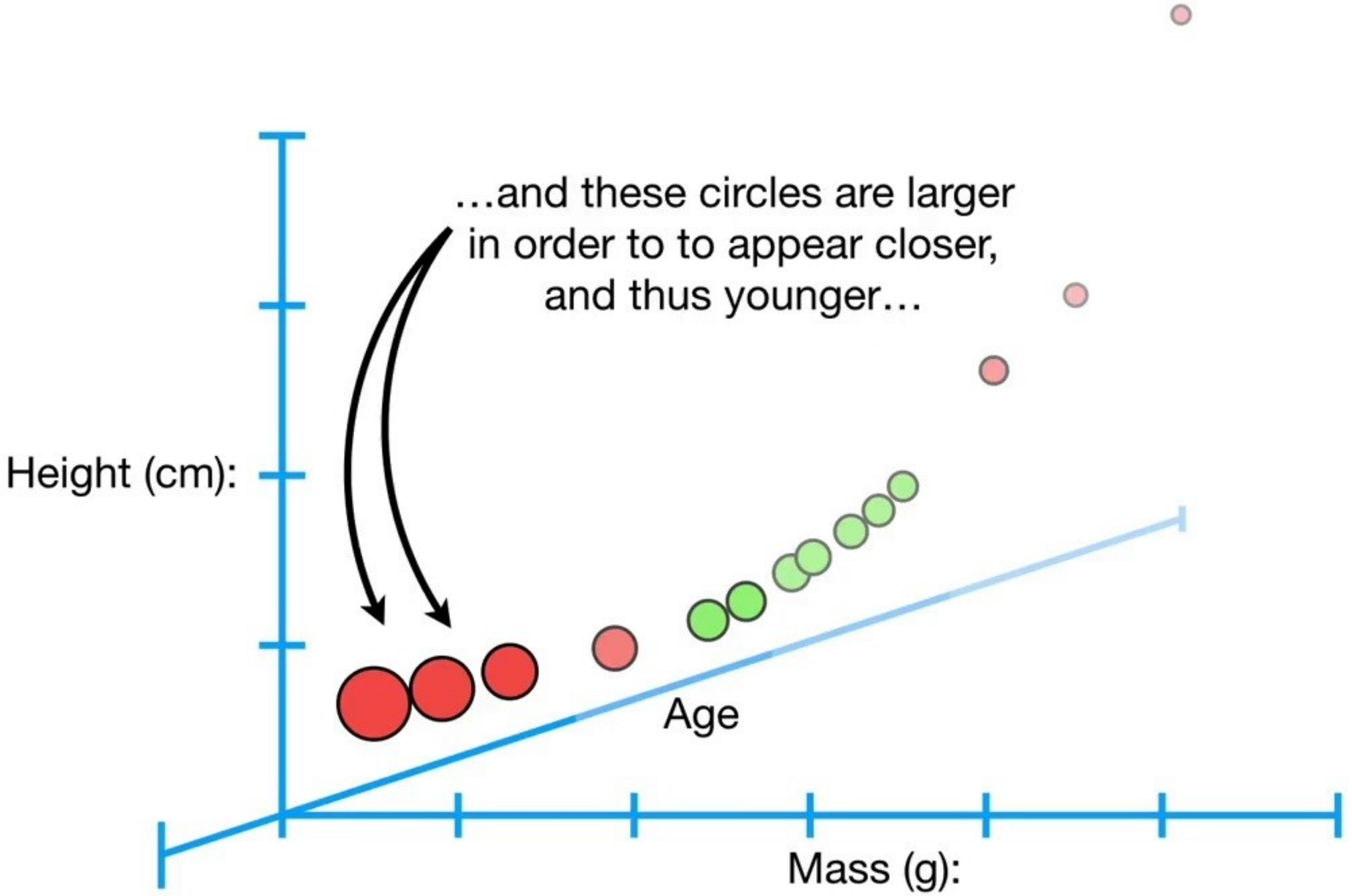

Now, If each each
observation had a ***mass***…
Height (cm):
Age
Mass (g):

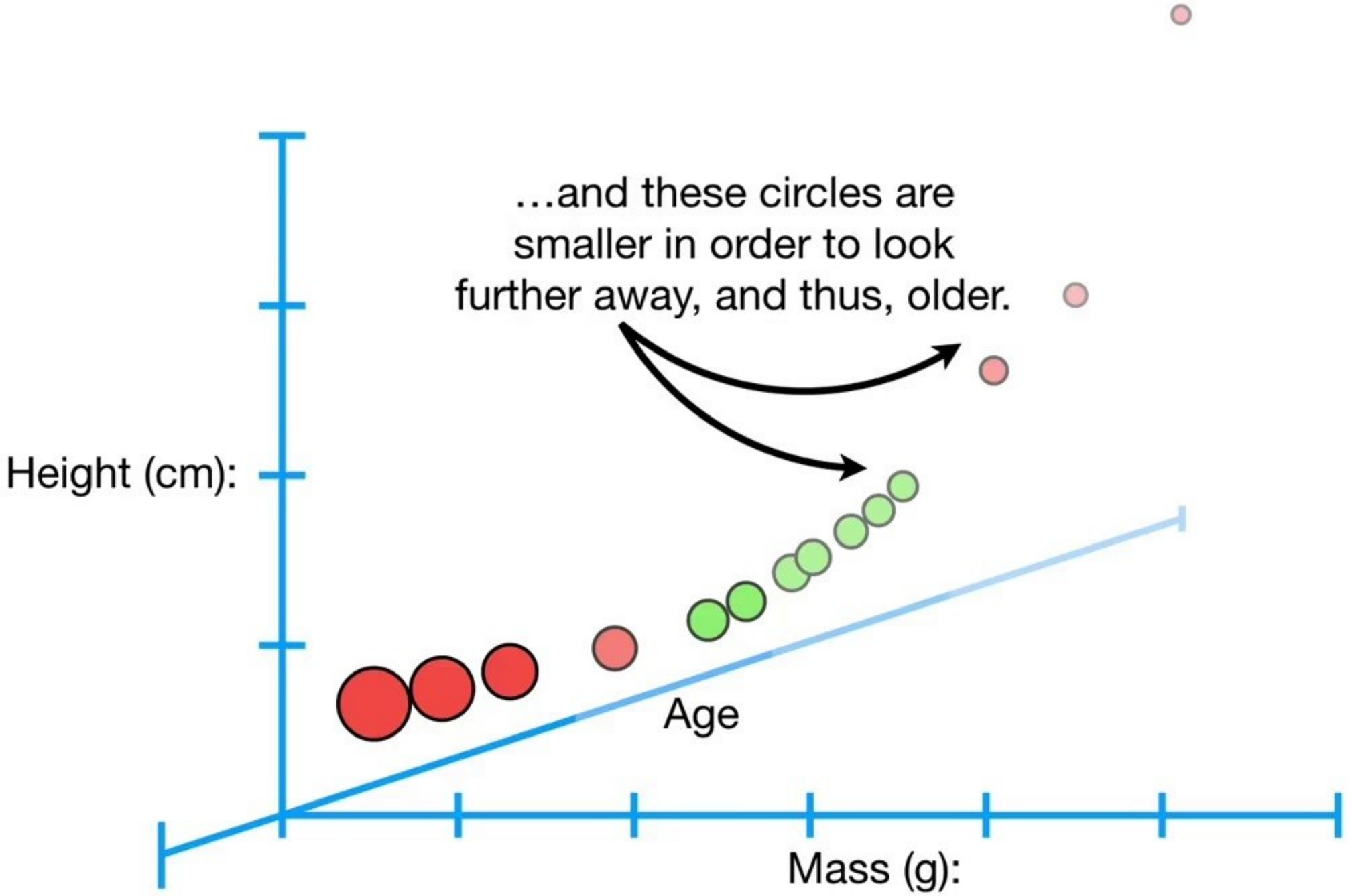

…a height…
Height (cm):
Age
Mass (g):

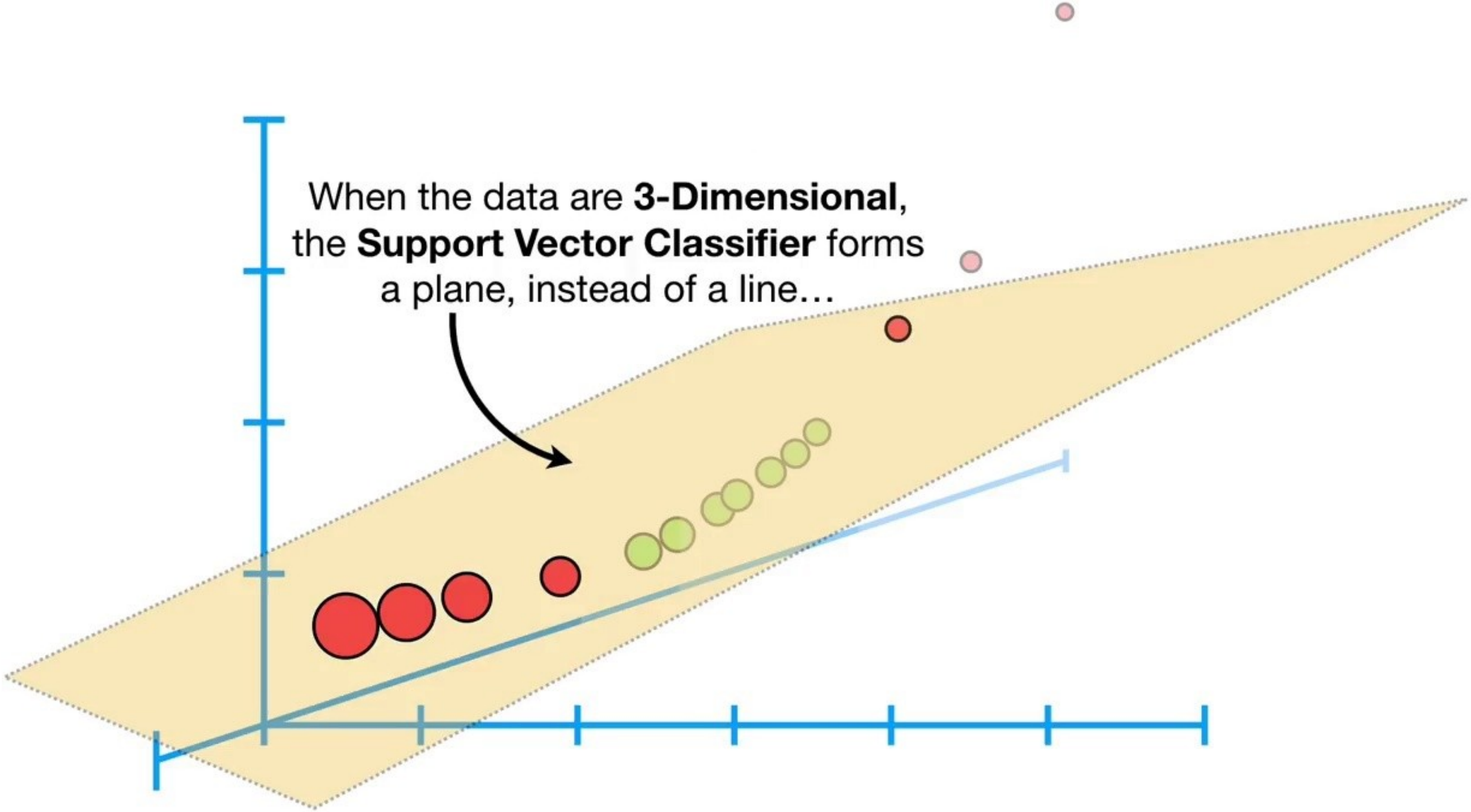

…and an ***age***…
Height (cm):
Age
Mass (g):

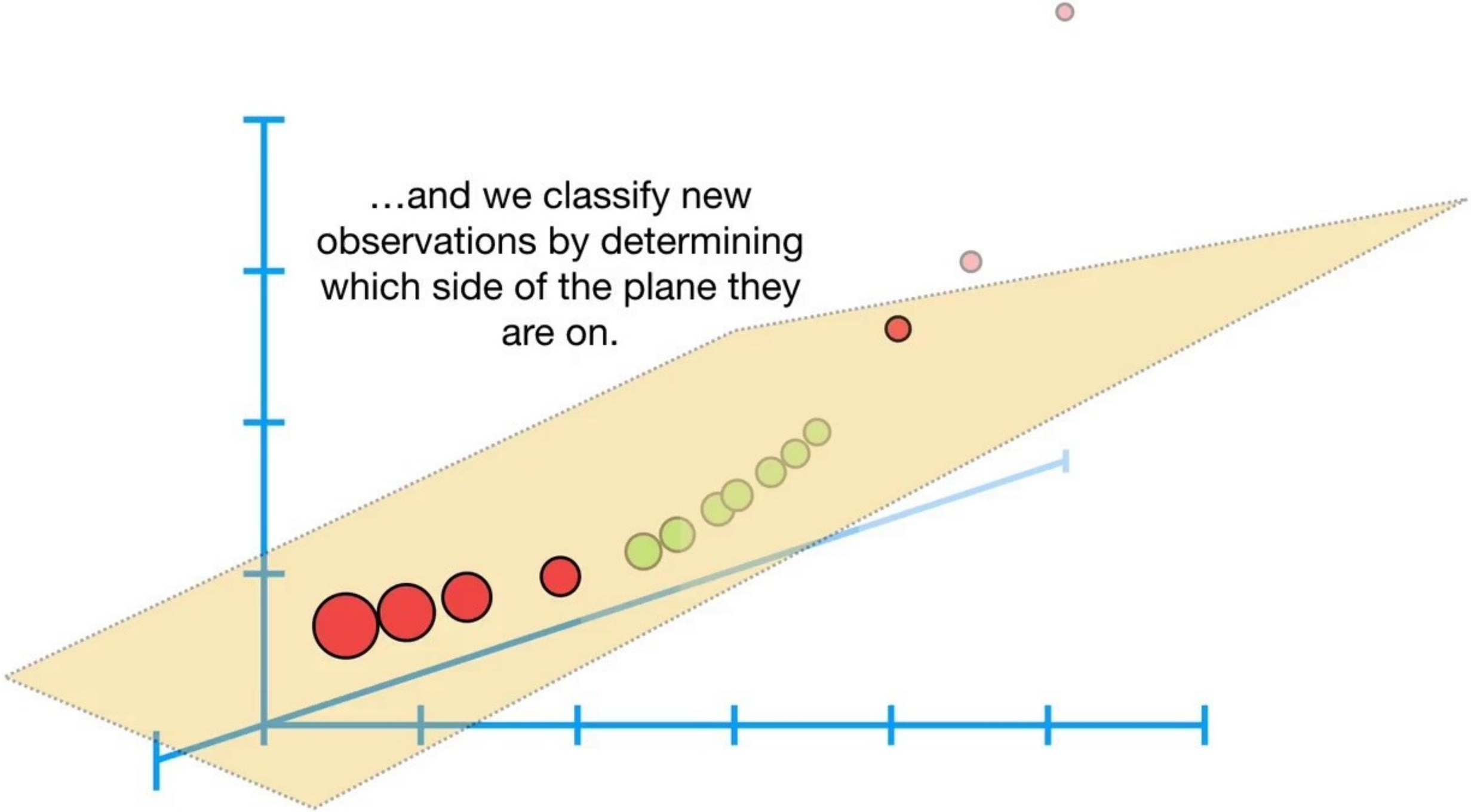

…then the data would
be **3-Dimensional**.
Height (cm):
Age
Mass (g):

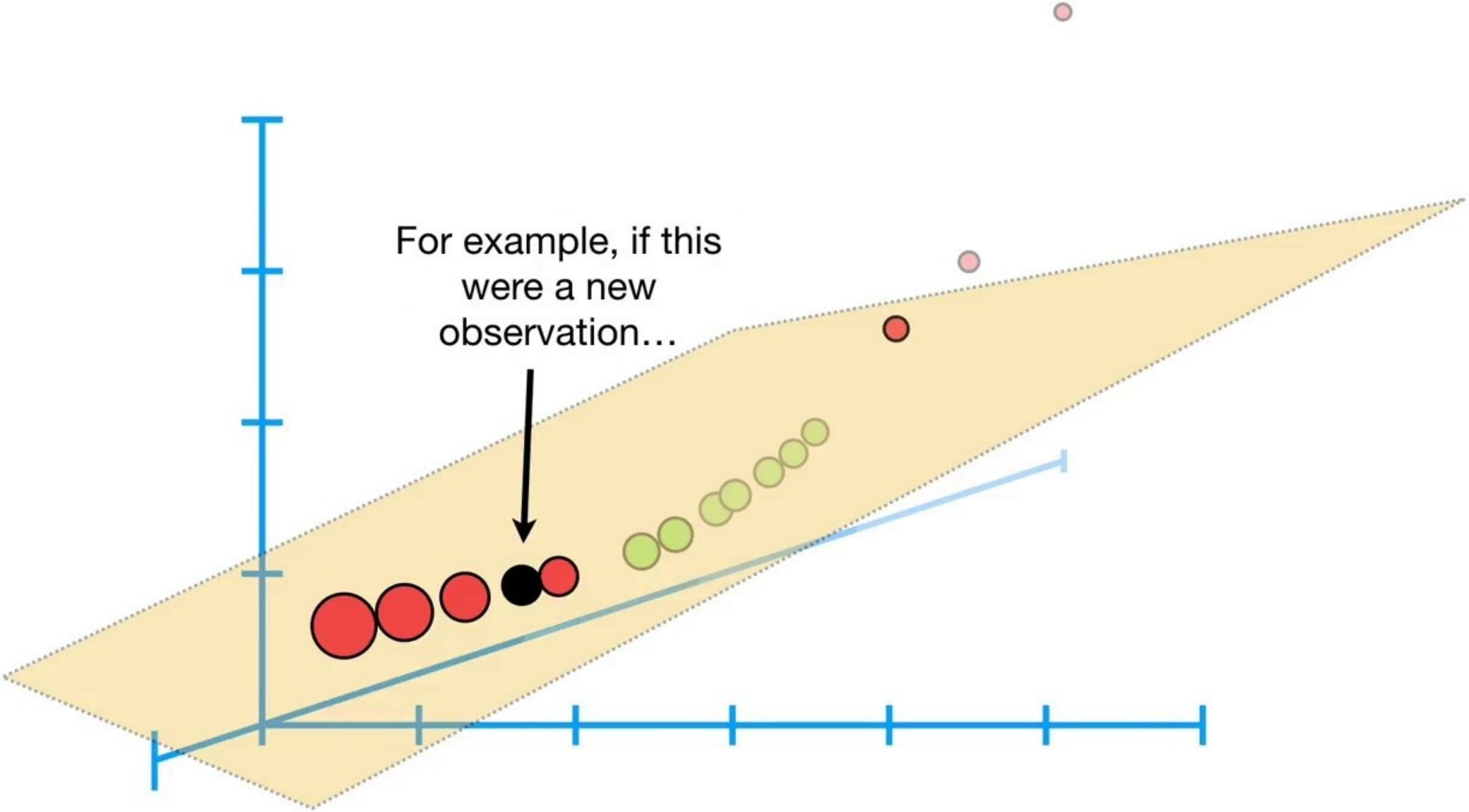

NOTE: The axis that age is on is supposed to represent depth…
Height (cm):
Age
Mass (g):

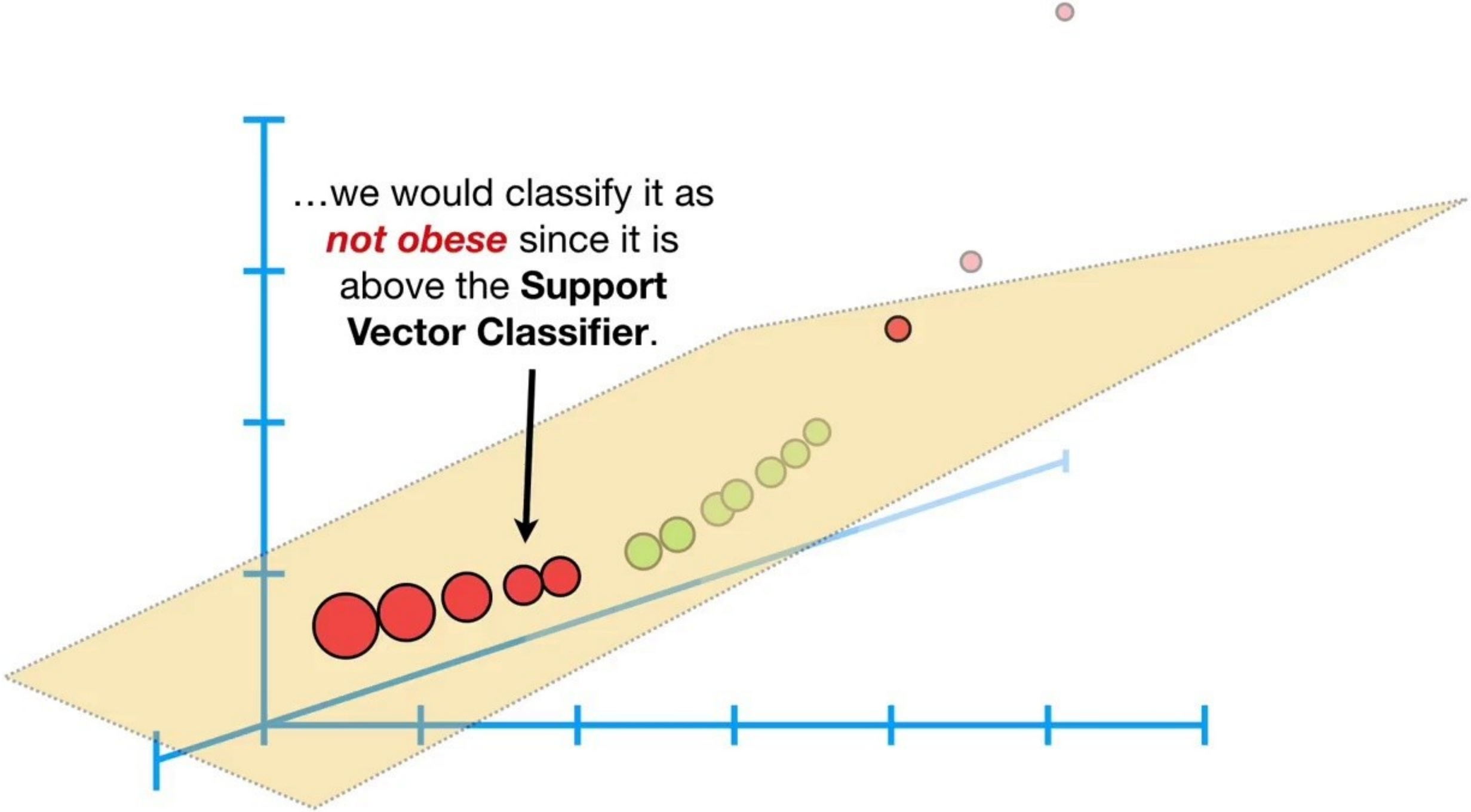

…and these circles are larger
in order to to appear closer,
and thus younger…
Height (cm):
Age
Mass (g):


…and these circles are
smaller in order to look
further away, and thus, older.
Height (cm):
Age
Mass (g):

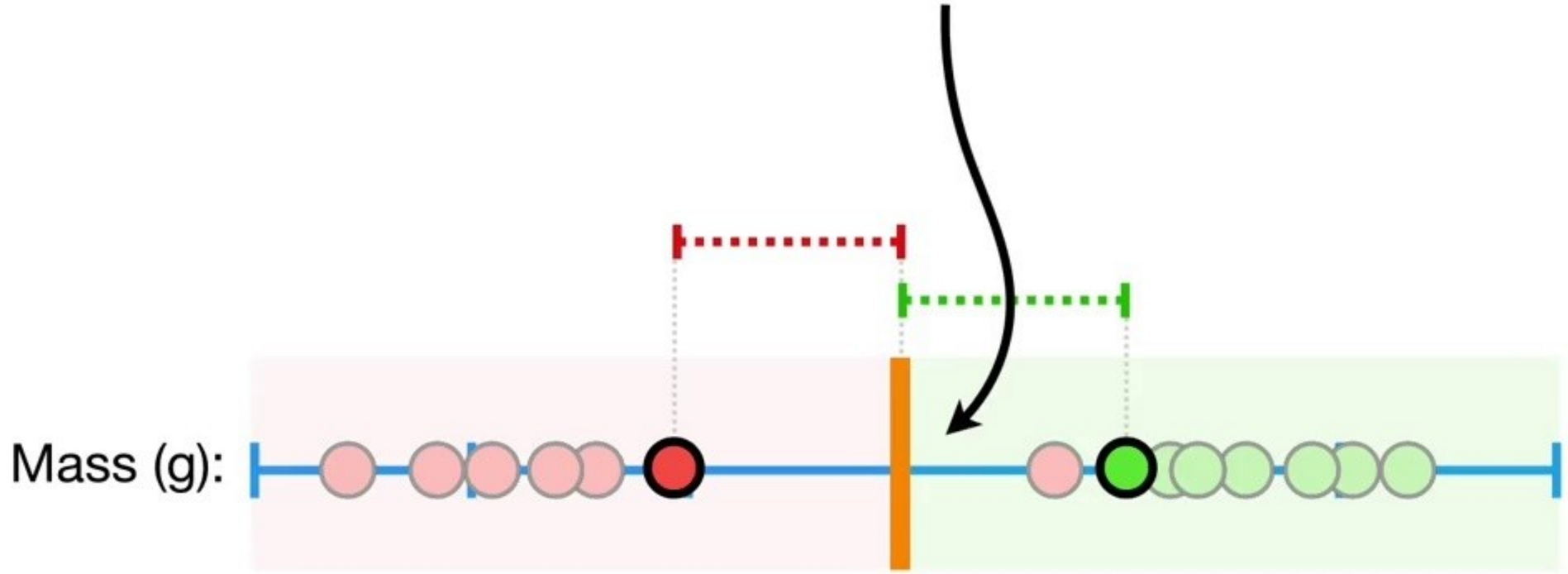

When the data are **3-Dimensional**,
the **Support Vector Classifier** forms
a plane, instead of a line…

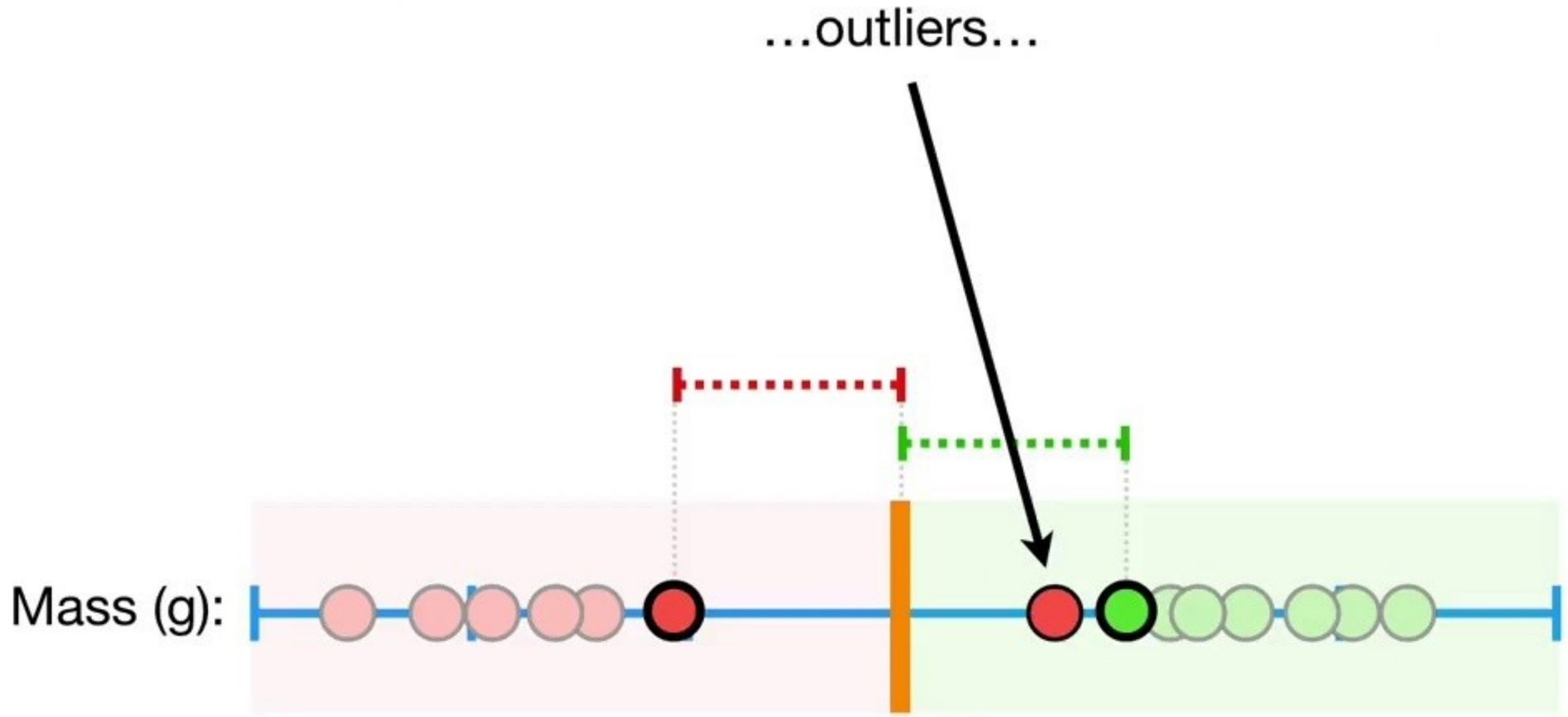

…and we classify new observations by determining which side of the plane they are on.


For example, if this were a new observation…

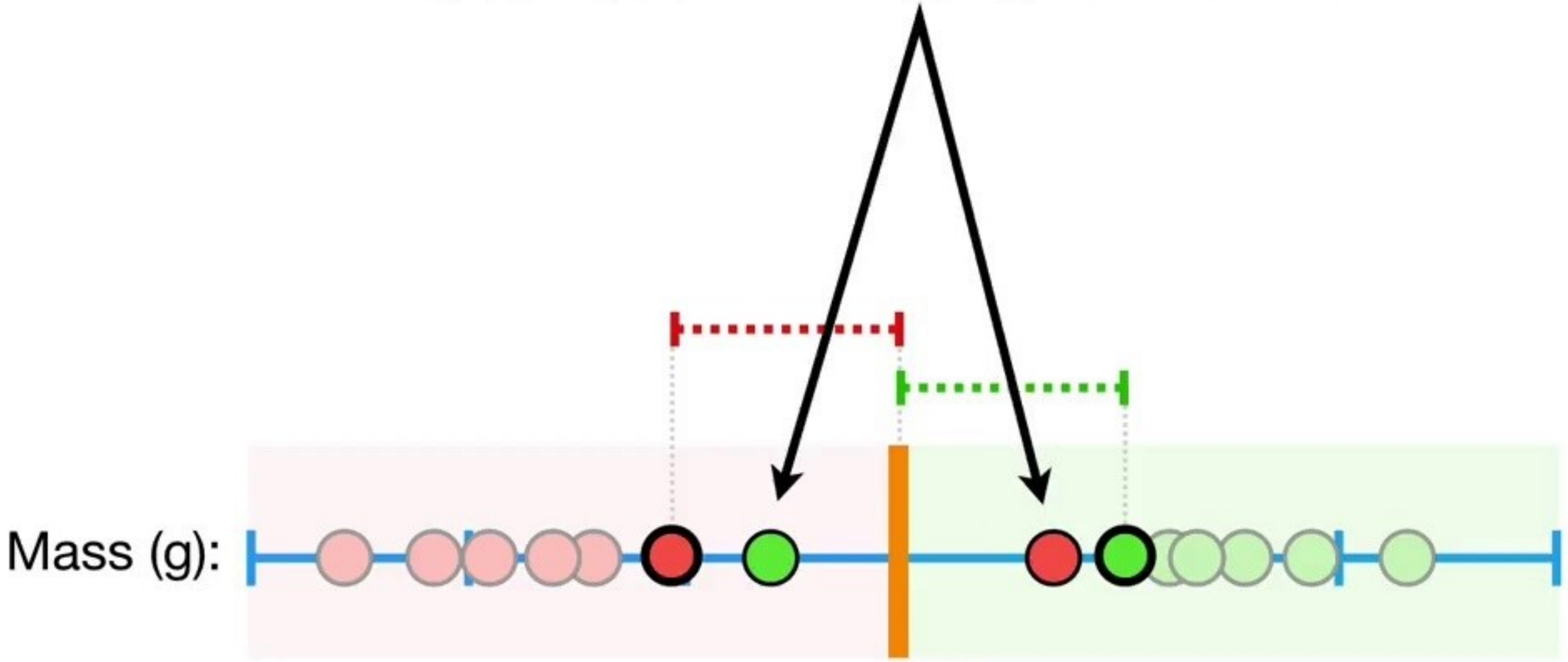

…we would classify it as
not obese since it is
above the Support
Vector Classifier.

Support Vector Classifiers seem pretty cool because they can handle…

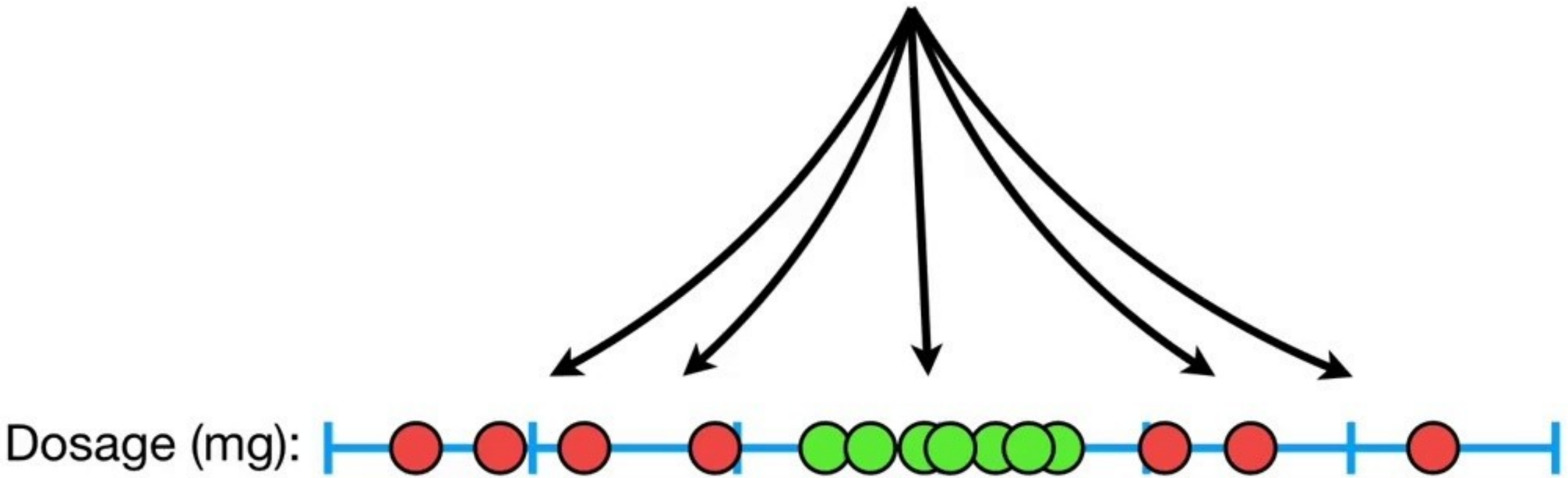



…outliers…
Mass (g):

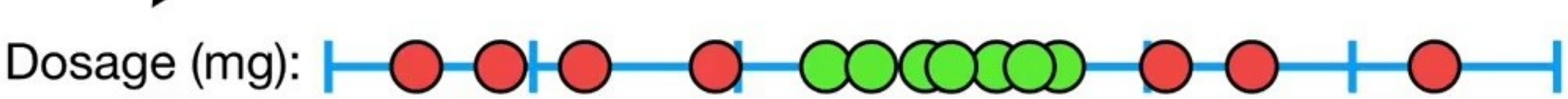
…and, because they allow misclassifications,
they can handle overlapping classifications…



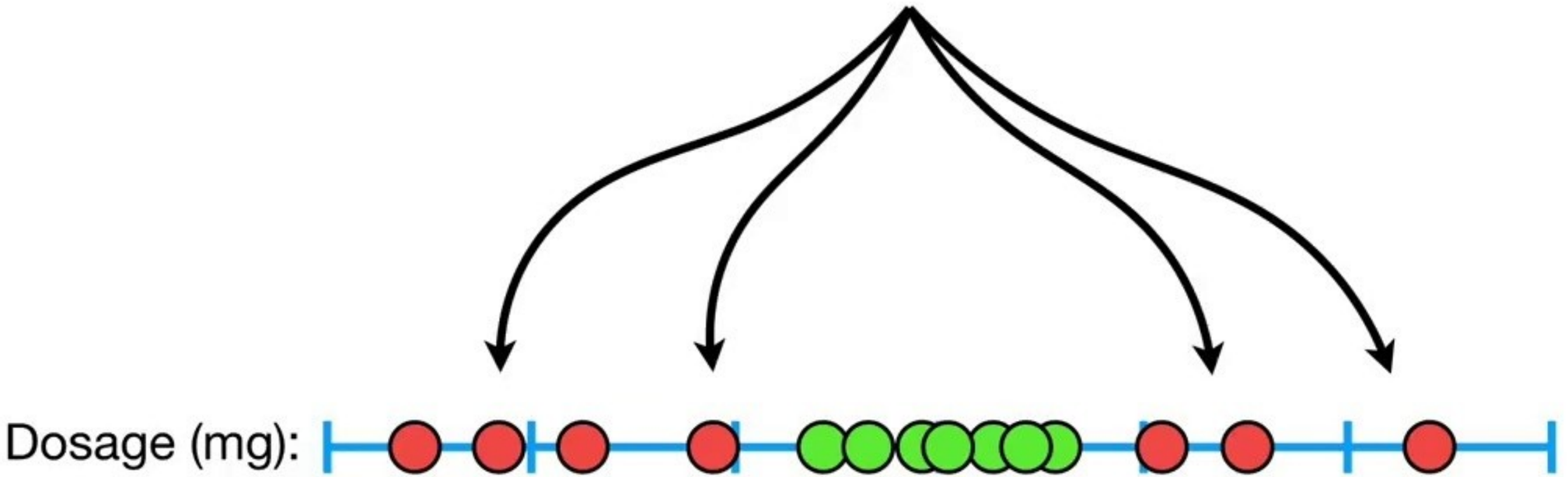
…but what if this was our training data and we had tons of overlap?



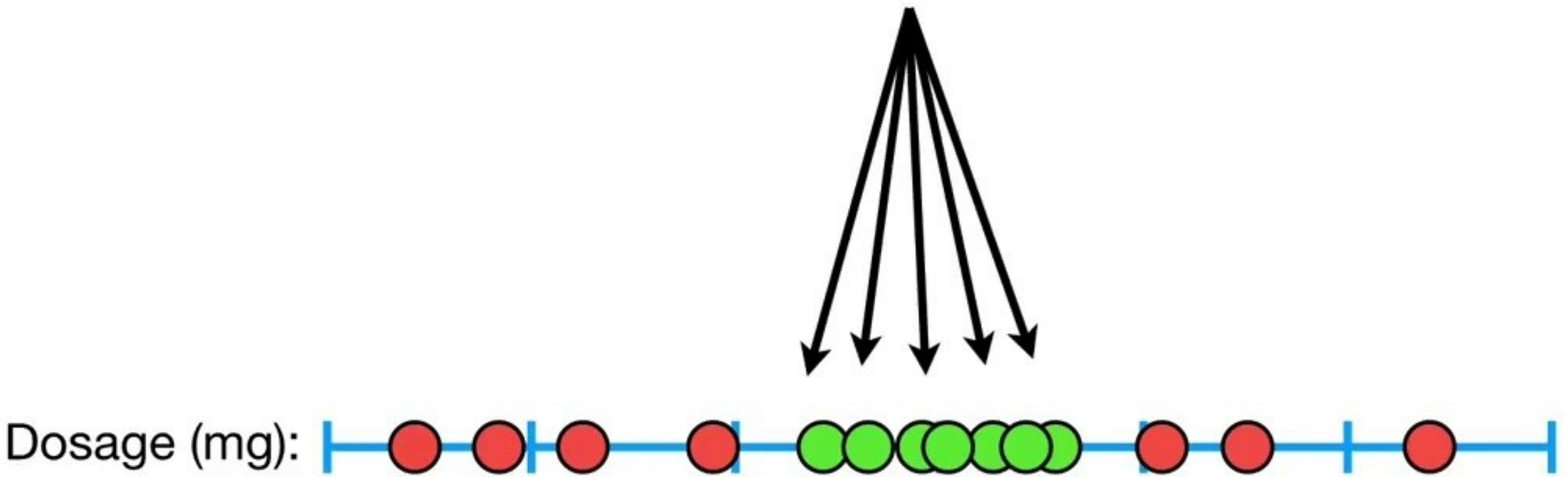
In this new example, with tons of overlap, we are now looking at **Drug Dosages**…



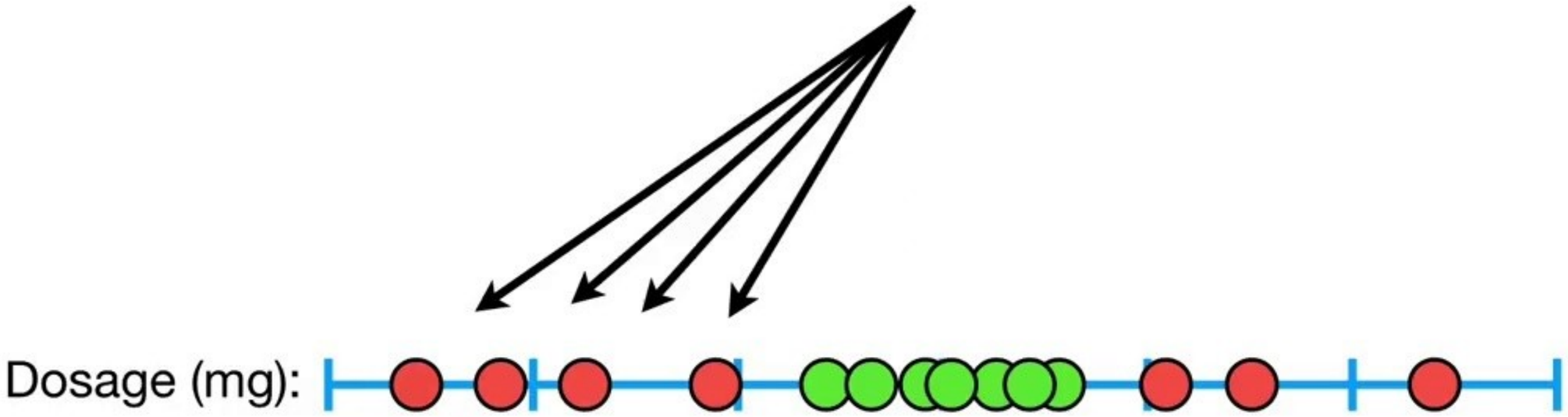
…and the **red dots** represent
patients that were ***not cured***…

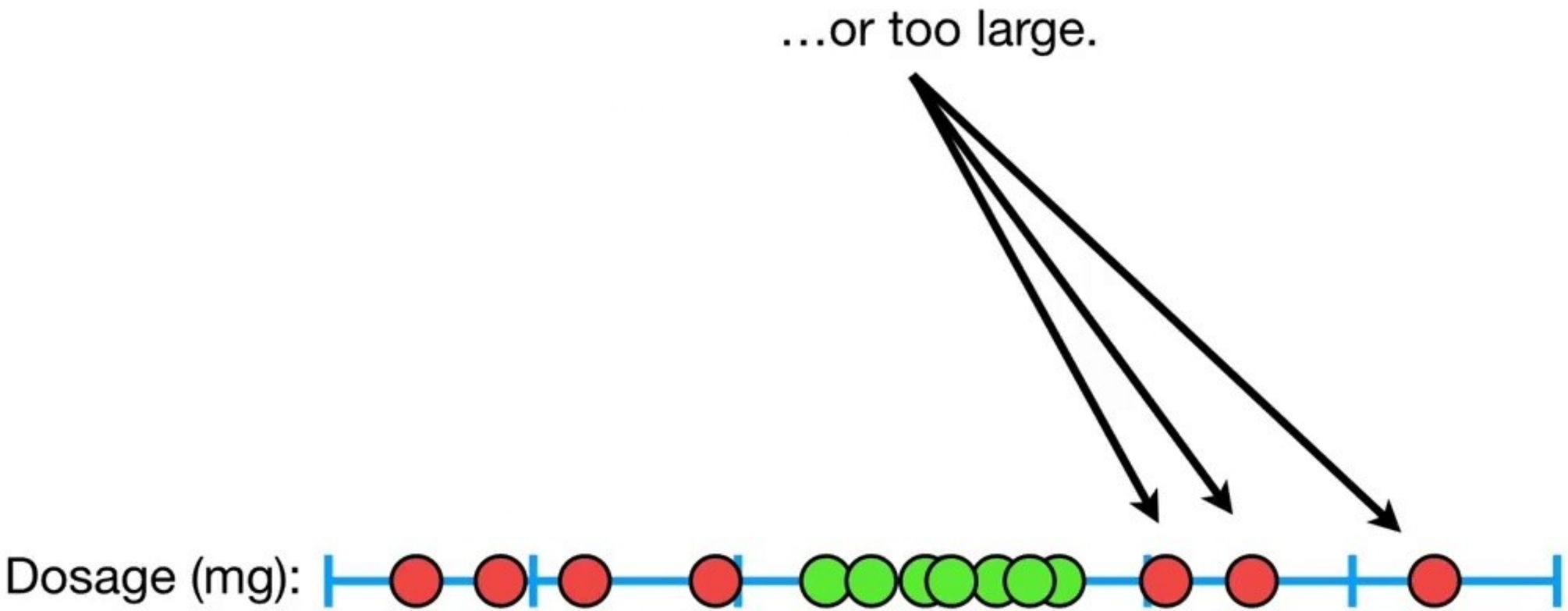


…and the **green dots** represent
patients that were ***cured***.

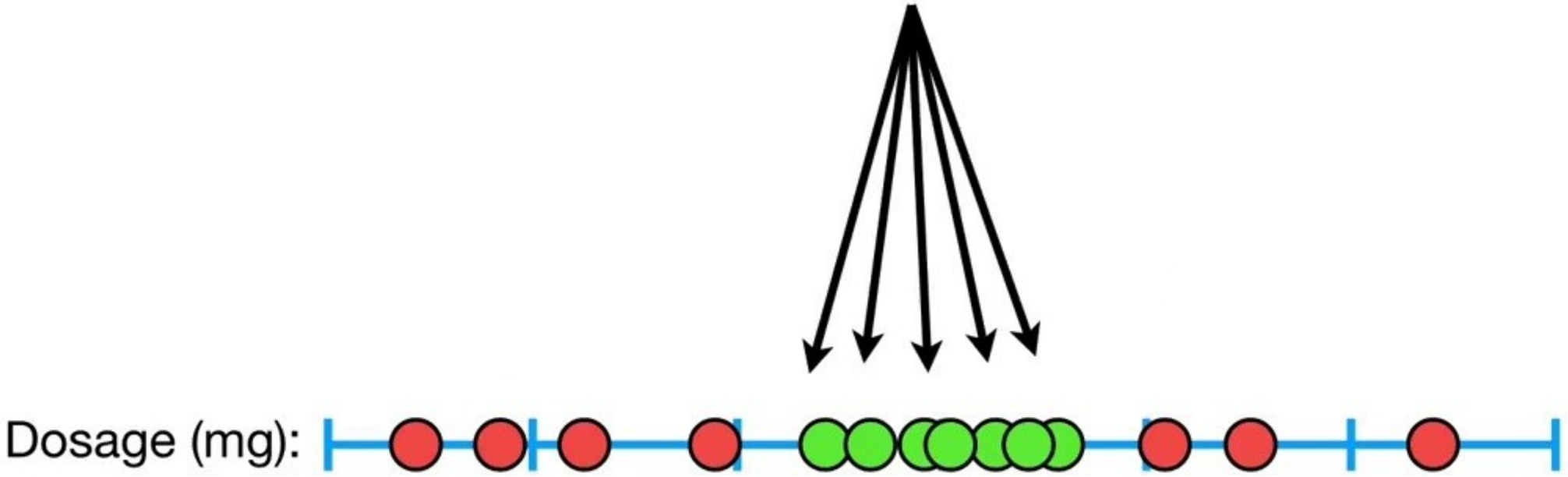


In other words, the drug doesn't work if the dosage is too small…

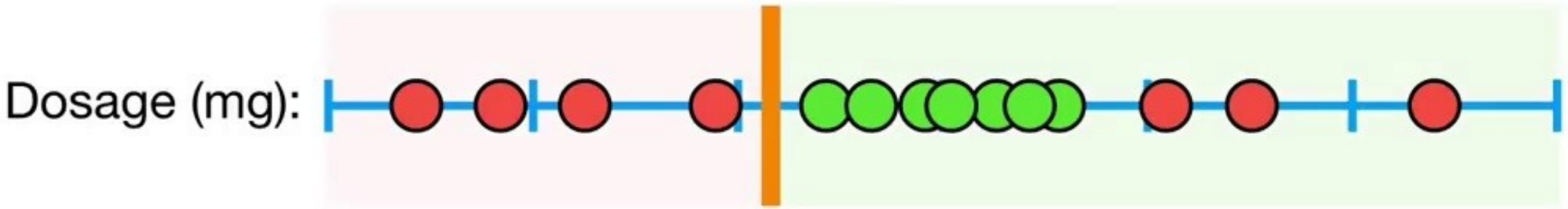



…or too large.
Dosage (mg):

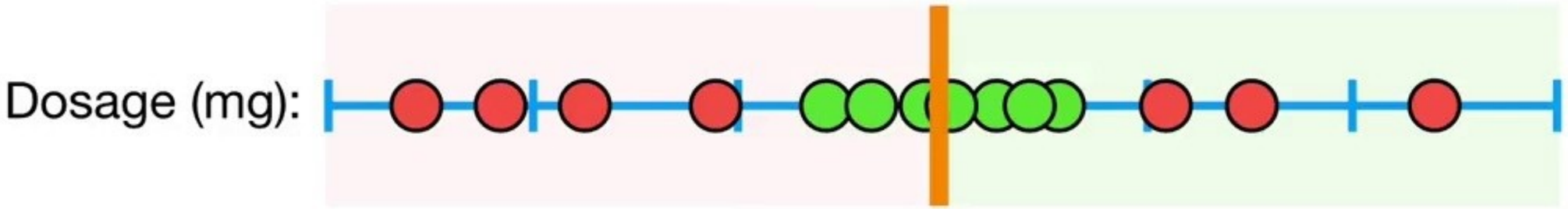
It only works when the
dosage is just right.



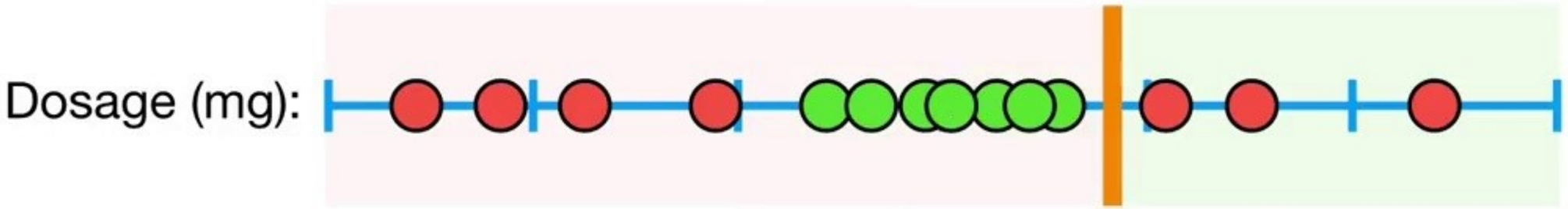
Now, no matter where we put the classifier, we will make a lot of misclassifications.



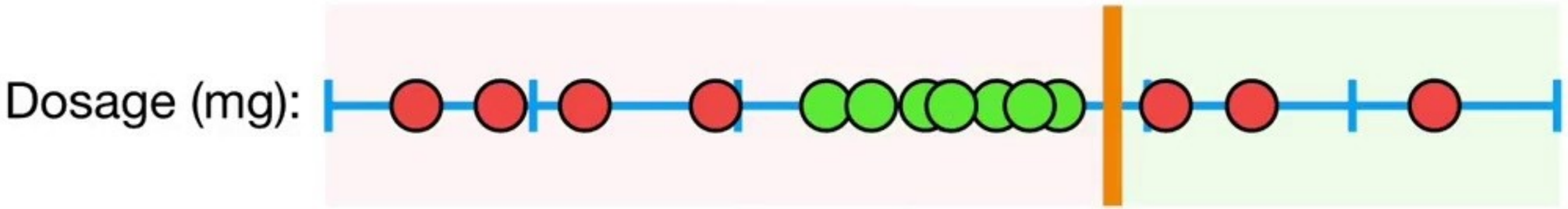
Now, no matter where we put the classifier, we will make a lot of misclassifications.



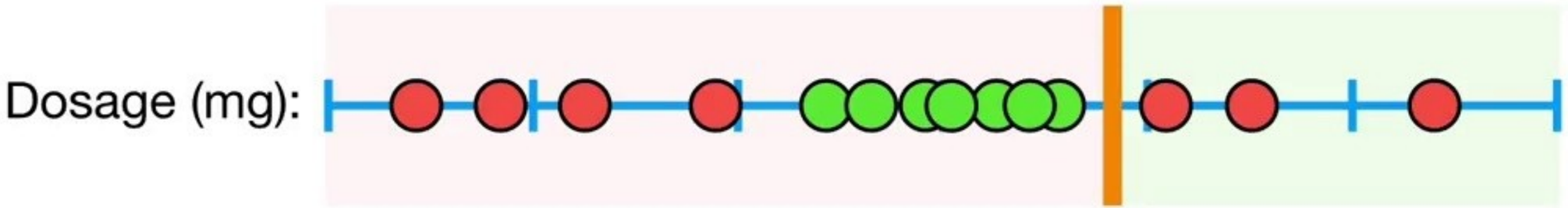
Now, no matter where we put the classifier, we will make a lot of misclassifications.



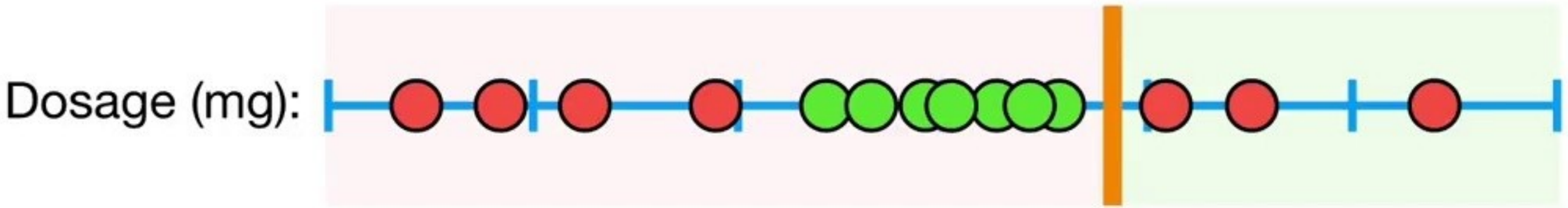
So **Support Vector Classifiers** are are only semi-cool, since they don't perform well with this type of data.



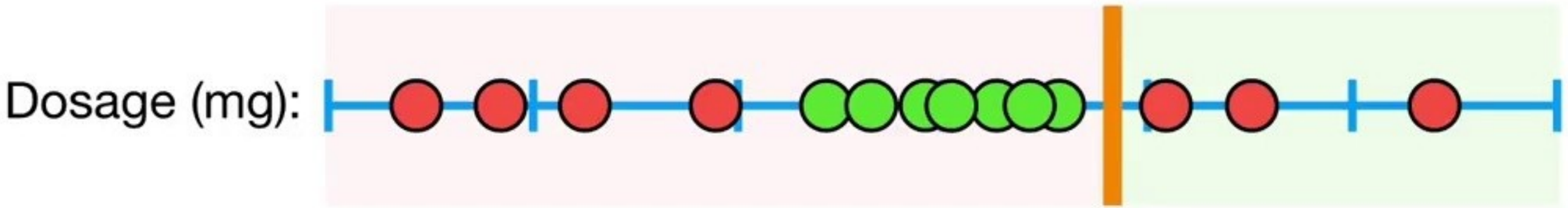
Can we do better than **Maximal Margin Classifiers** and **Support Vector Classifiers**?



YES!!!

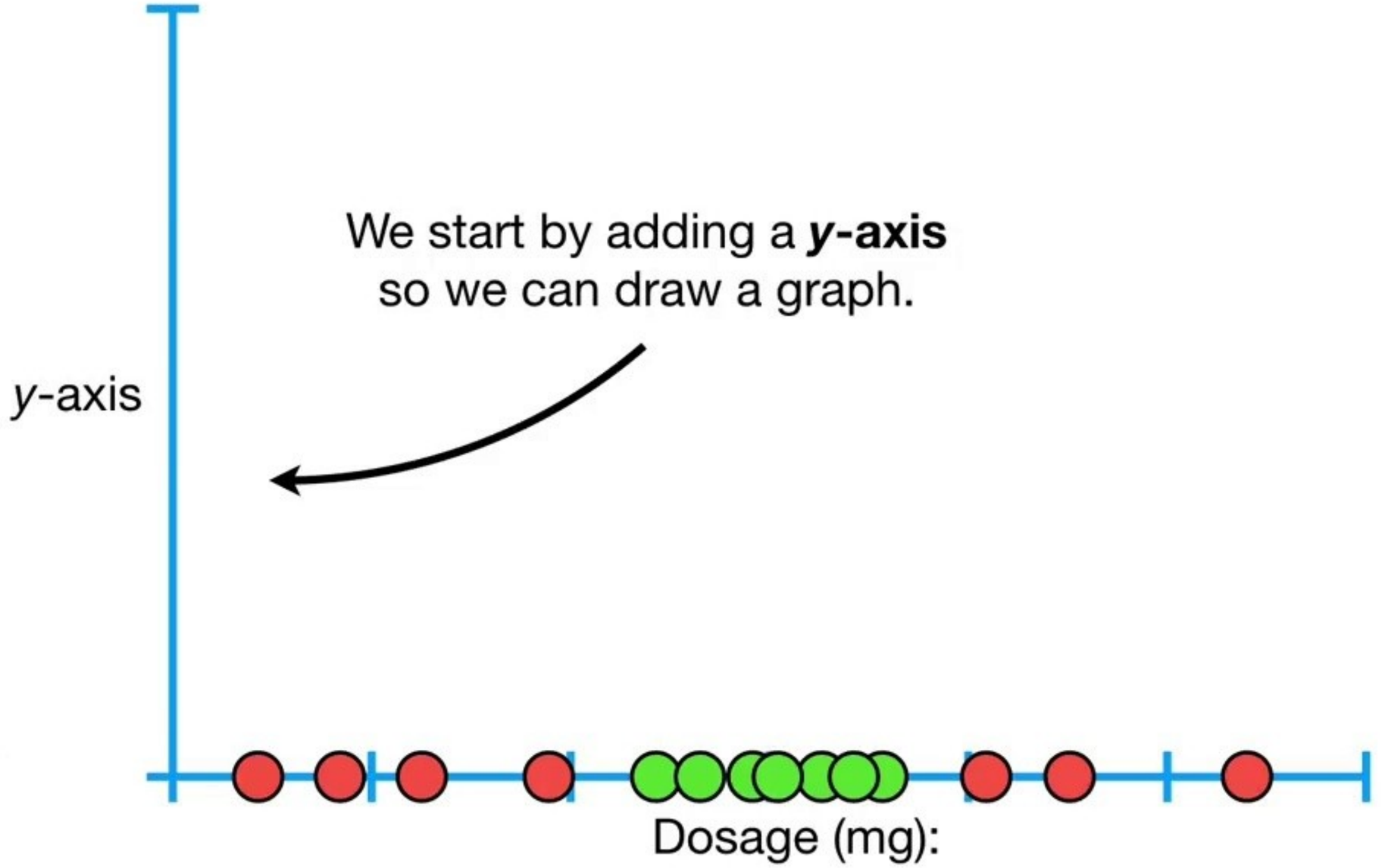


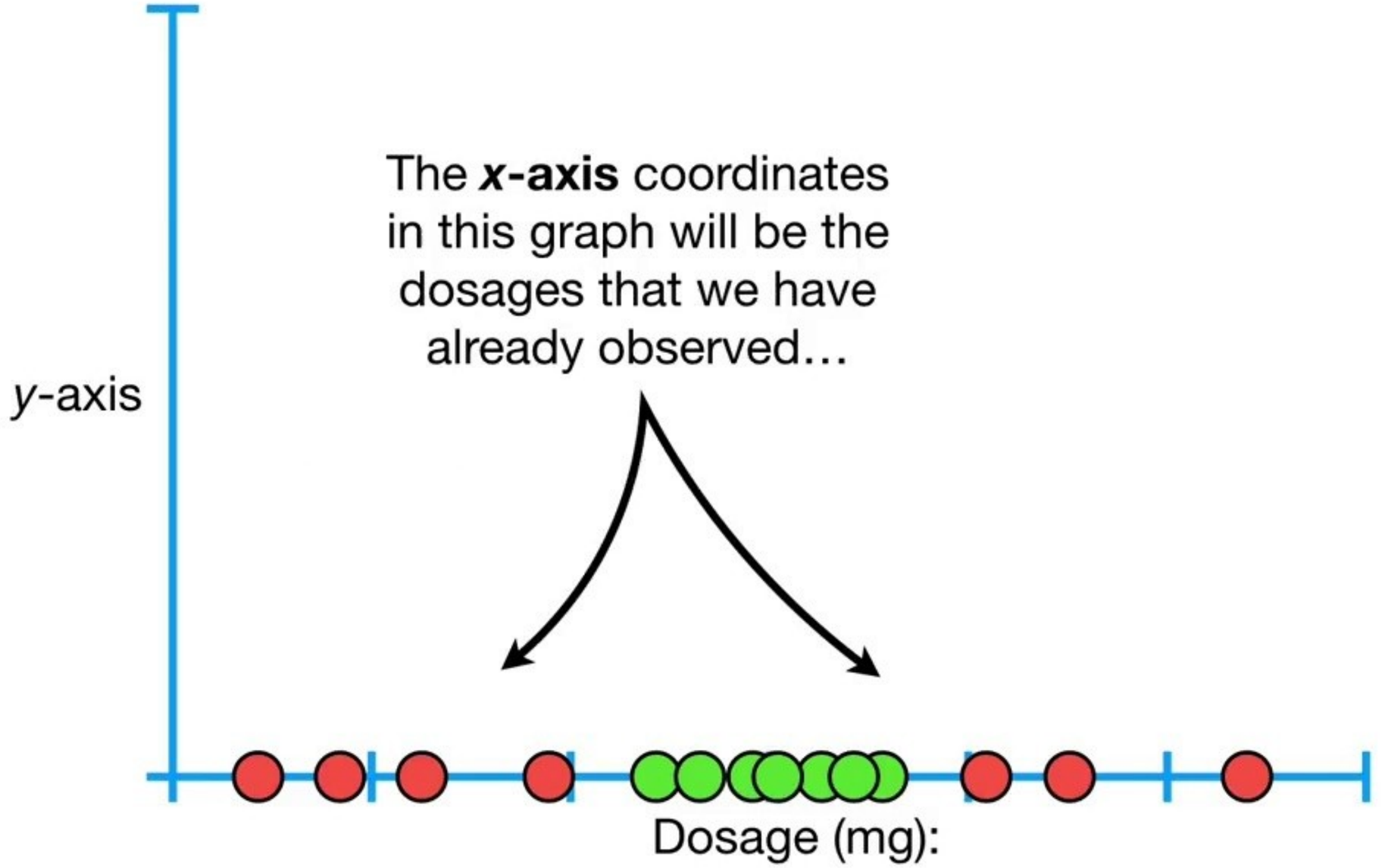
Since **Maximal Margin Classifiers** and **Support Vector Classifiers** can't handle this data, it's high time we talked about…

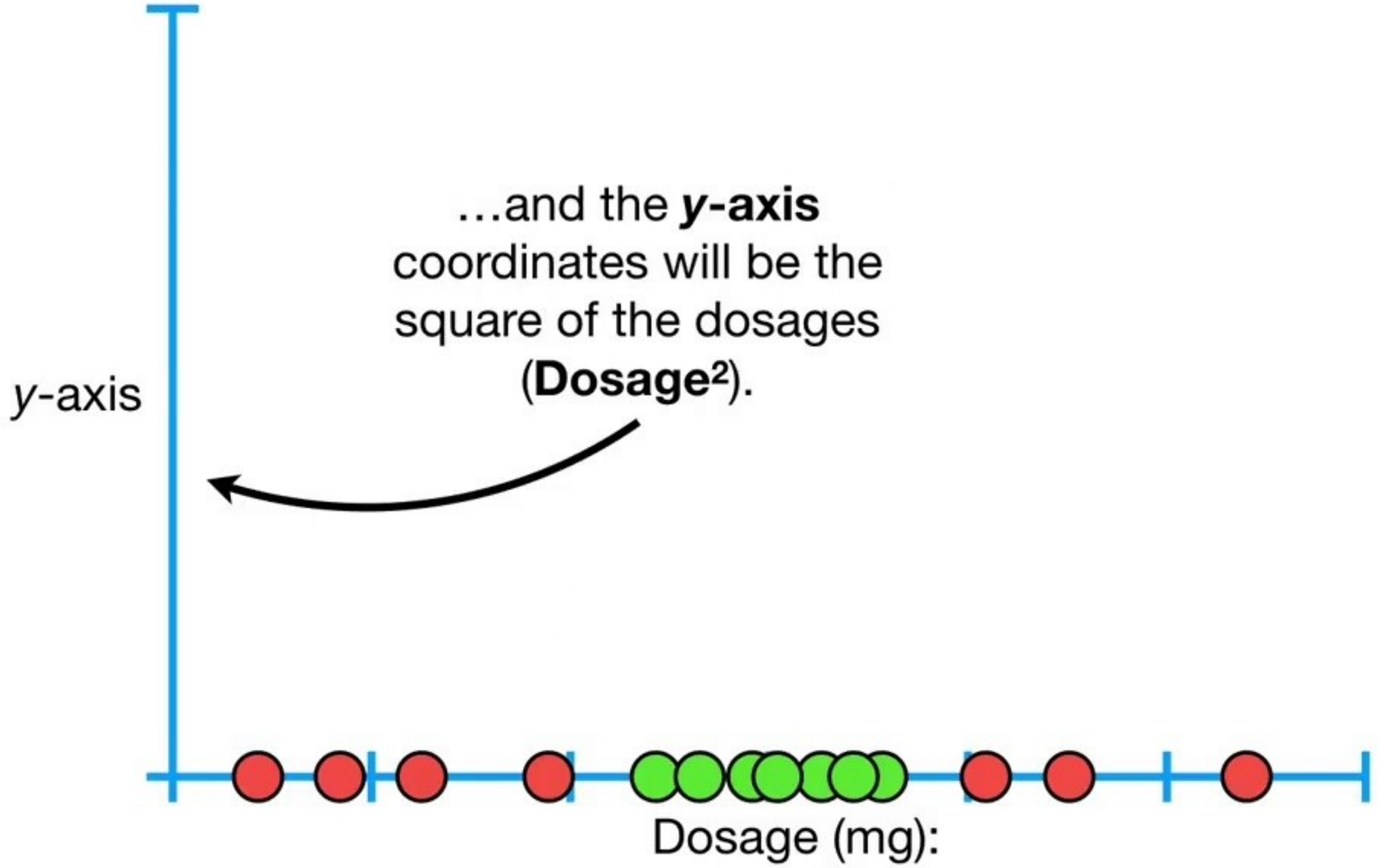


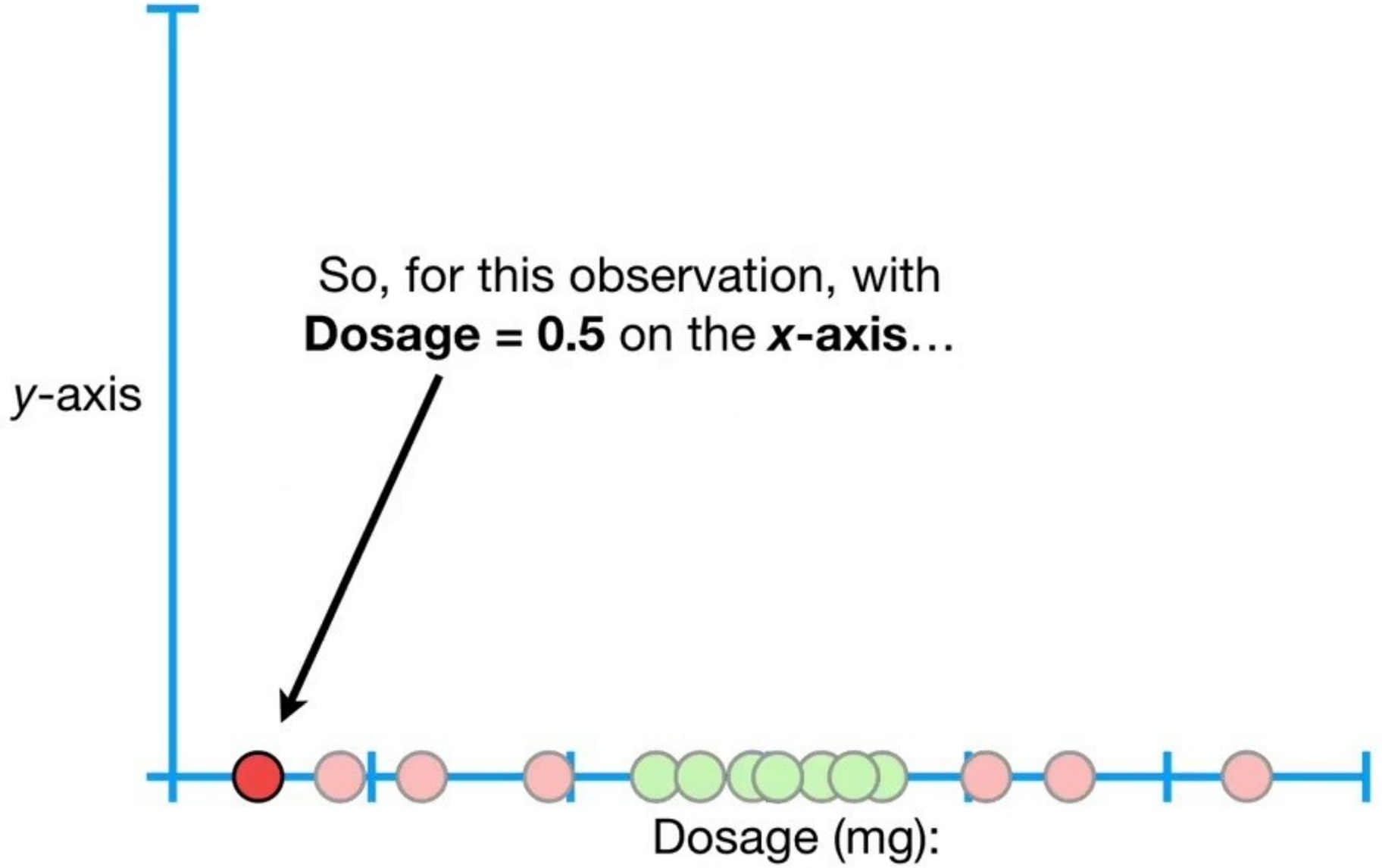
Support Vector Machines!!!

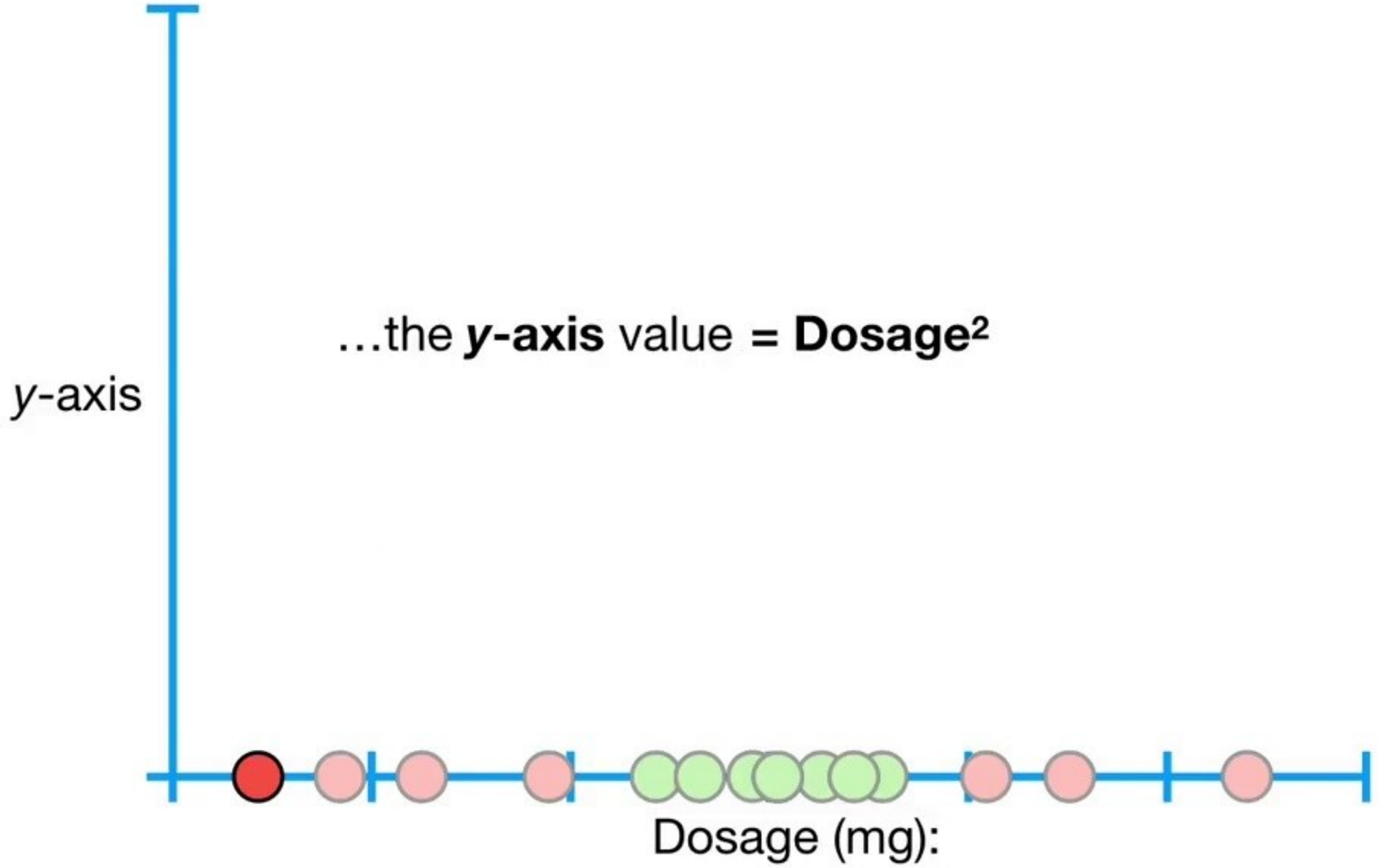
So let's start by getting get an intuitive sense of the main ideas behind **Support Vector Machines**.


We start by adding a **y-axis**
so we can draw a graph.
y-axis
Dosage (mg):

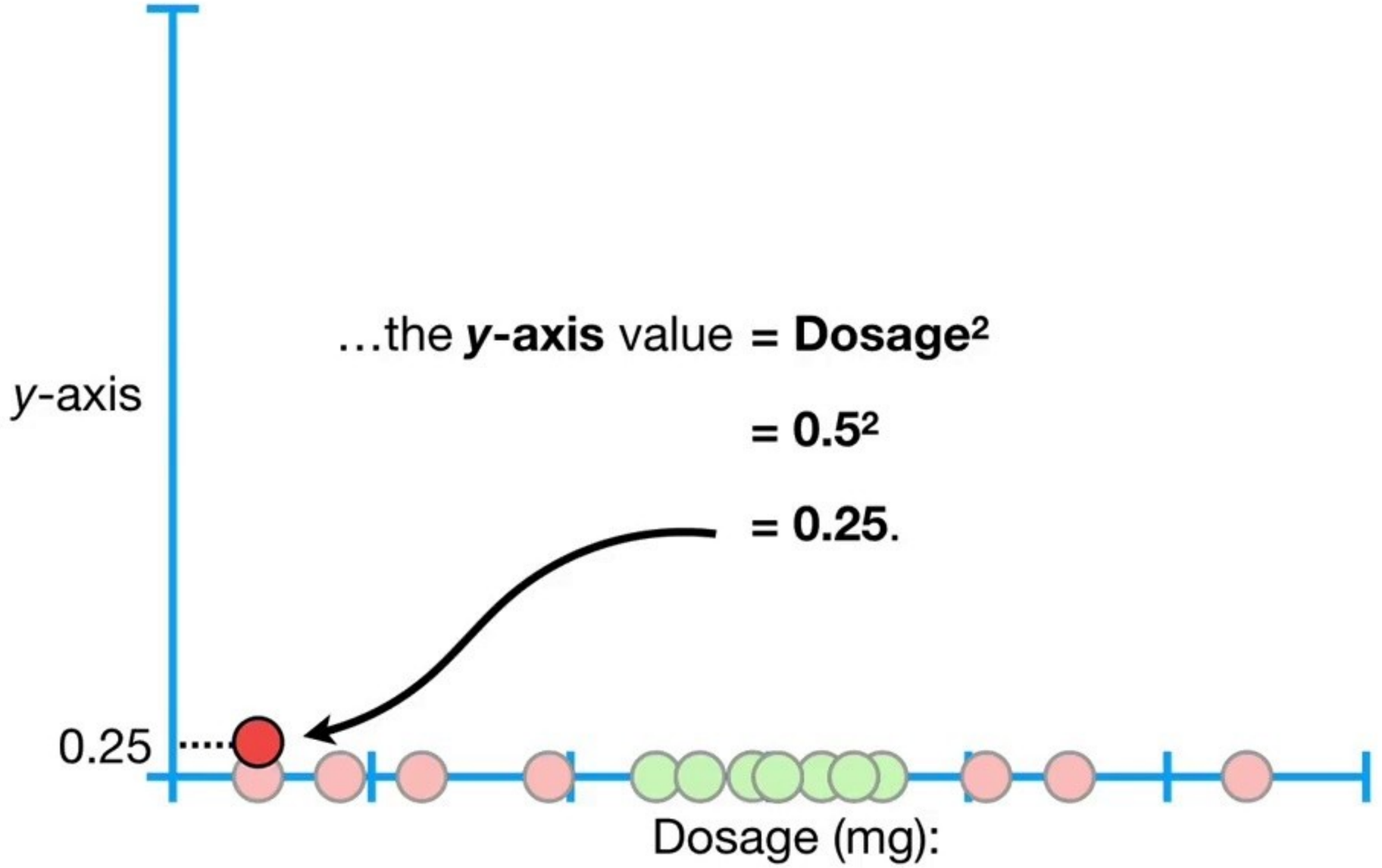

The **x-axis** coordinates in this graph will be the dosages that we have already observed…
y-axis
Dosage (mg):

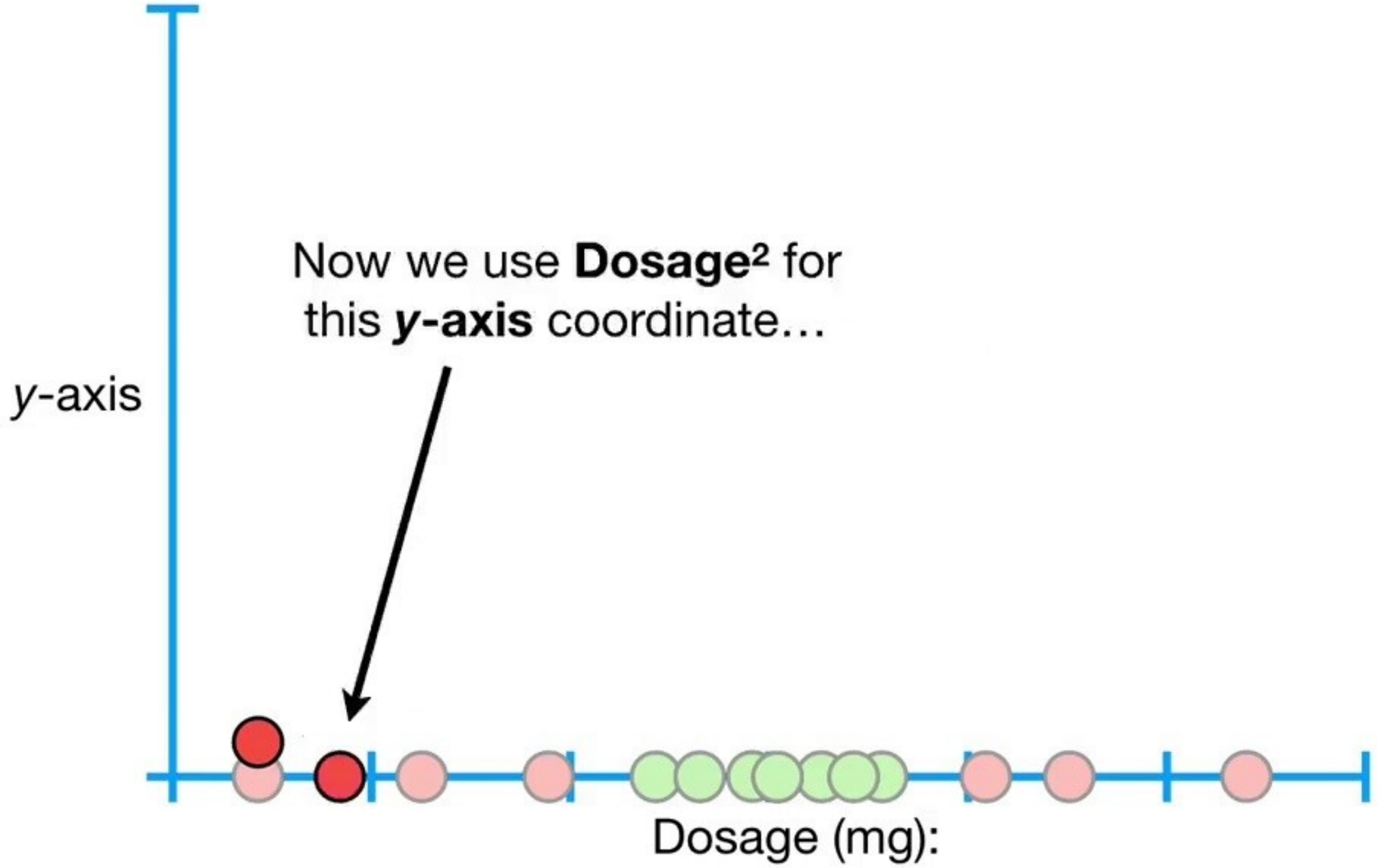

…and the **y-axis** coordinates will be the square of the dosages (**Dosage²**).
y-axis
Dosage (mg):

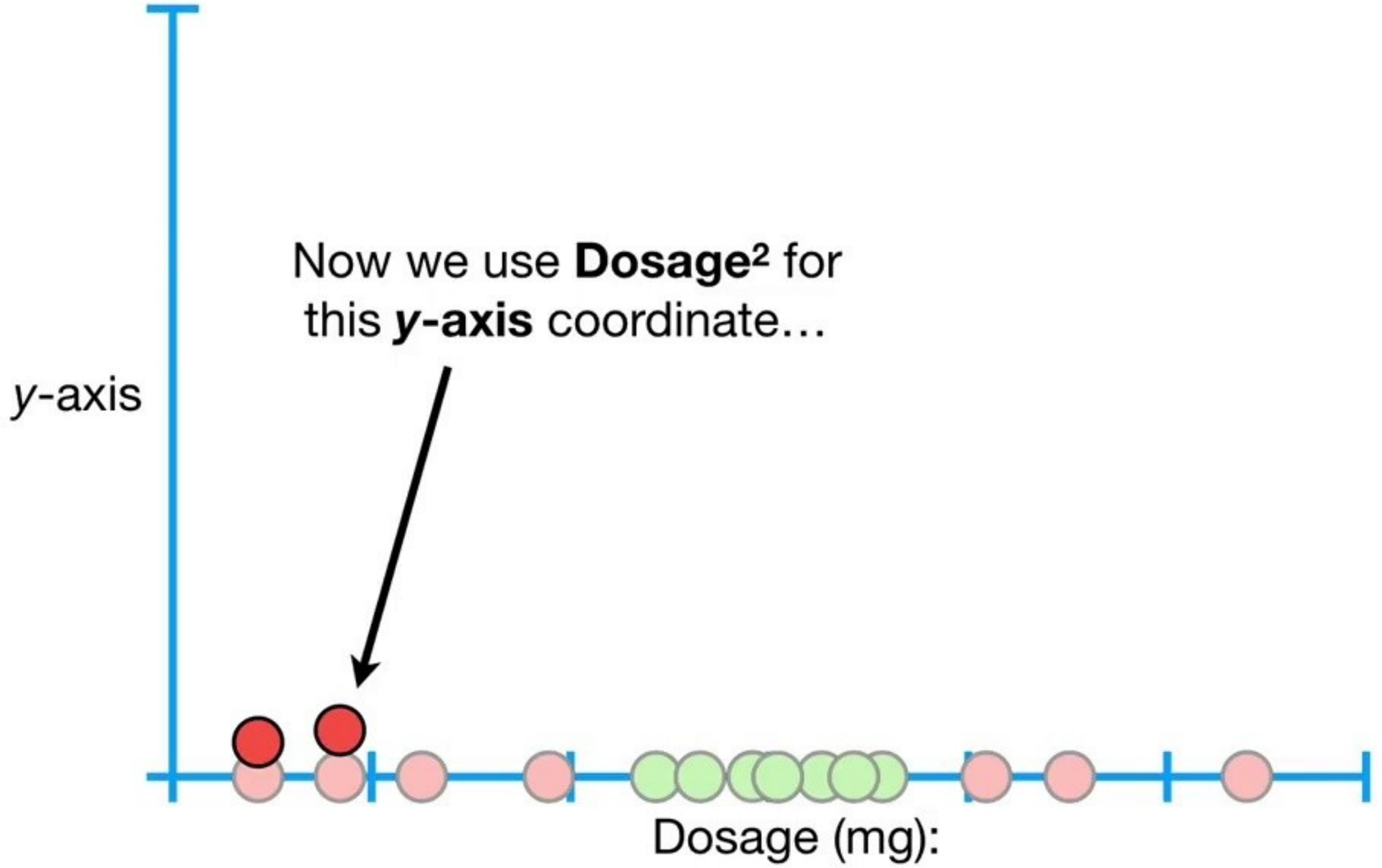

So, for this observation, with
Dosage = 0.5 on the ***x*-axis**…
y-axis
Dosage (mg):

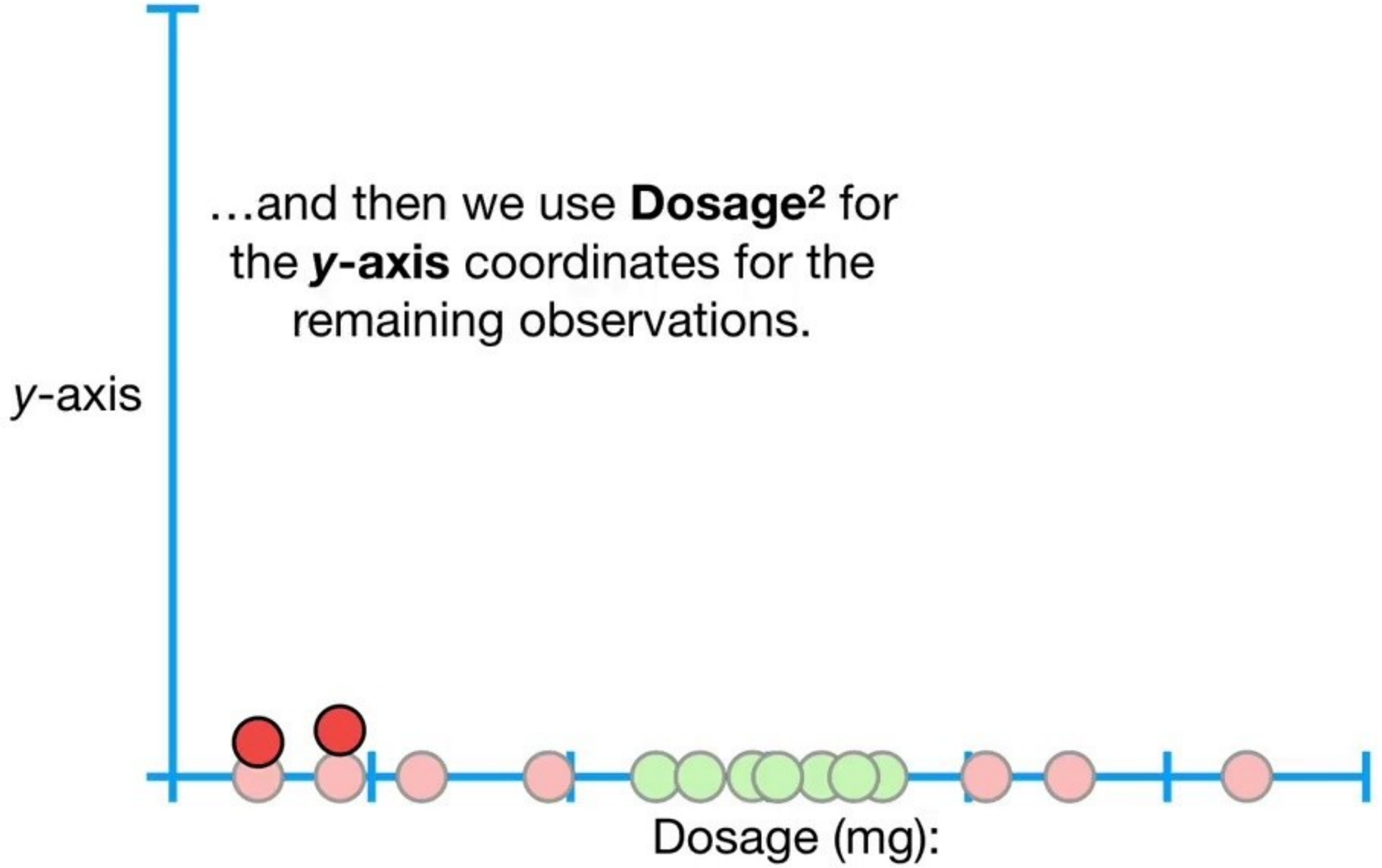

…the y-axis value = Dosage²
y-axis
Dosage (mg):

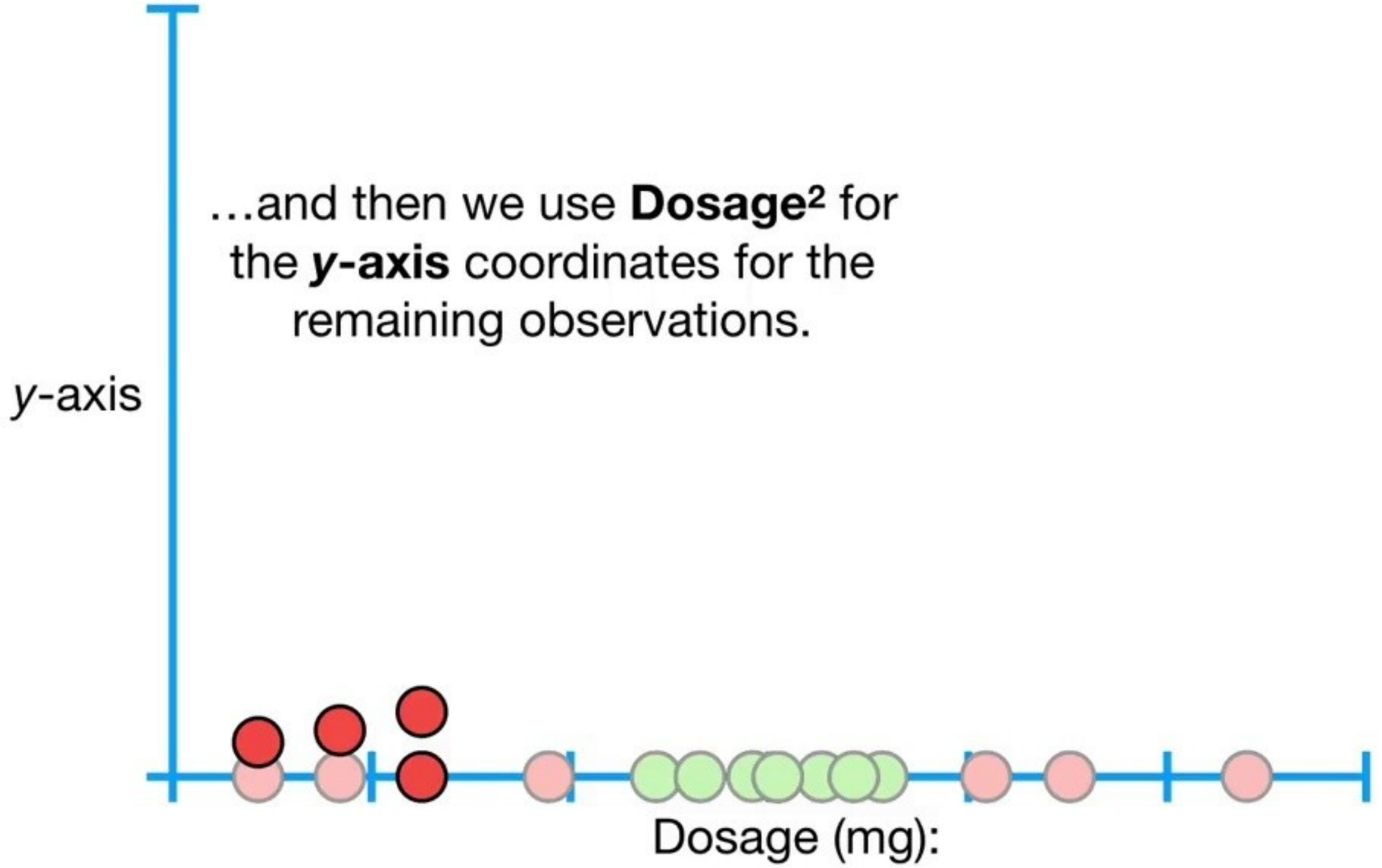

y-axis
…the y-axis value = Dosage²
= 0.5²
Dosage (mg):

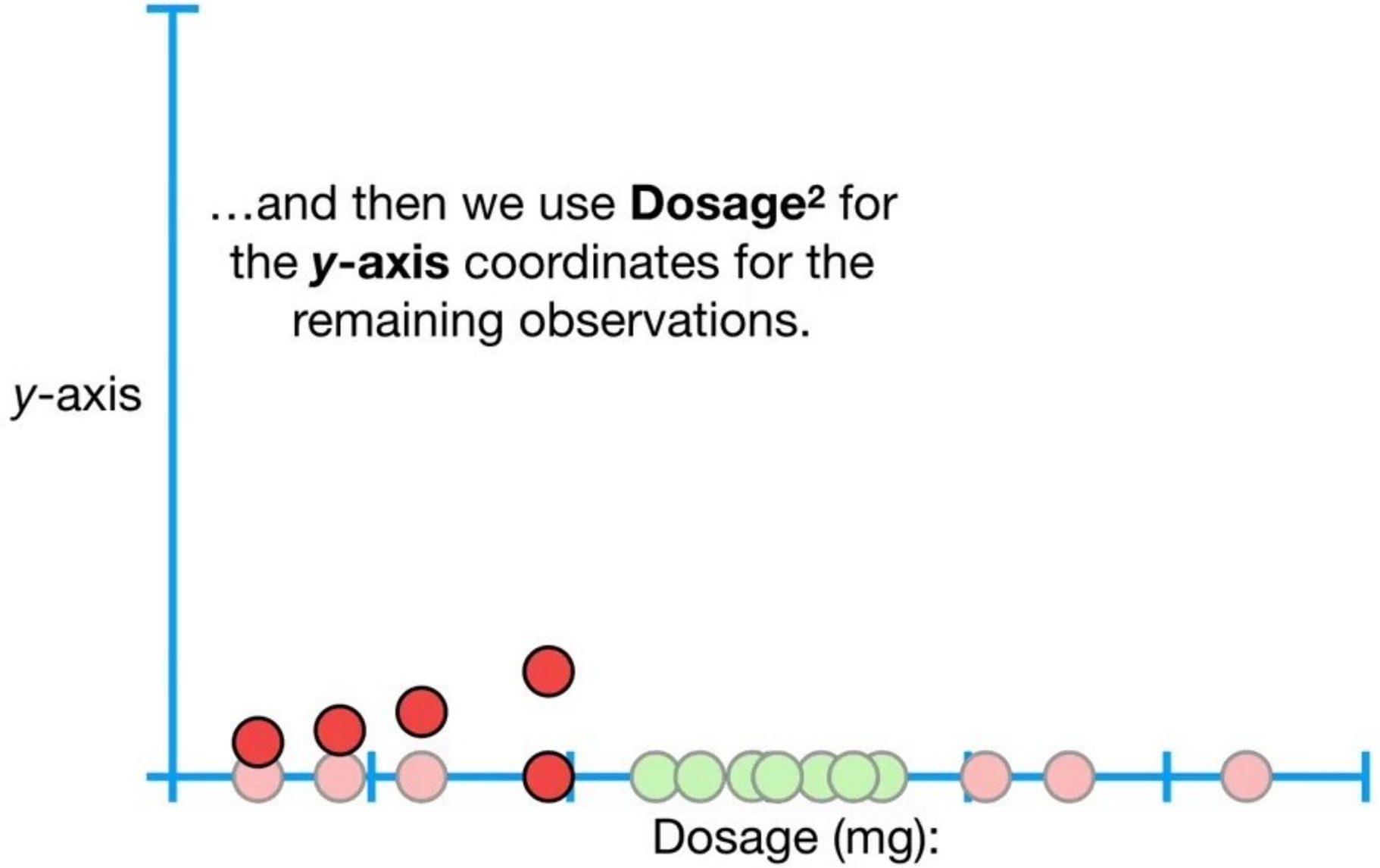

…the y-axis value = Dosage²
= 0.5²
= 0.25.
y-axis
0.25
Dosage (mg):

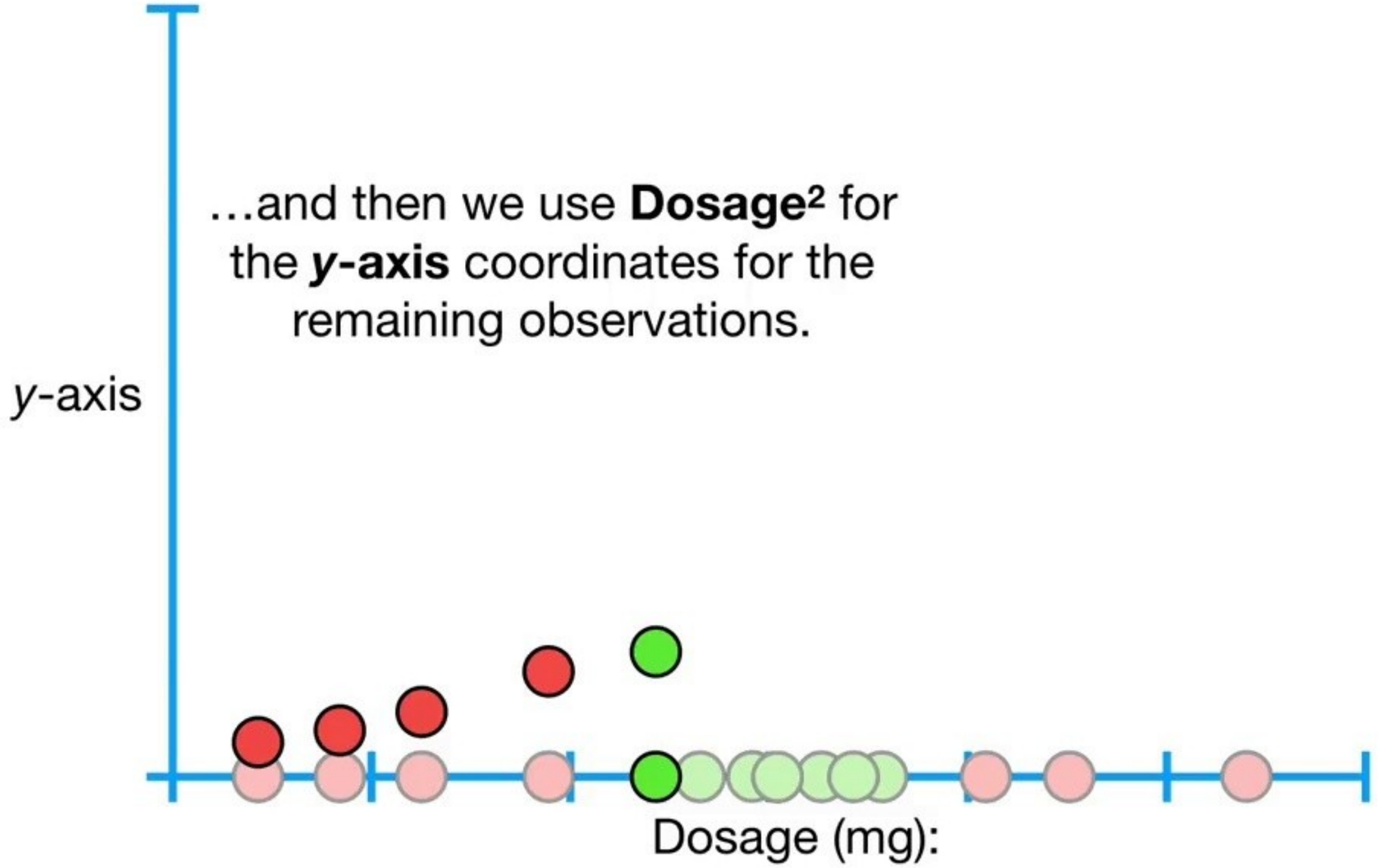

Now we use **Dosage²** for this ***y*-axis** coordinate…
y-axis
Dosage (mg):

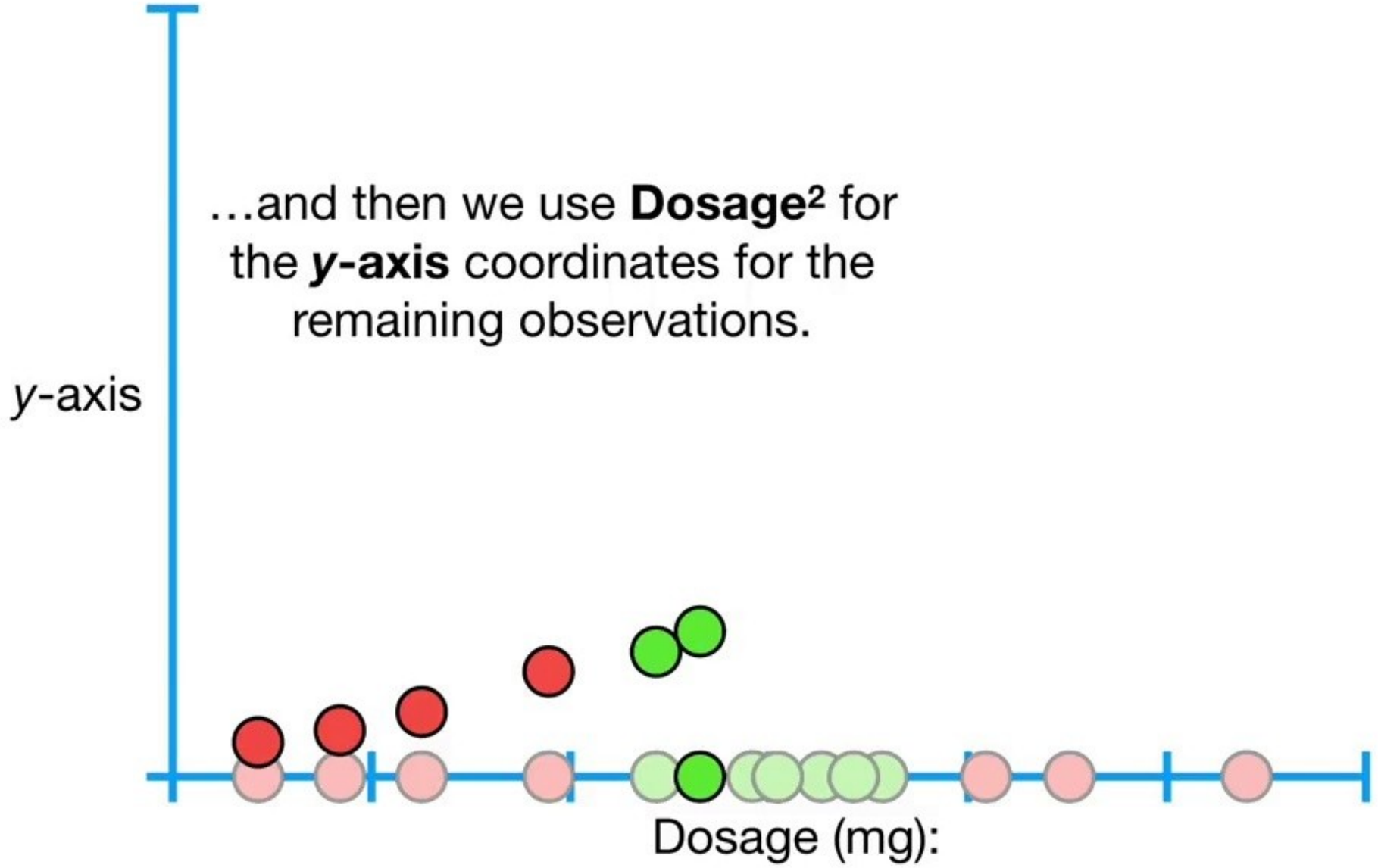

Now we use **Dosage²** for this ***y*-axis** coordinate…
y-axis
Dosage (mg):

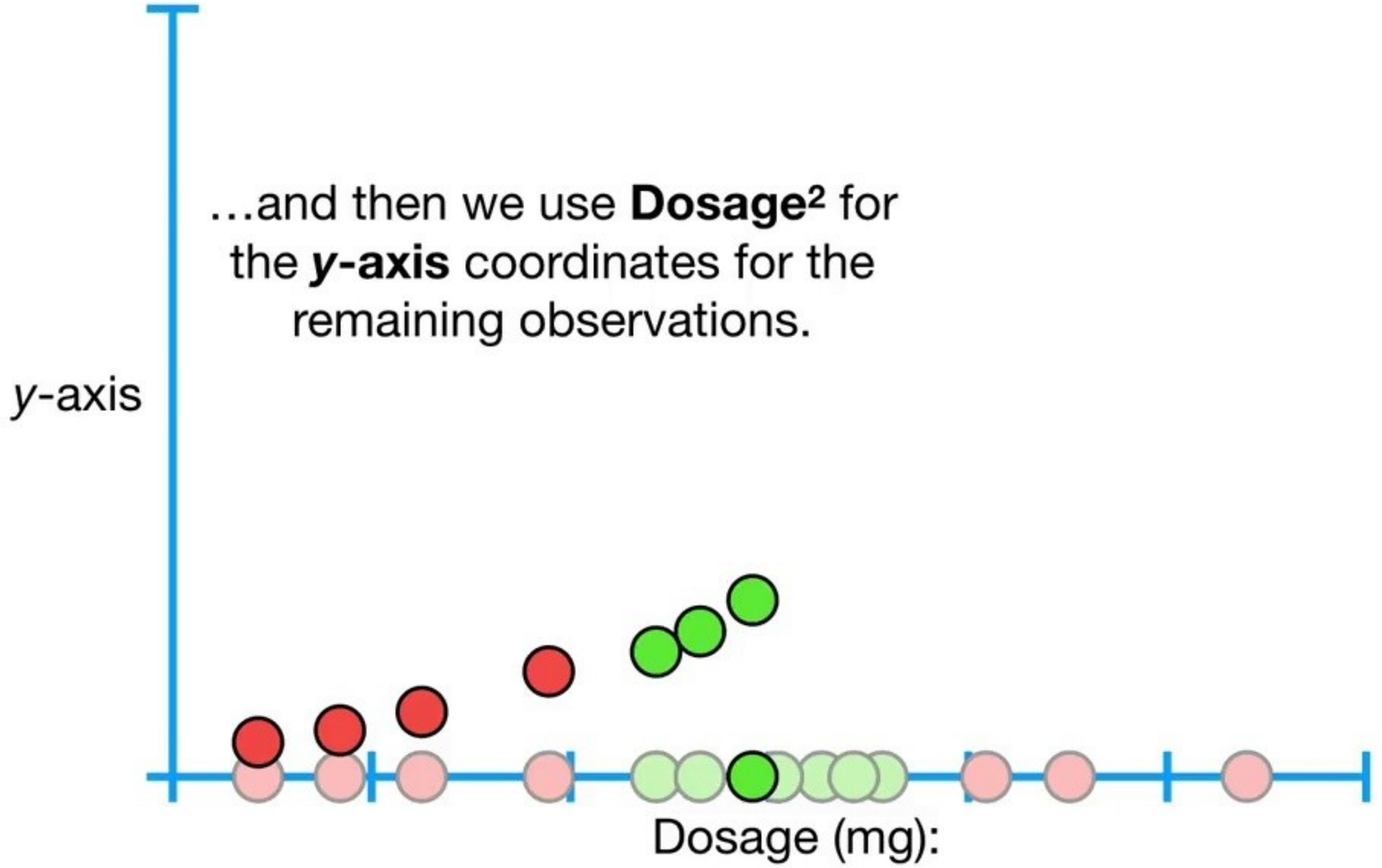

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

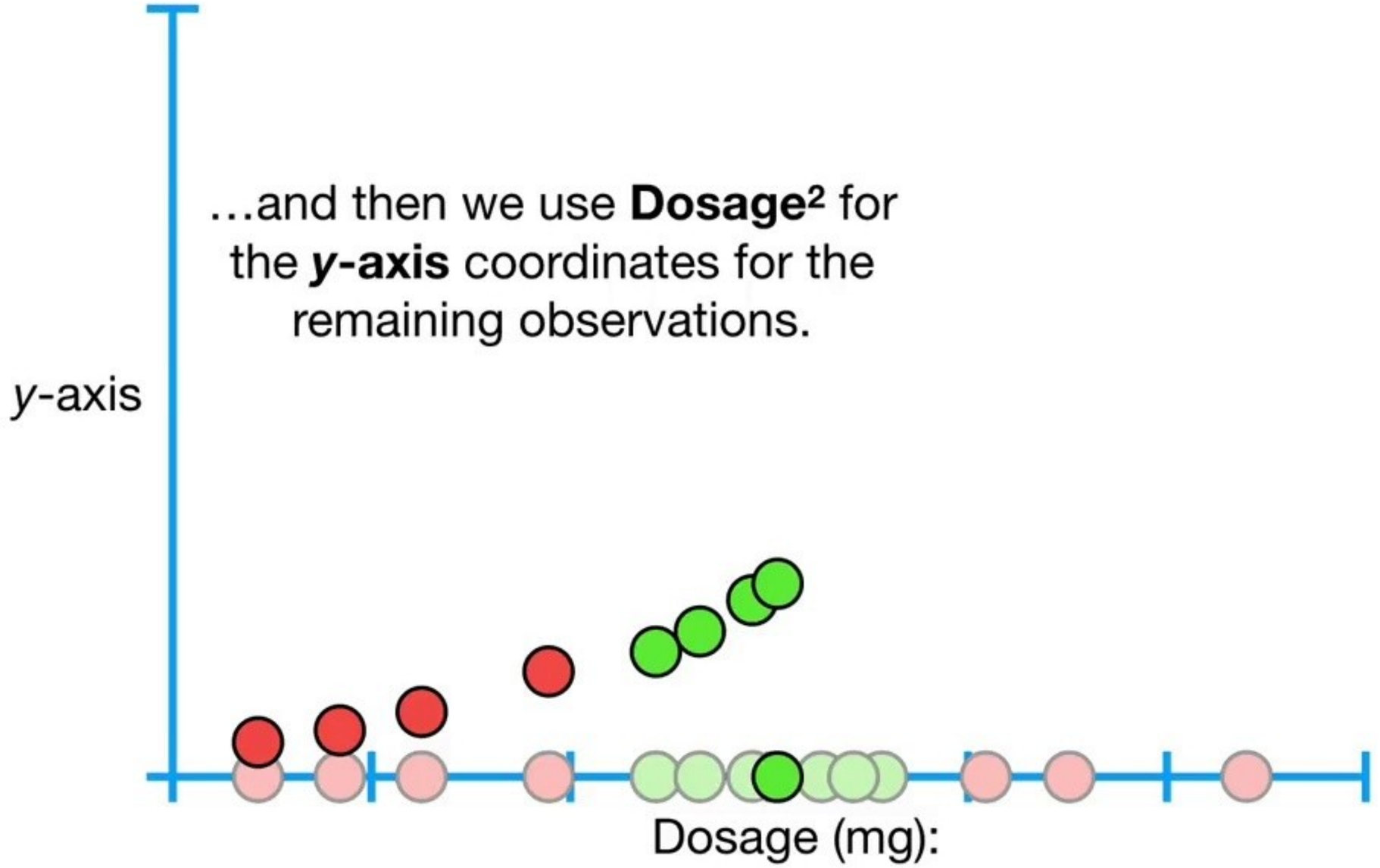

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

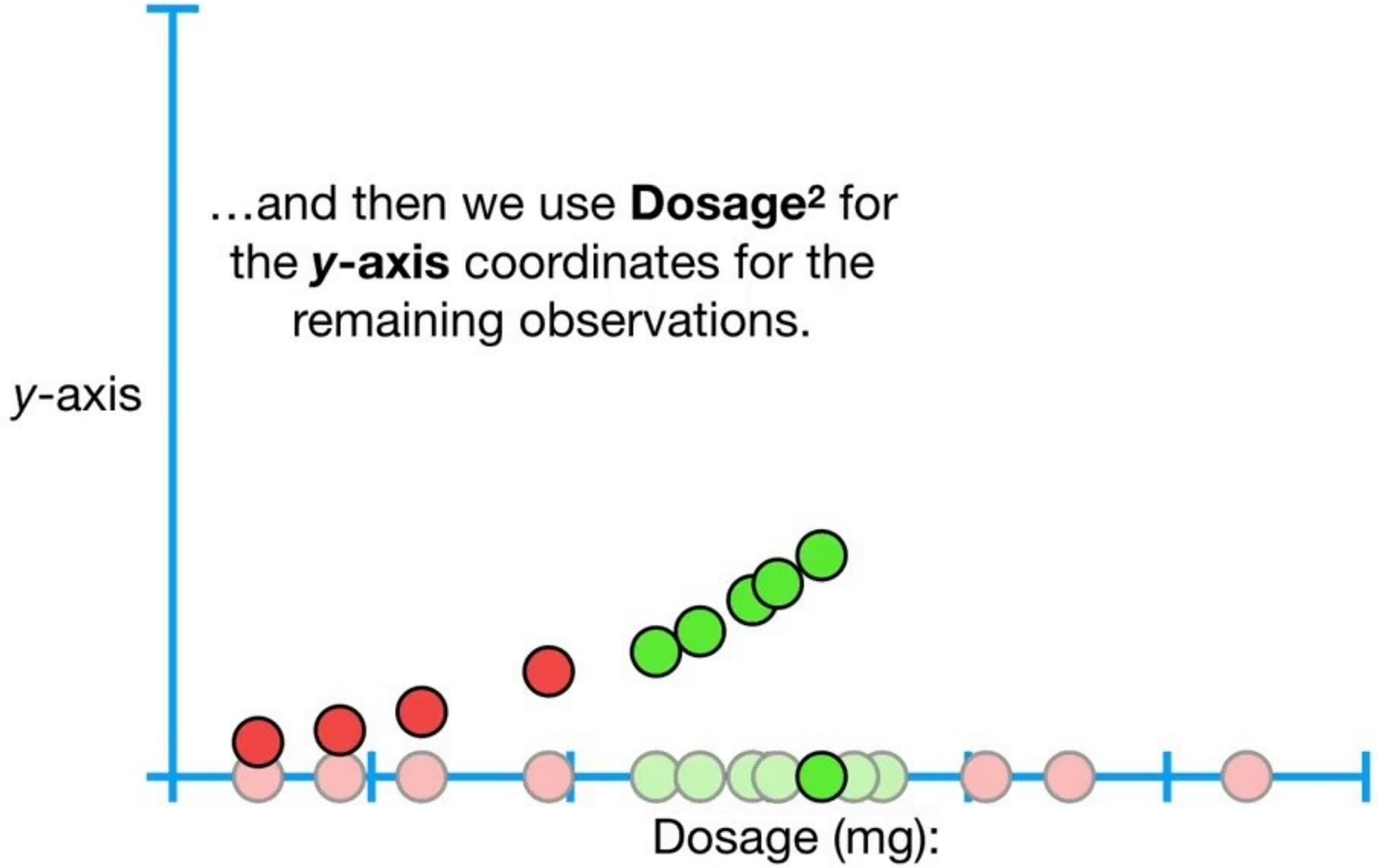

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

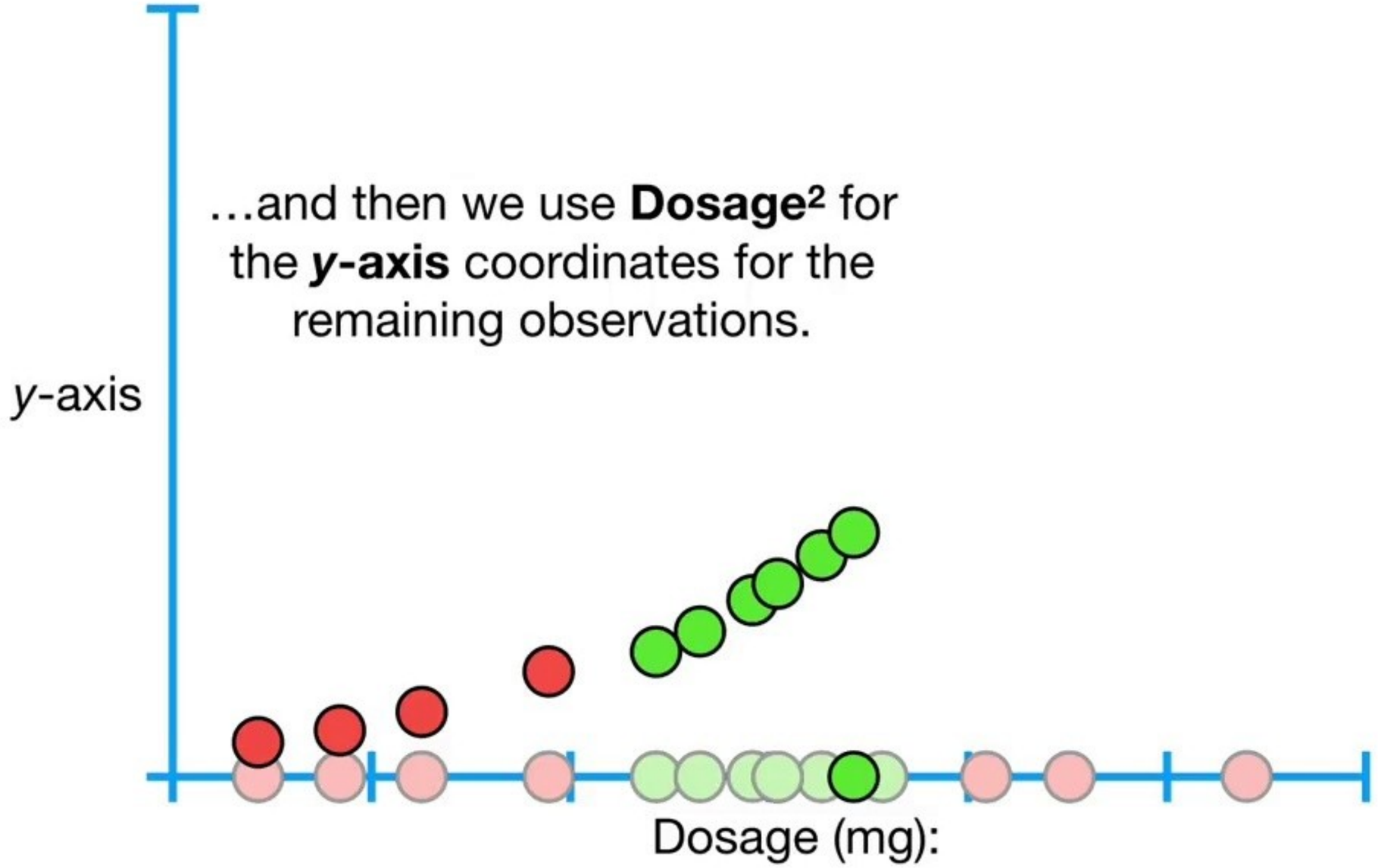

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

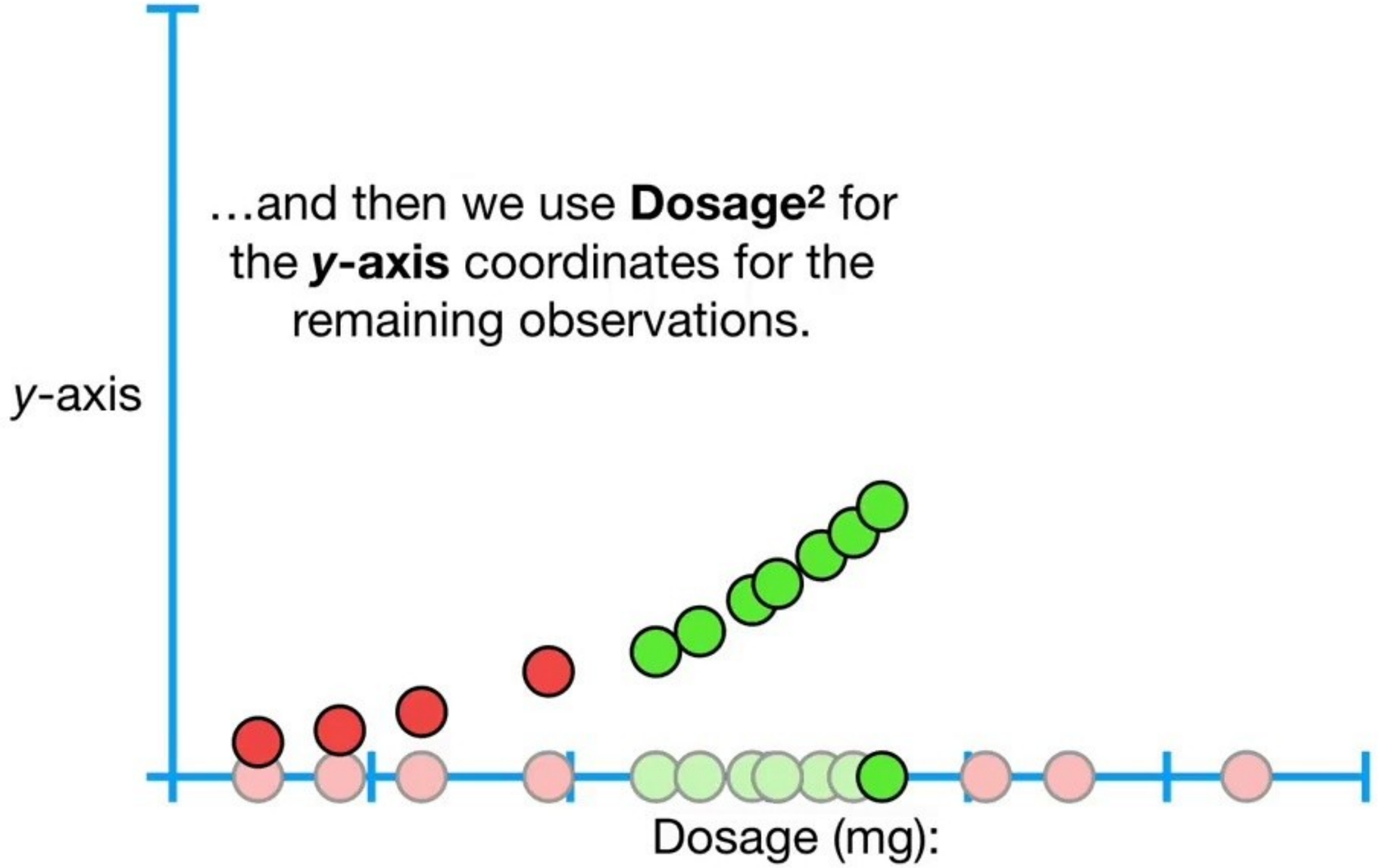

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

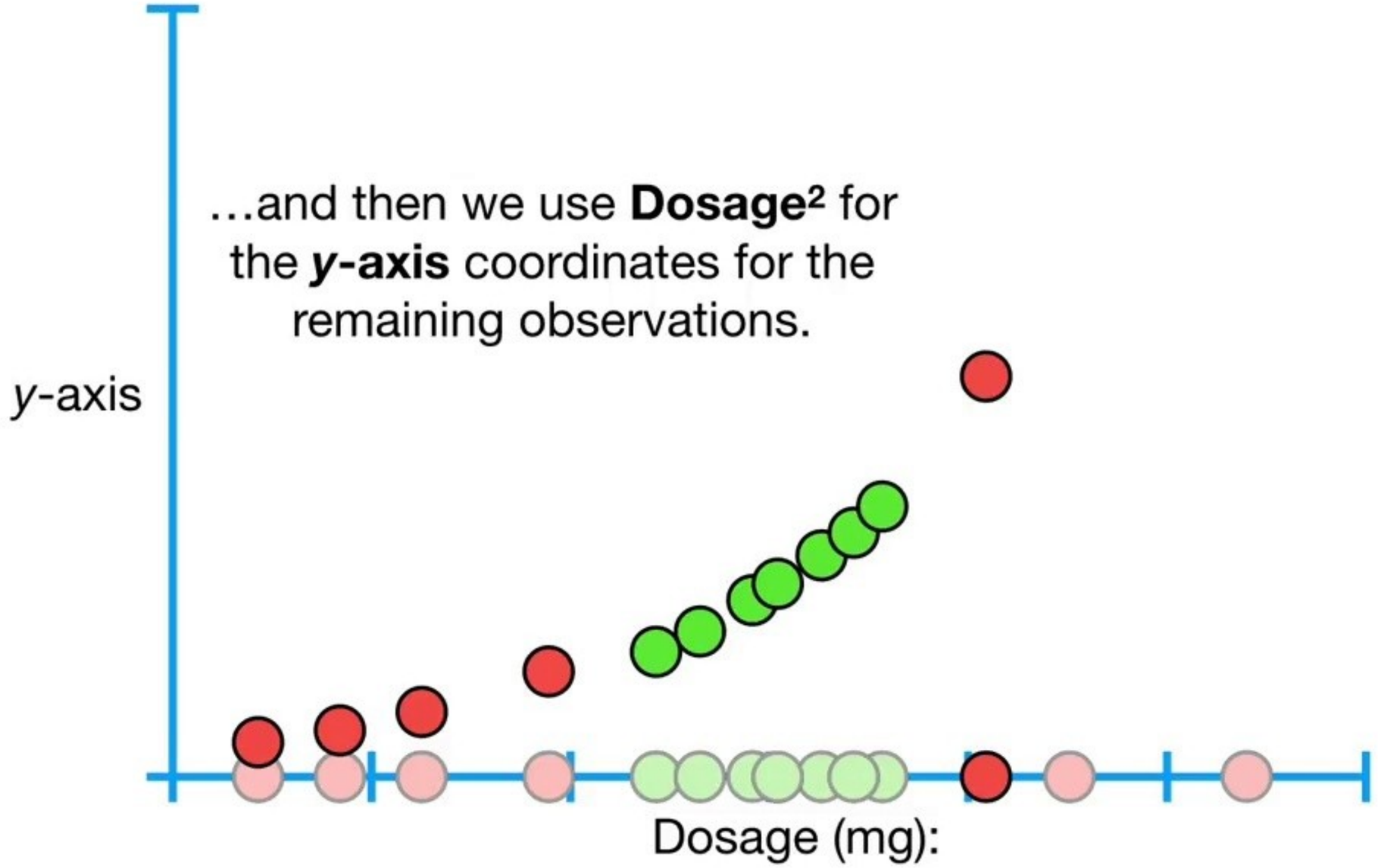

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

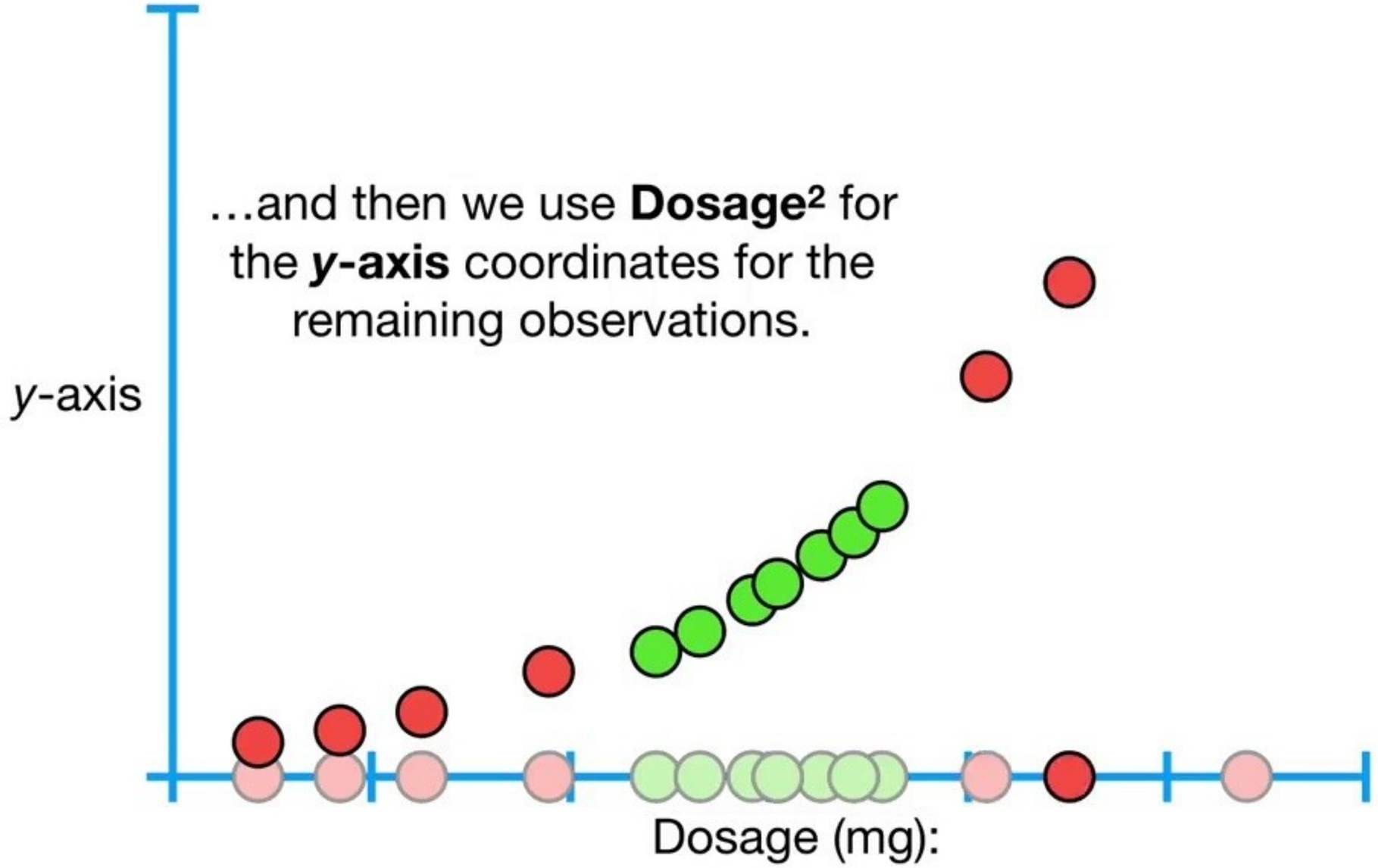

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

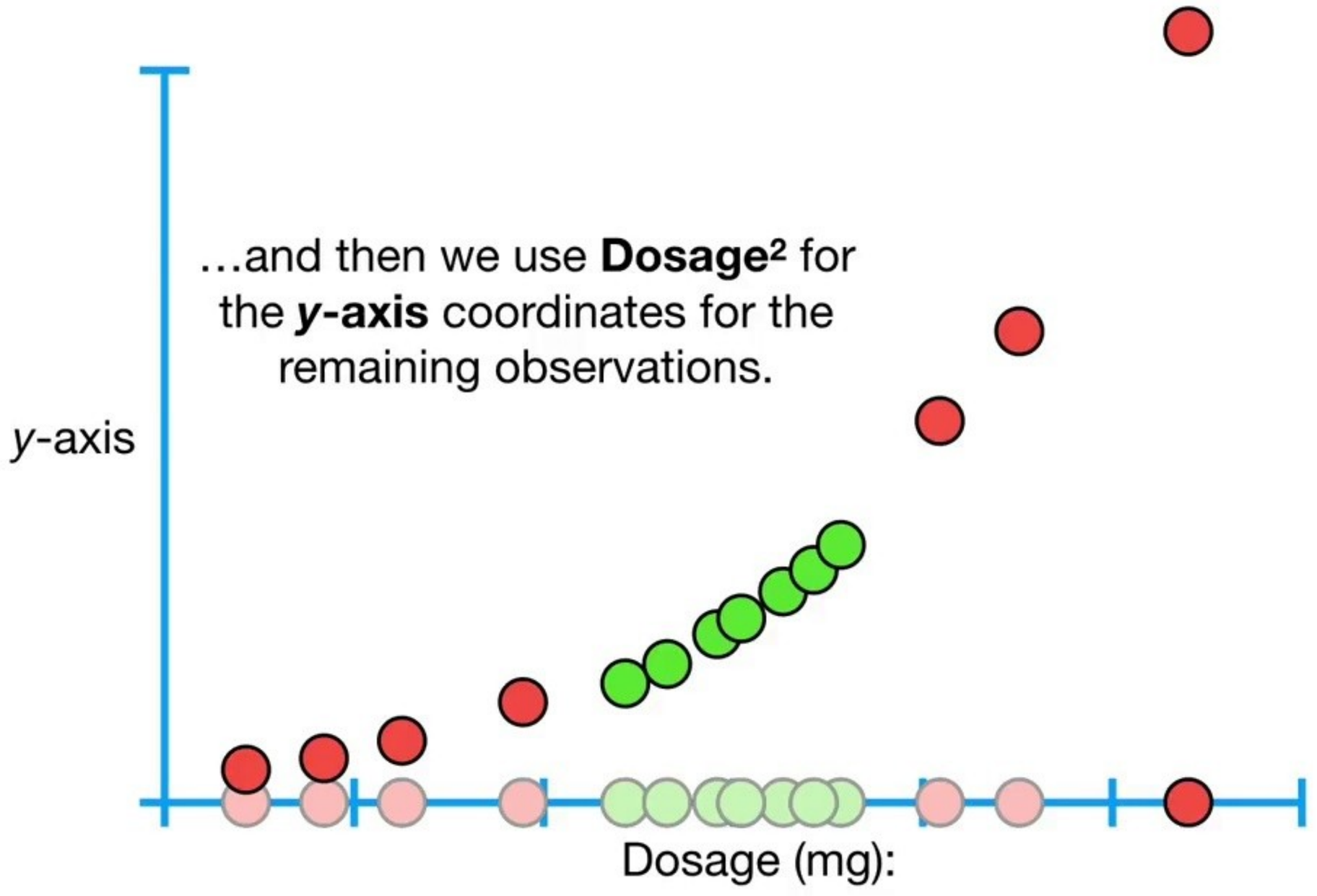

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

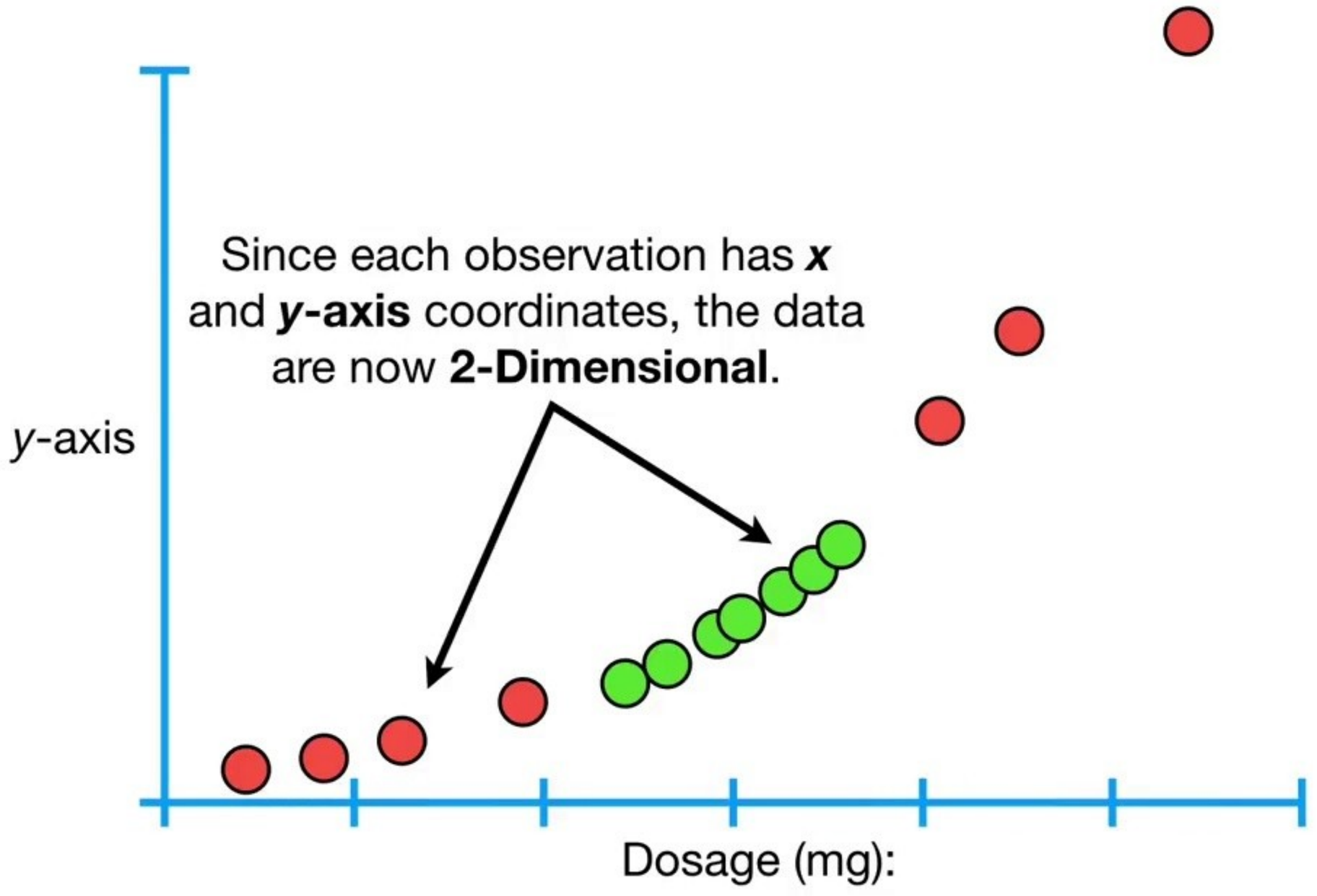

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

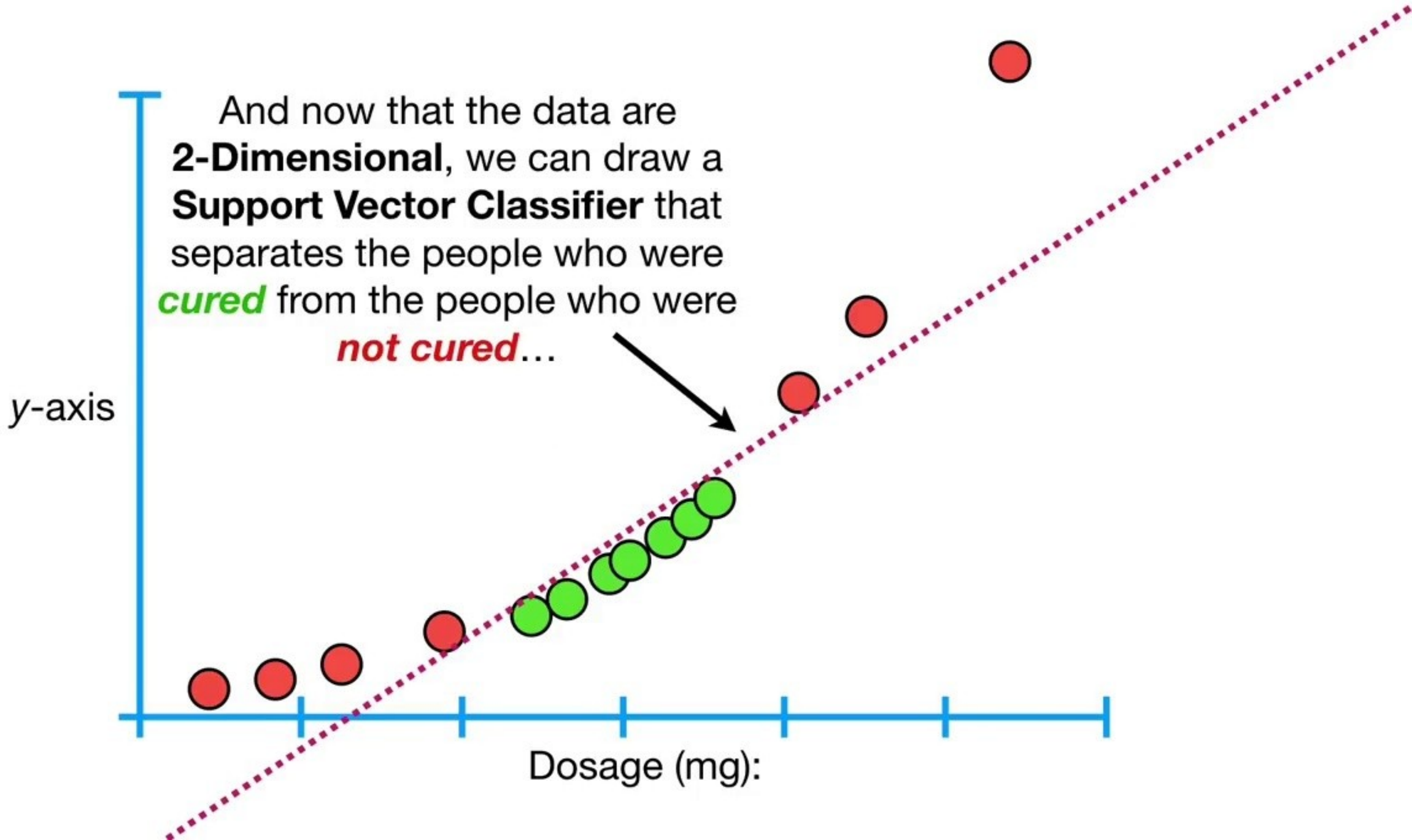

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

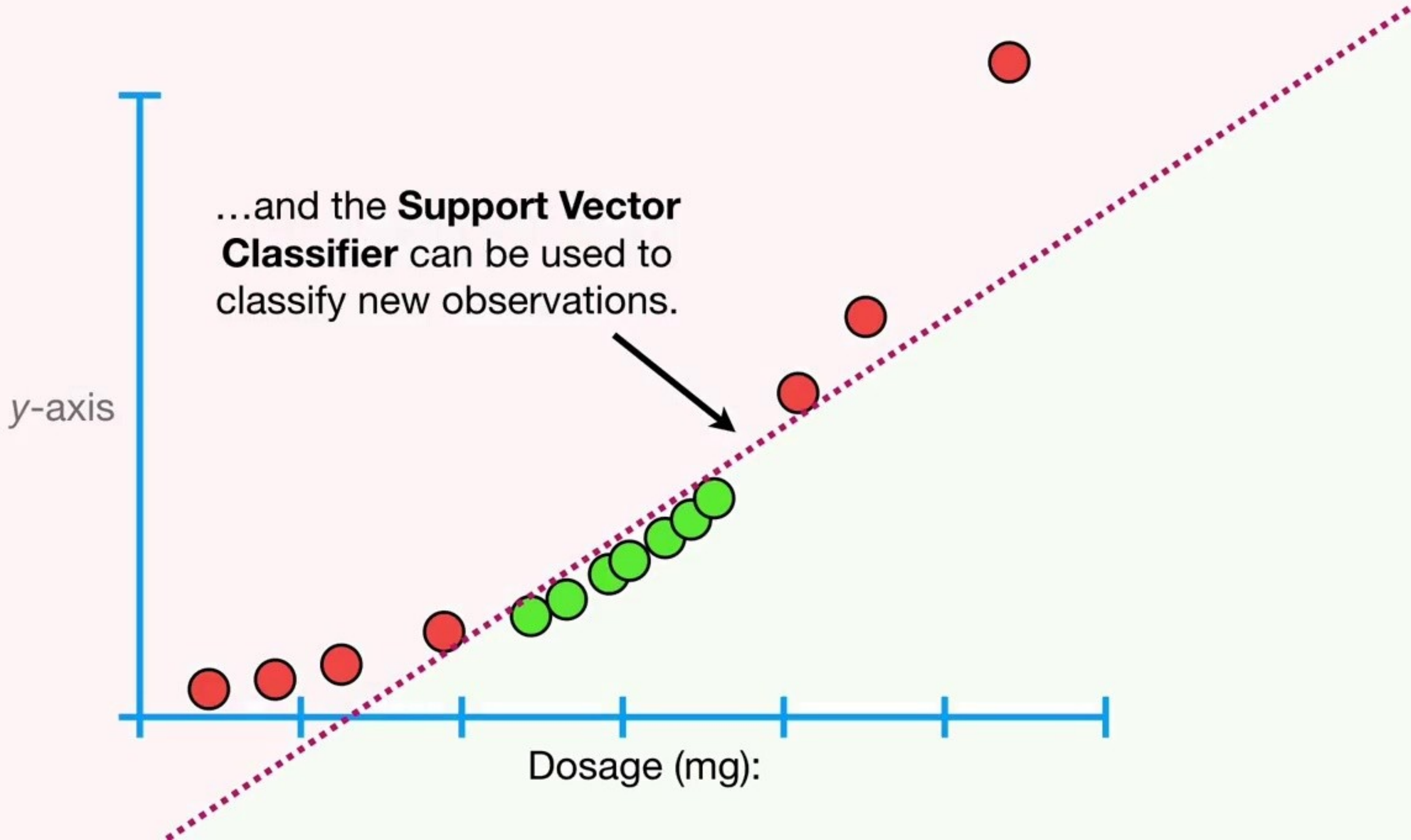

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

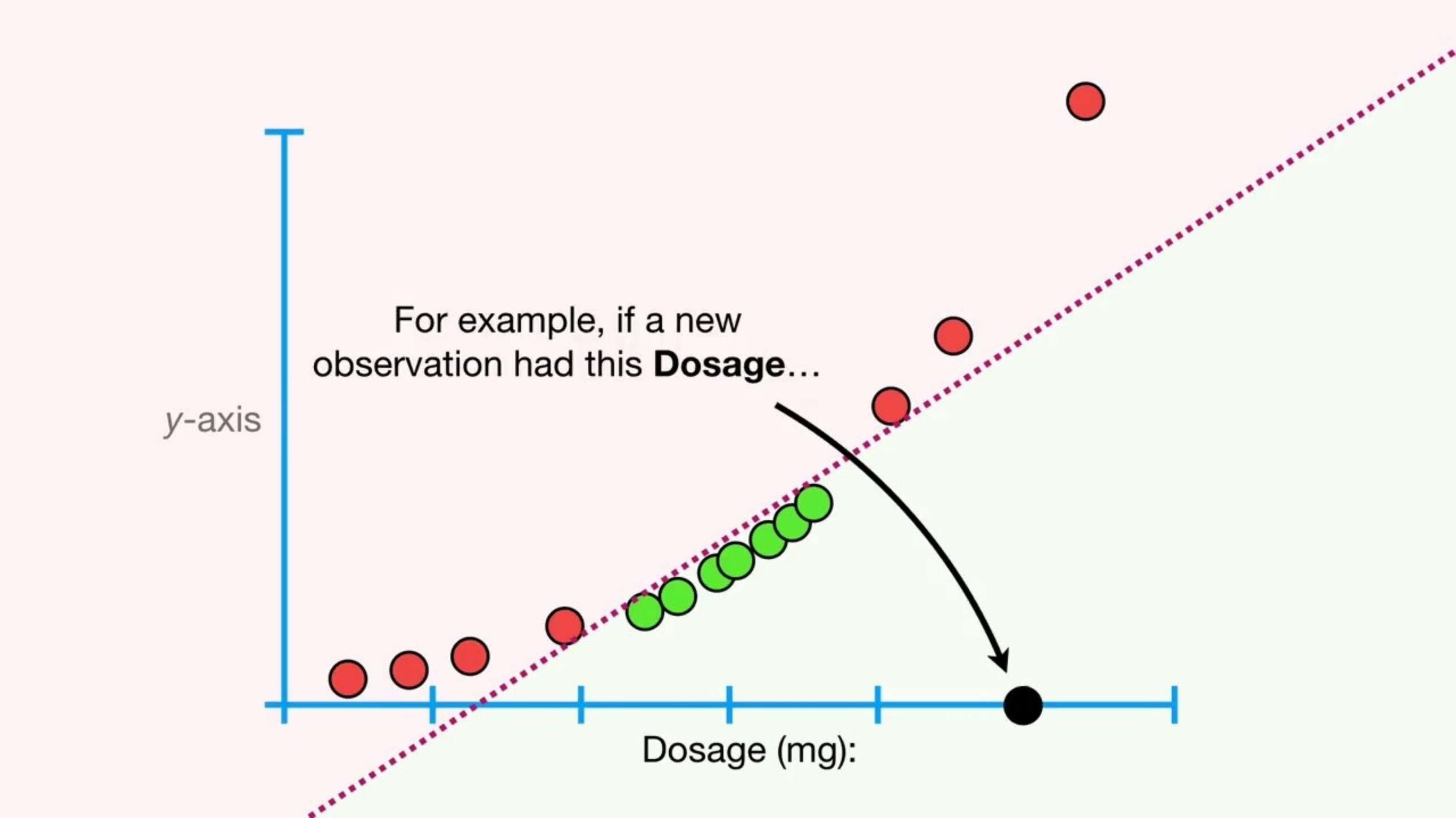

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

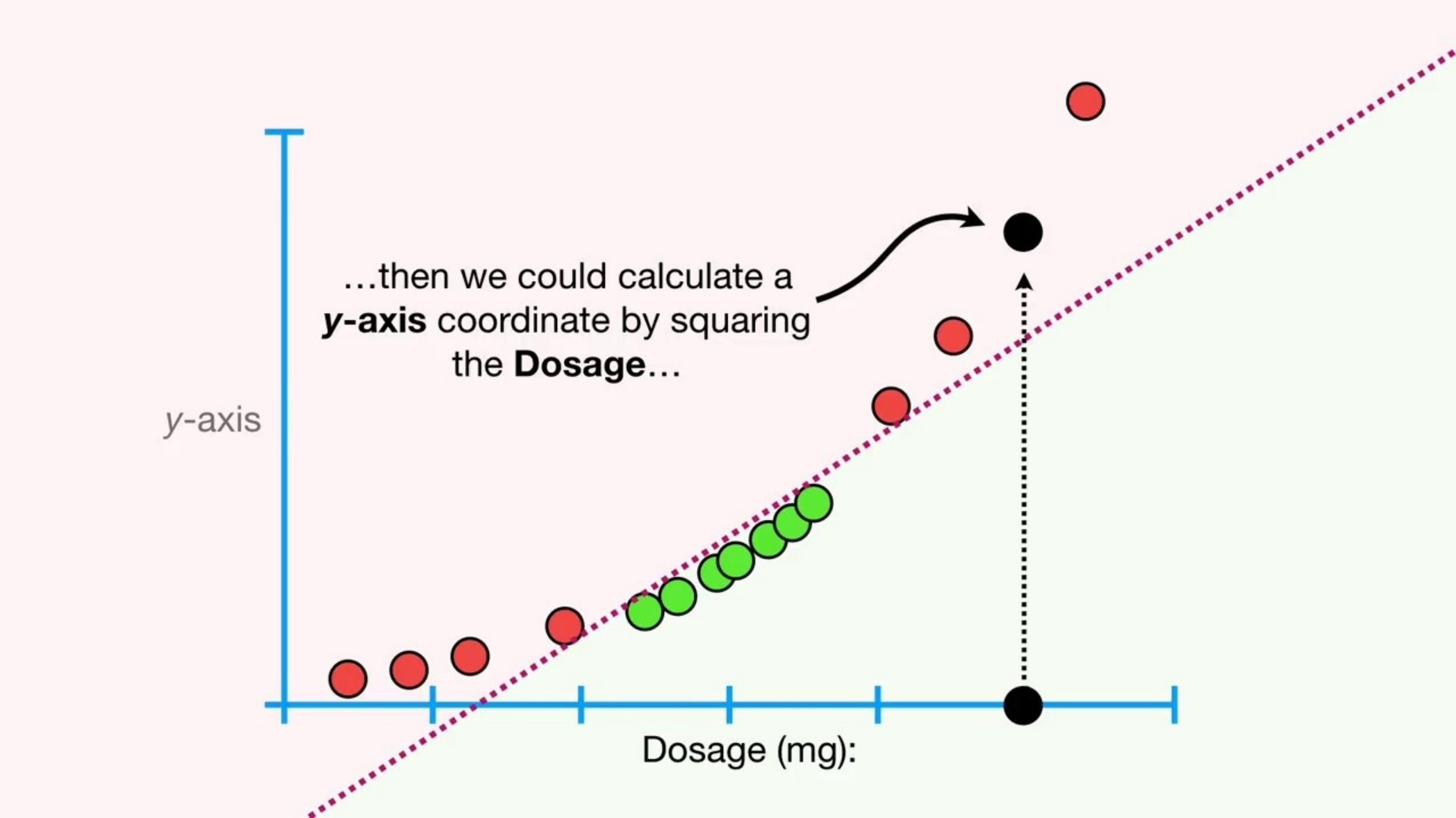

…and then we use **Dosage²** for the ***y*-axis** coordinates for the remaining observations.
y-axis
Dosage (mg):

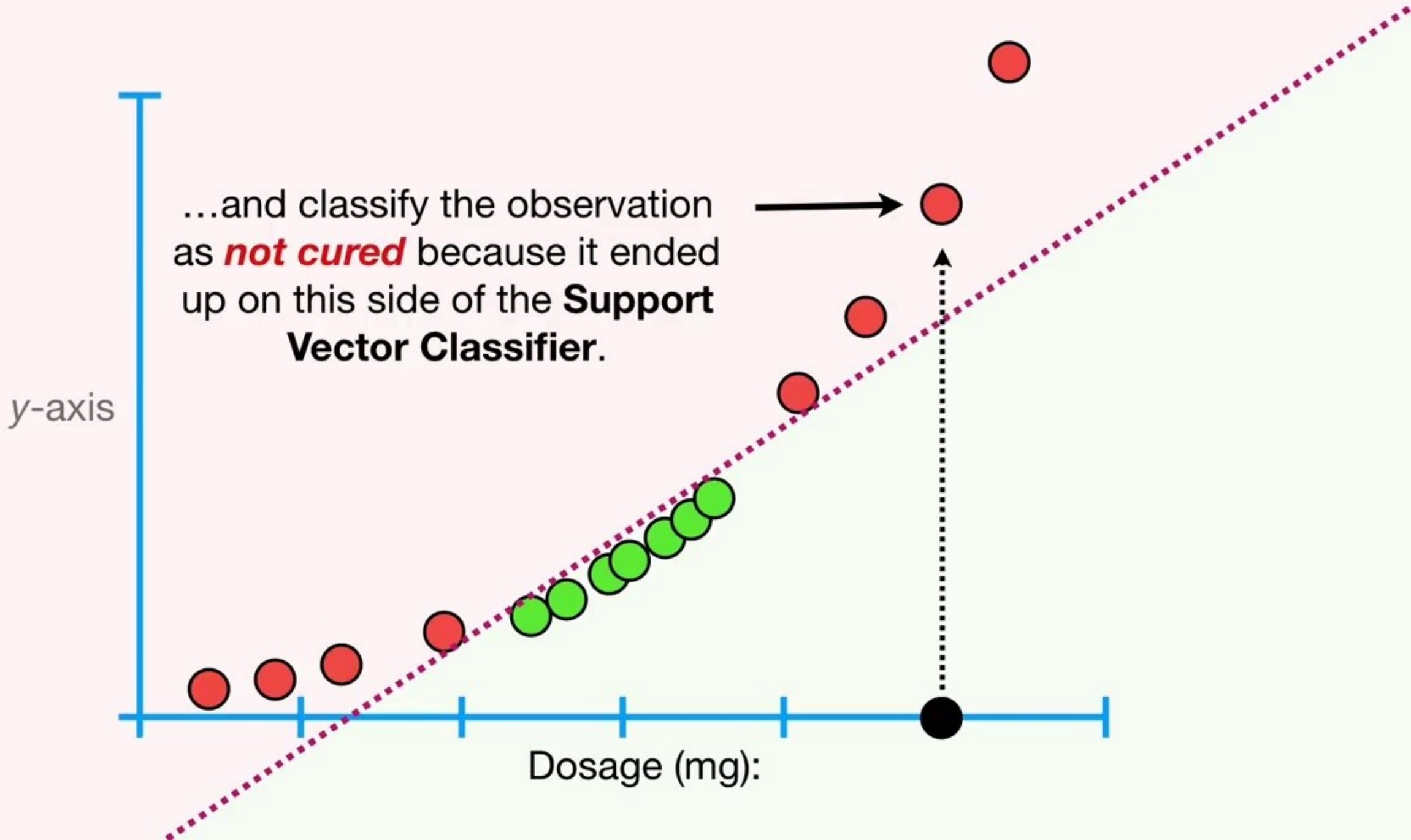

Since each observation has *x* and ***y*-axis** coordinates, the data are now **2-Dimensional**.
y-axis
Dosage (mg):

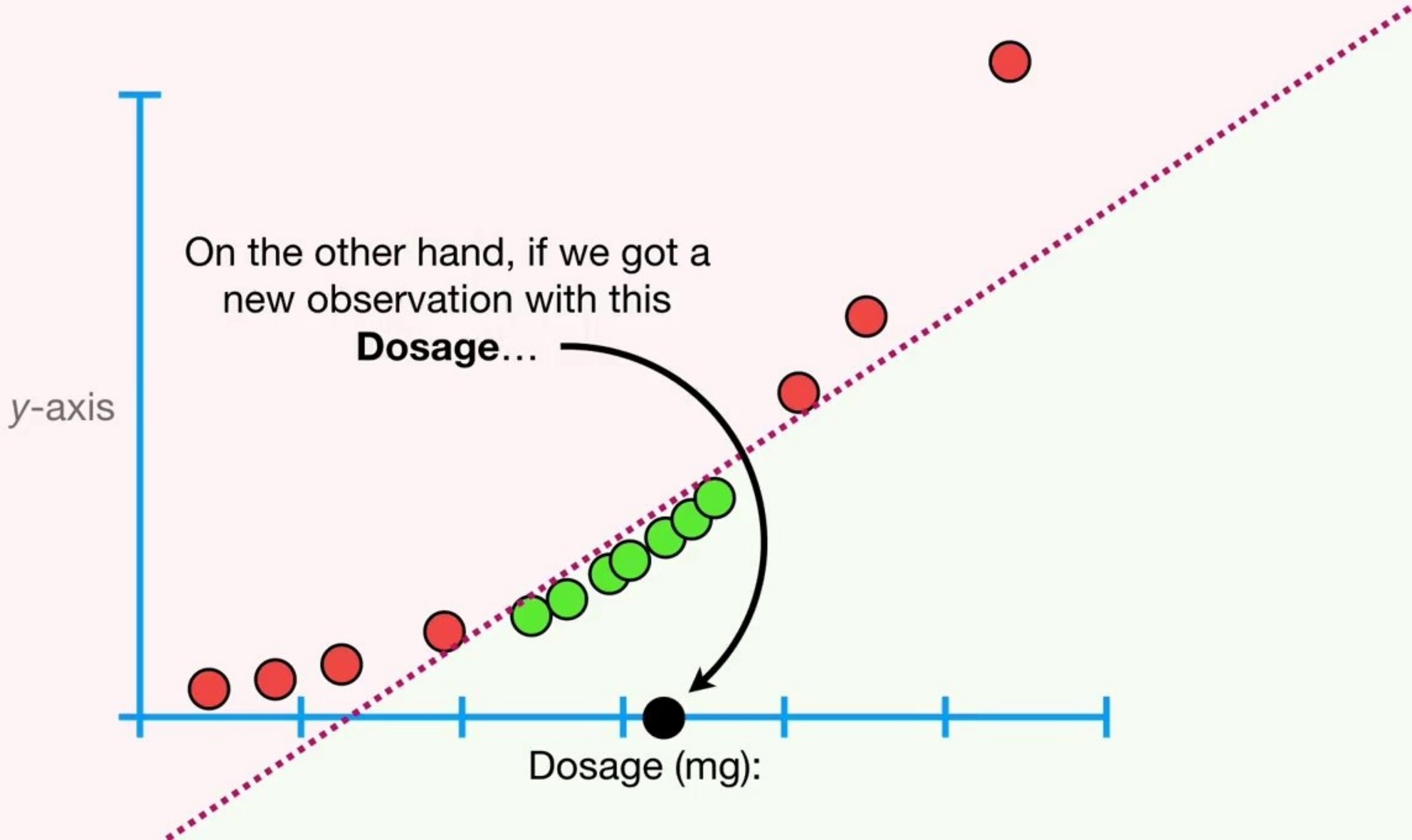

And now that the data are
2-Dimensional, we can draw a
Support Vector Classifier that
separates the people who were
cured from the people who were
not cured…
y-axis
Dosage (mg):

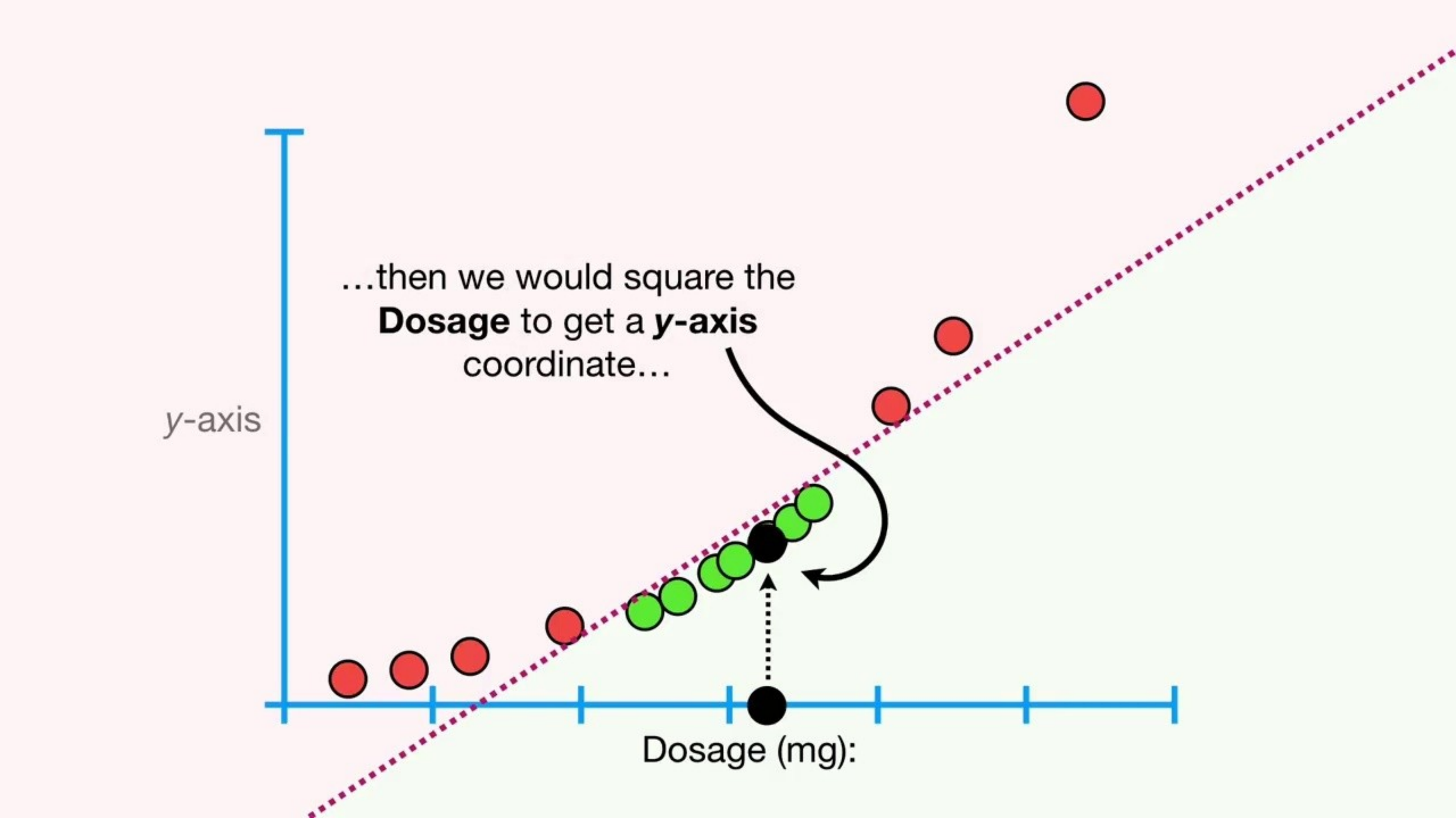

…and the **Support Vector Classifier** can be used to classify new observations.
y-axis
Dosage (mg):

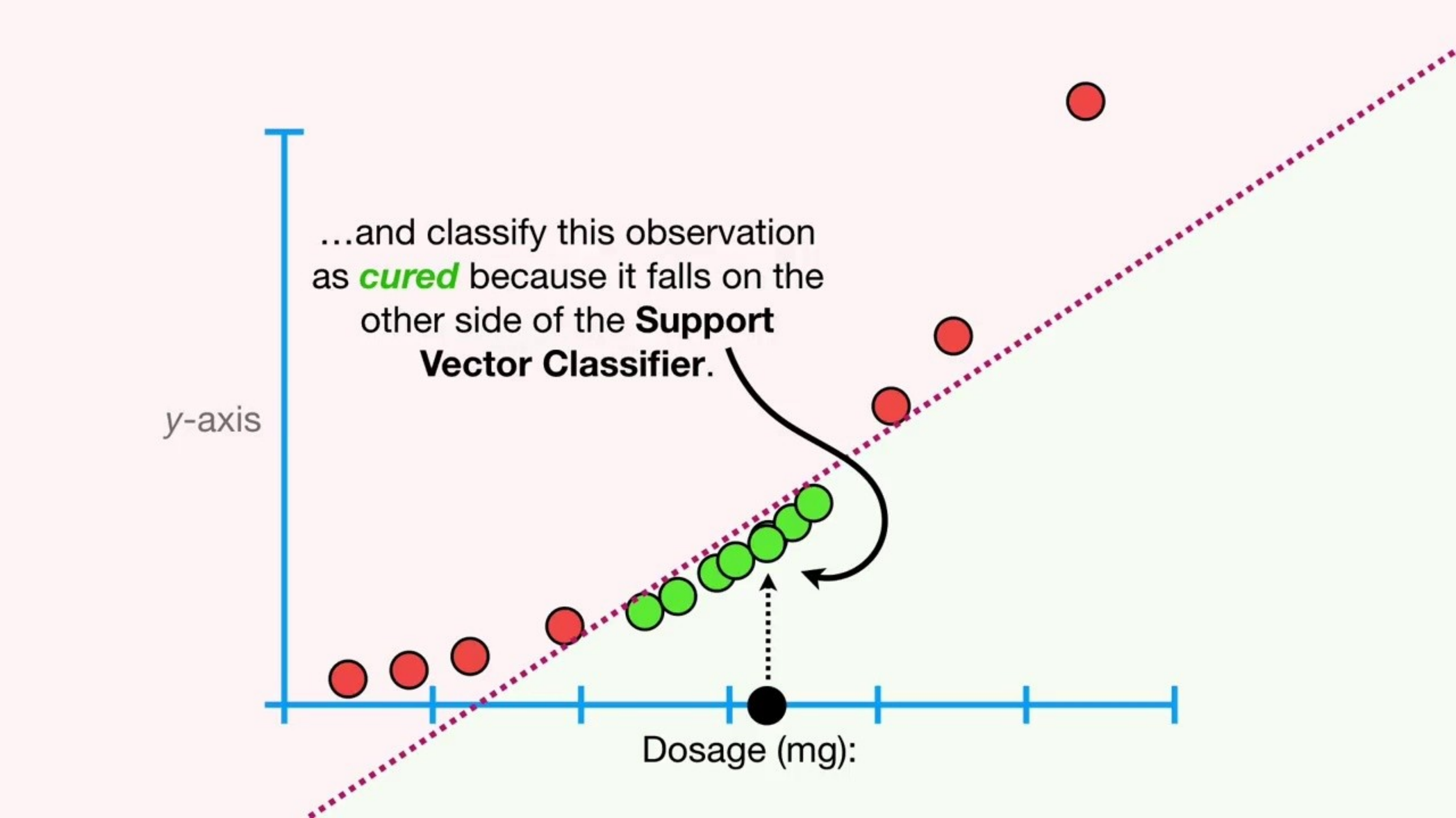

For example, if a new observation had this **Dosage**…
y-axis
Dosage (mg):

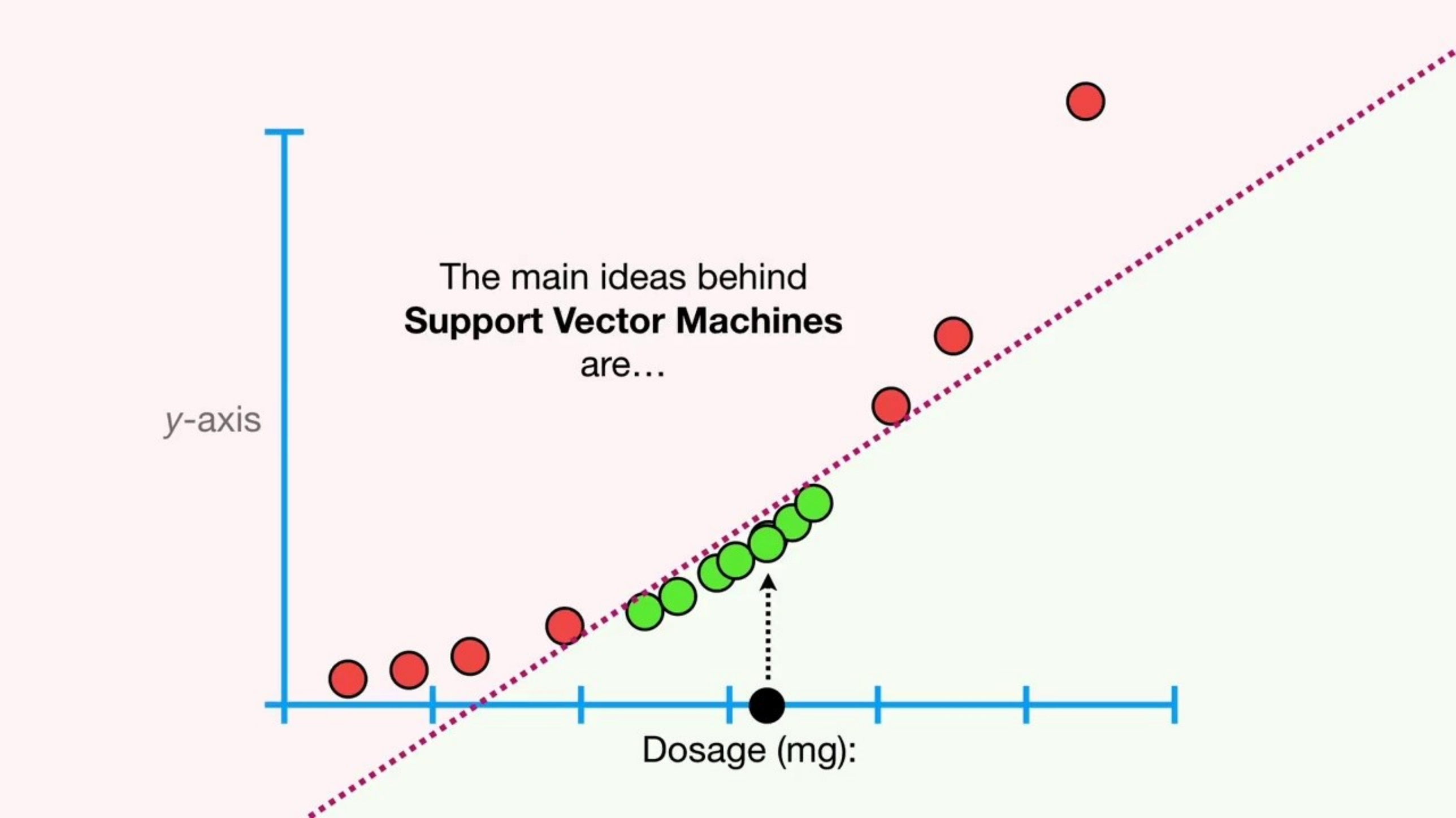

…then we could calculate a
***y*-axis** coordinate by squaring
the **Dosage**…
y-axis
Dosage (mg):

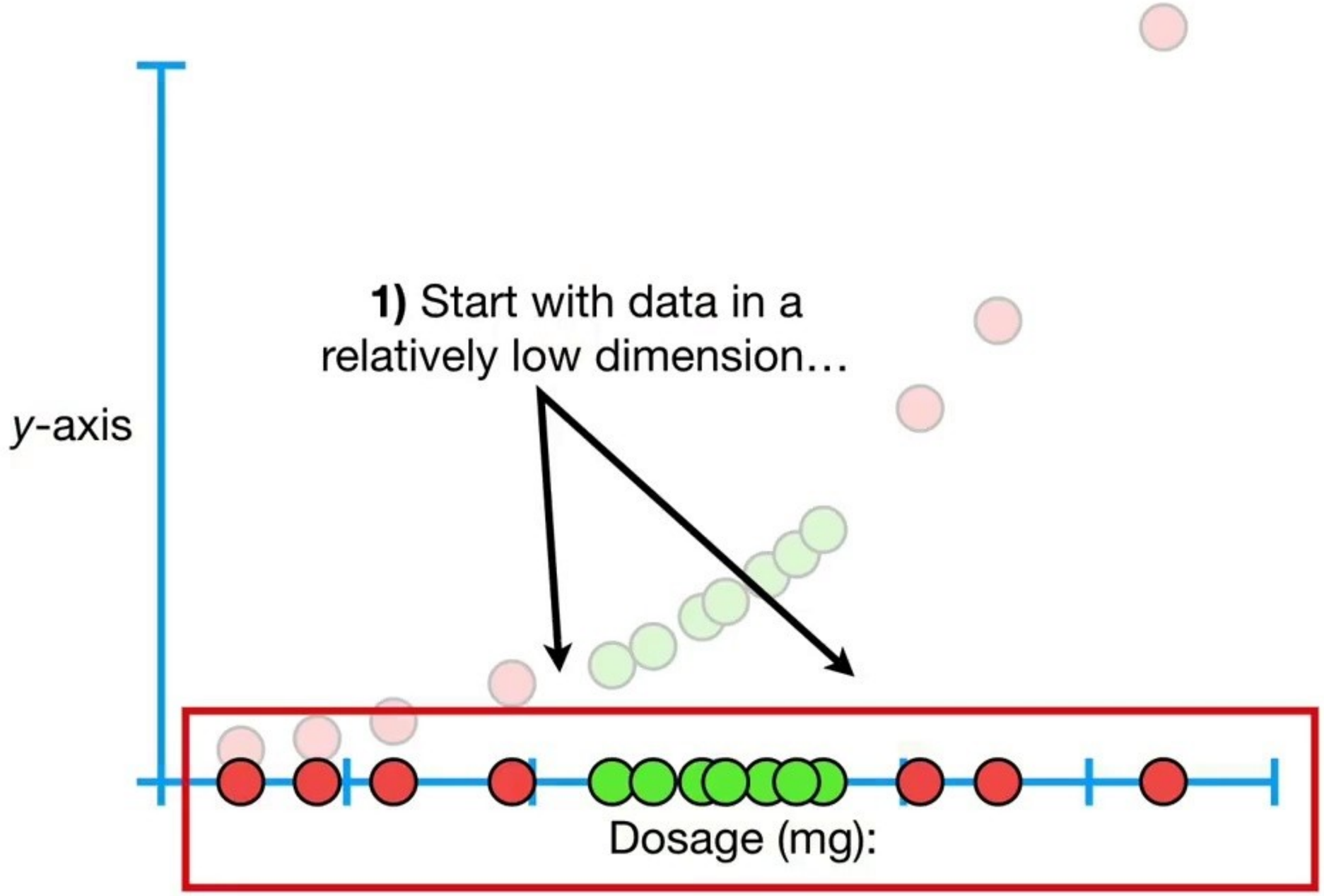

…and classify the observation as *not cured* because it ended up on this side of the **Support Vector Classifier**.
y-axis
Dosage (mg):

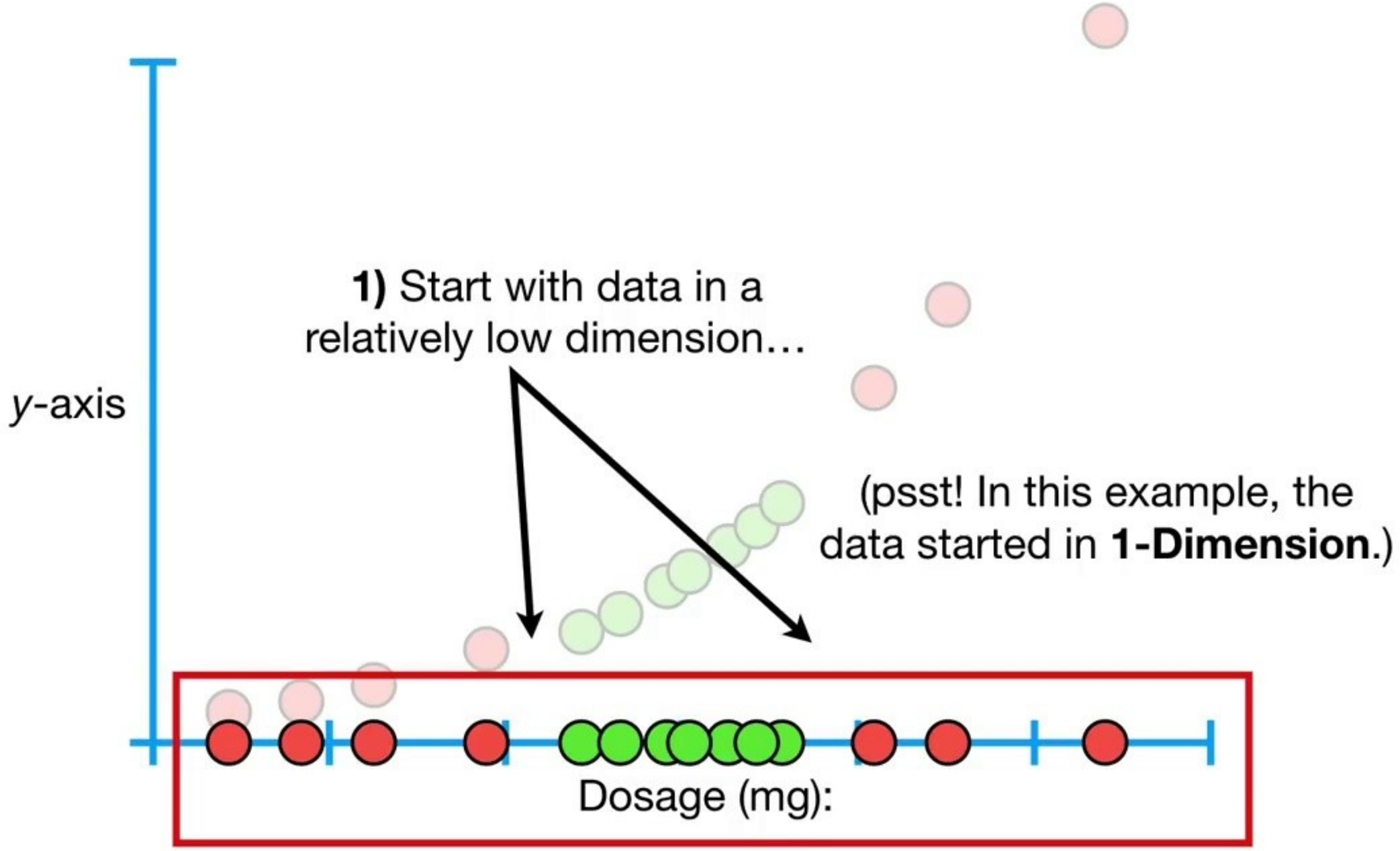

On the other hand, if we got a new observation with this **Dosage**…
y-axis
Dosage (mg):

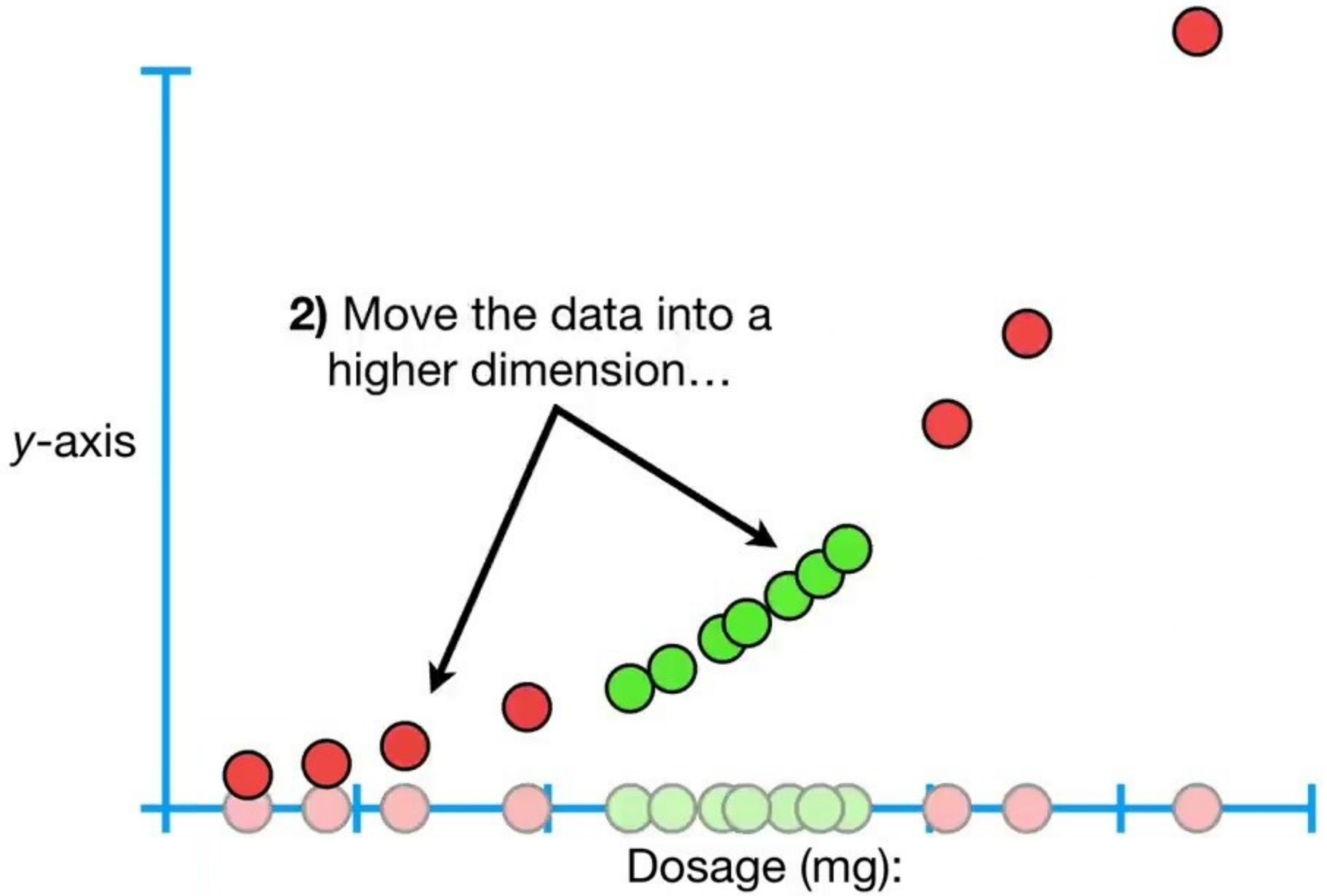

…then we would square the
Dosage to get a ***y*-axis**
coordinate…
y-axis
Dosage (mg):

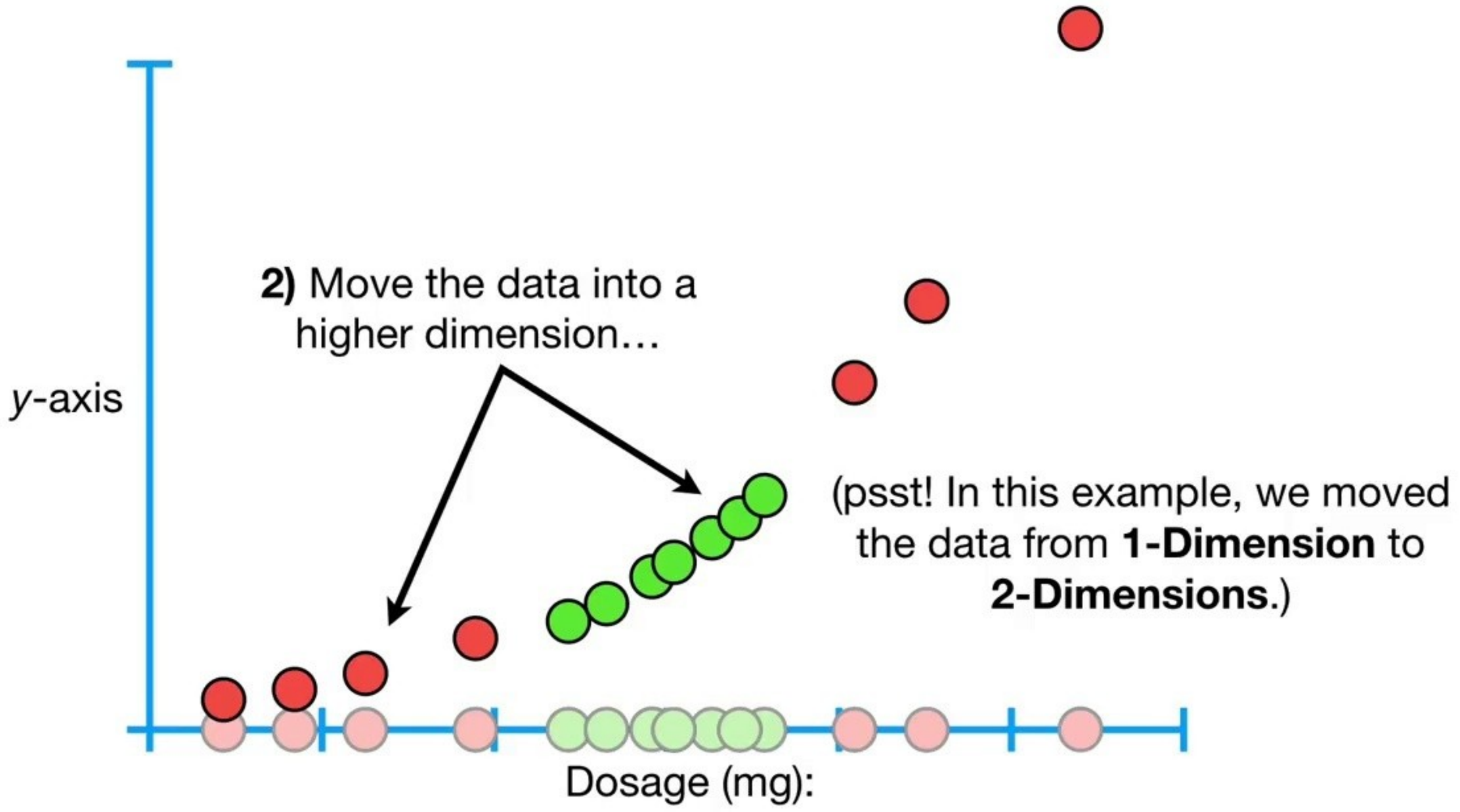

…and classify this observation as *cured* because it falls on the other side of the **Support Vector Classifier**.
y-axis
Dosage (mg):

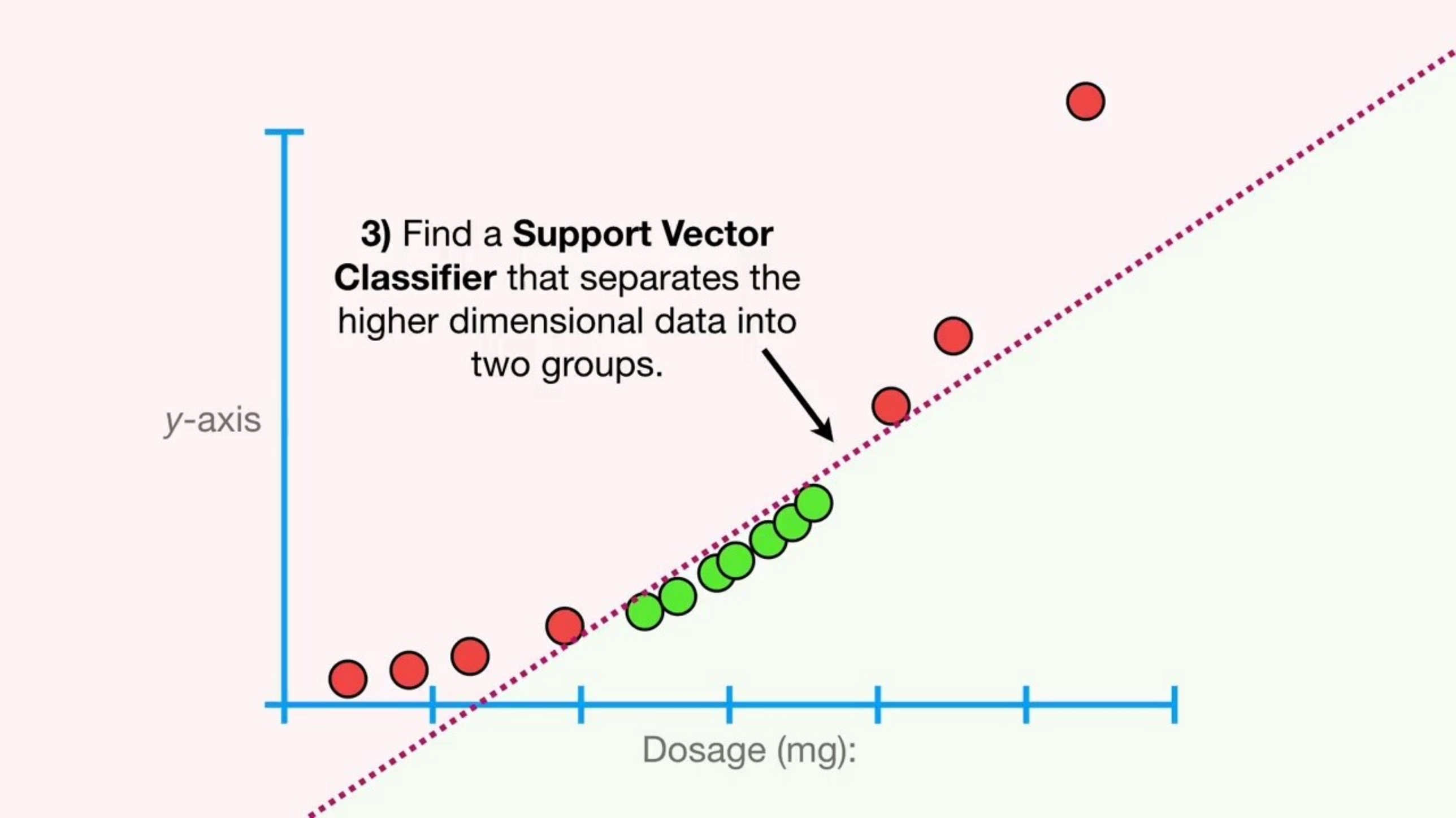

The main ideas behind
Support Vector Machines
are…
y-axis
Dosage (mg):

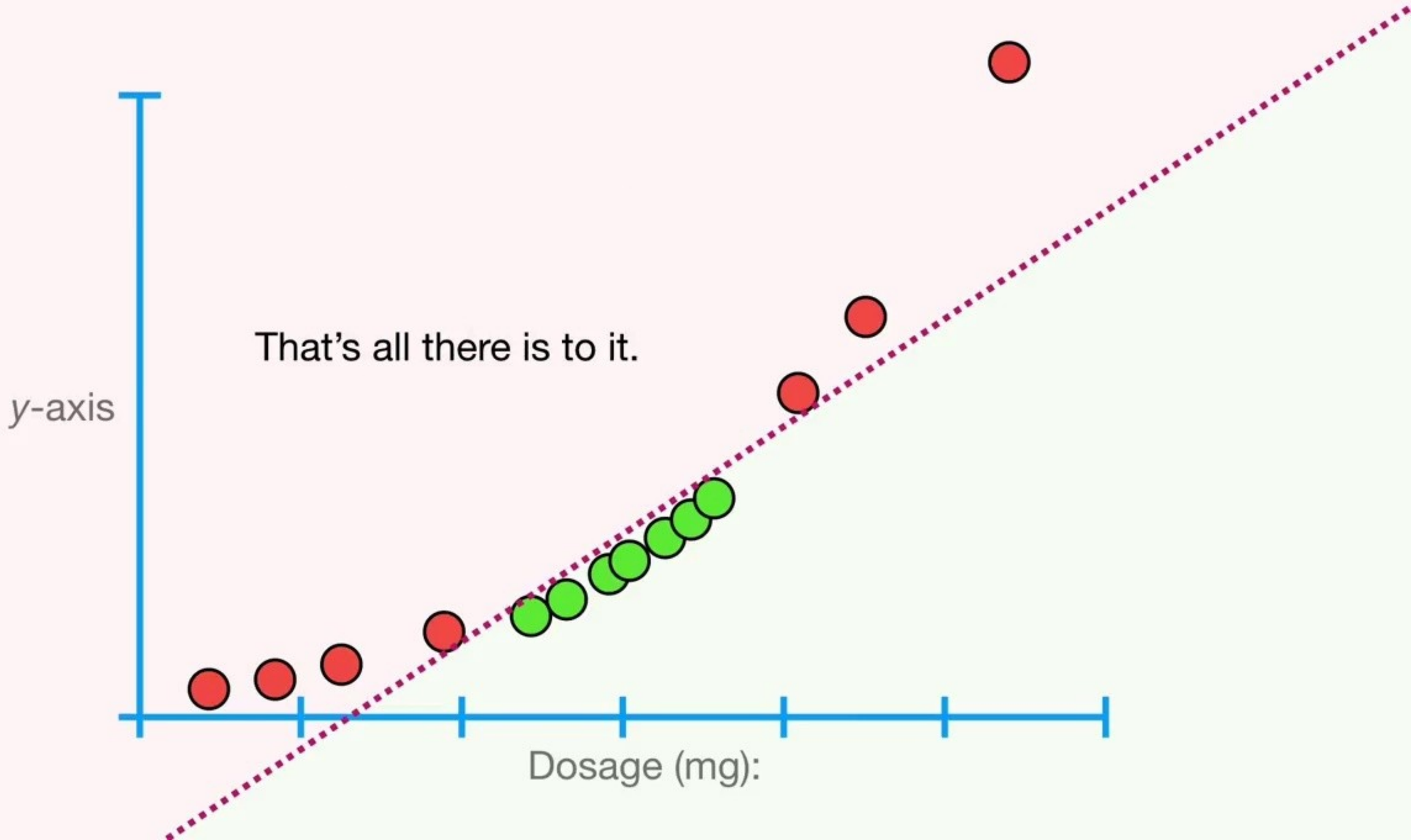

1) Start with data in a relatively low dimension…
y-axis
Dosage (mg):


y-axis
1) Start with data in a relatively low dimension…
(psst! In this example, the data started in 1-Dimension.)
Dosage (mg):

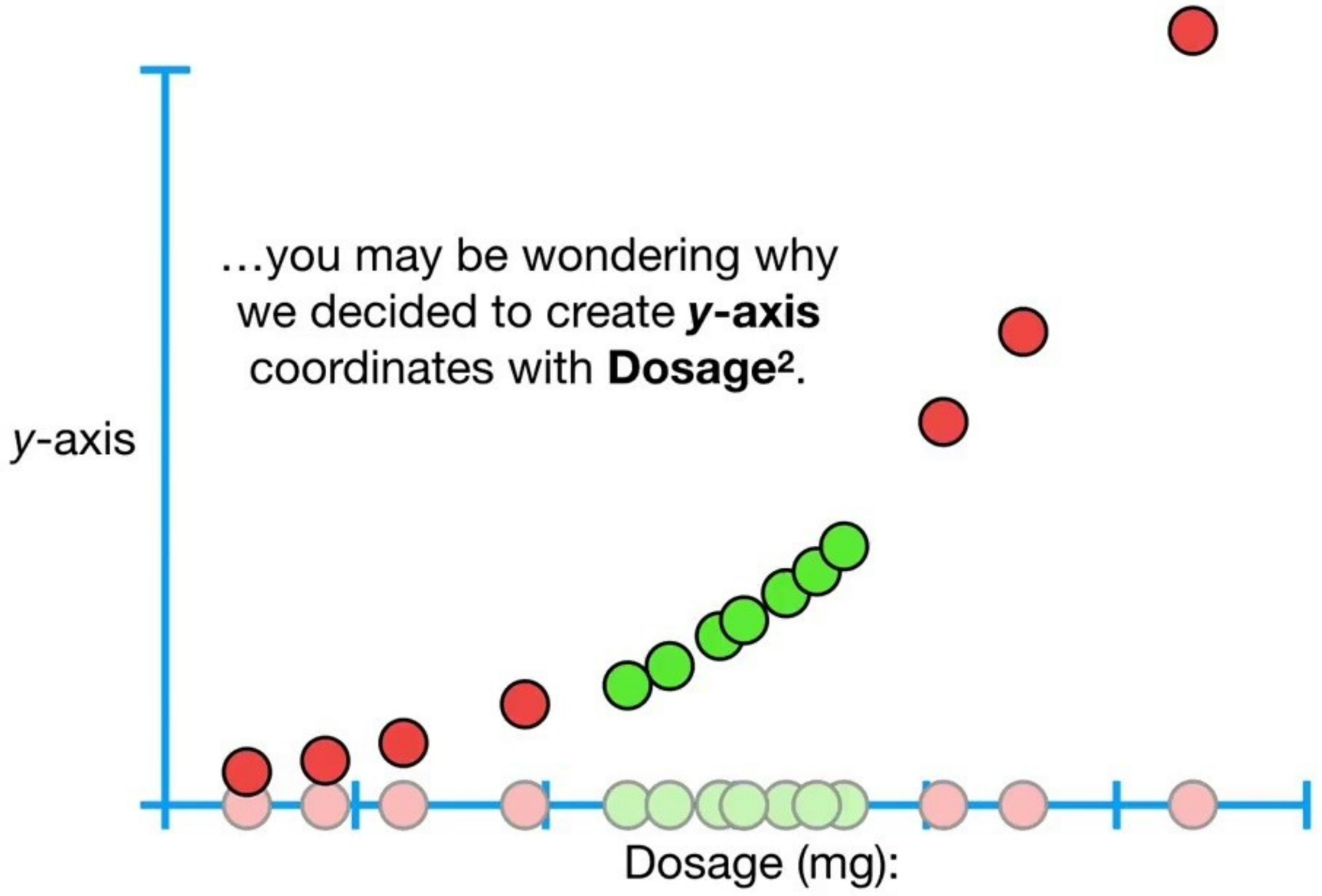

2) Move the data into a higher dimension…
y-axis
Dosage (mg):

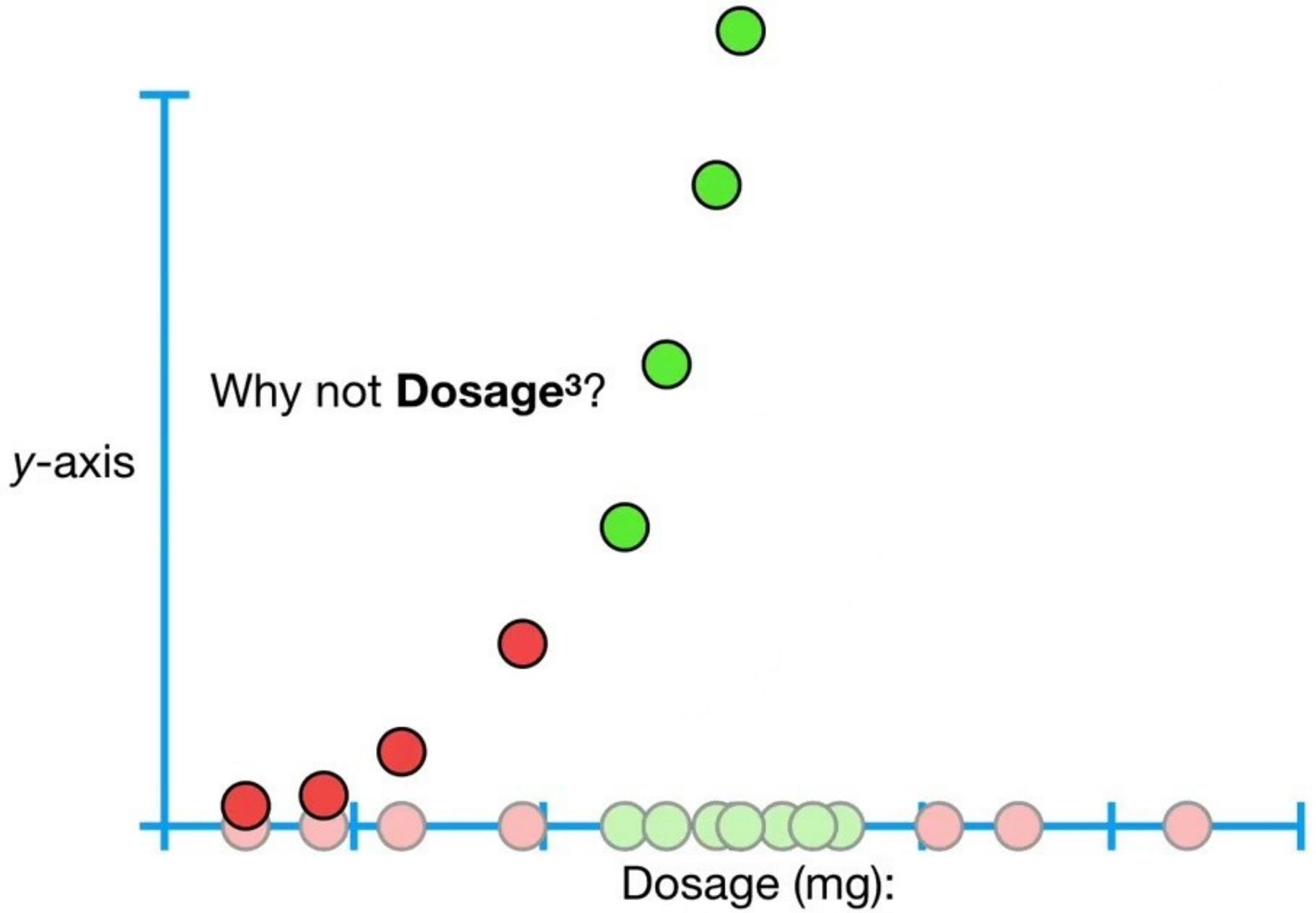

2) Move the data into a higher dimension…
y-axis
(psst! In this example, we moved the data from 1-Dimension to 2-Dimensions.)
Dosage (mg):

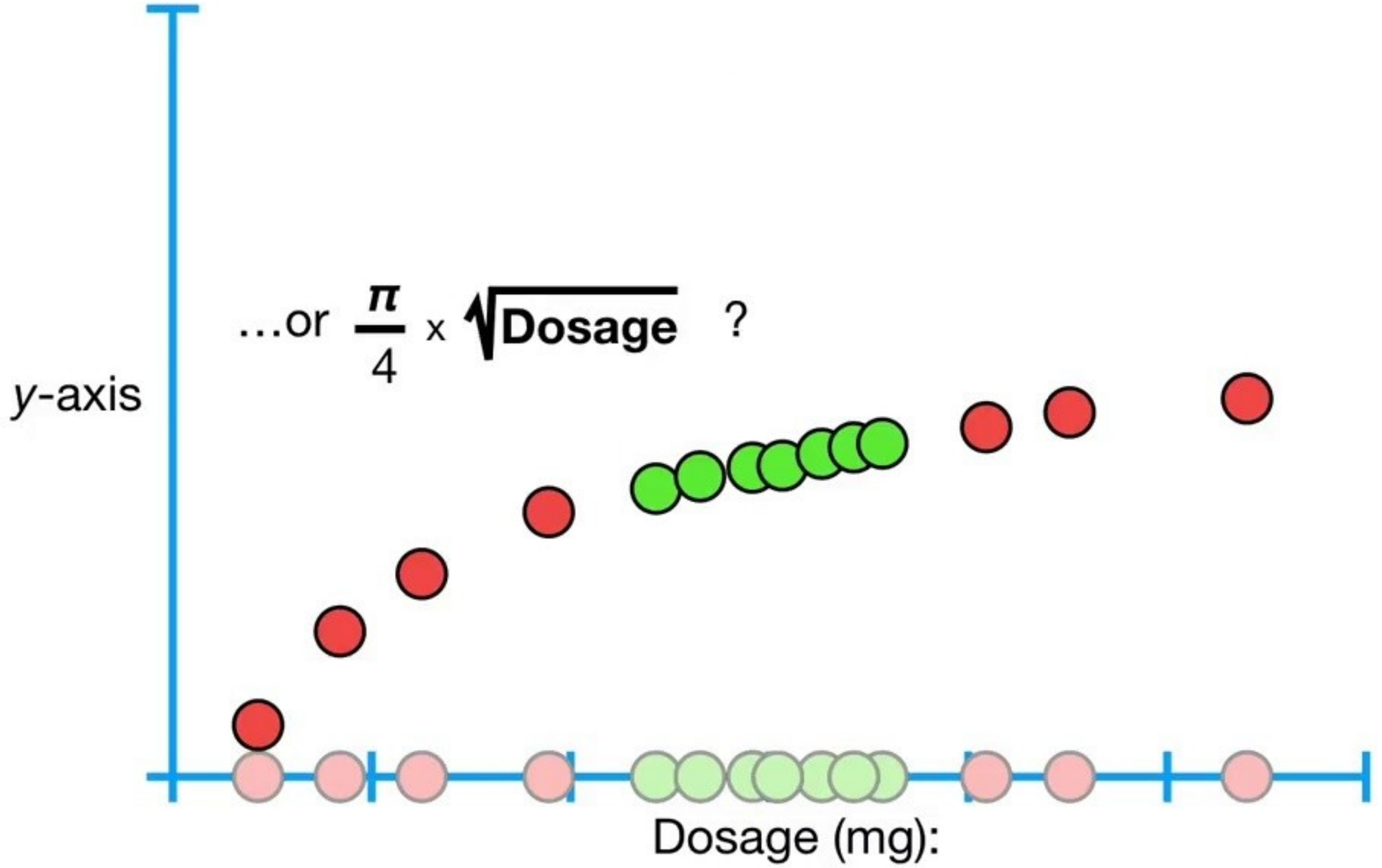

3) Find a **Support Vector Classifier** that separates the higher dimensional data into two groups.
y-axis
Dosage (mg):

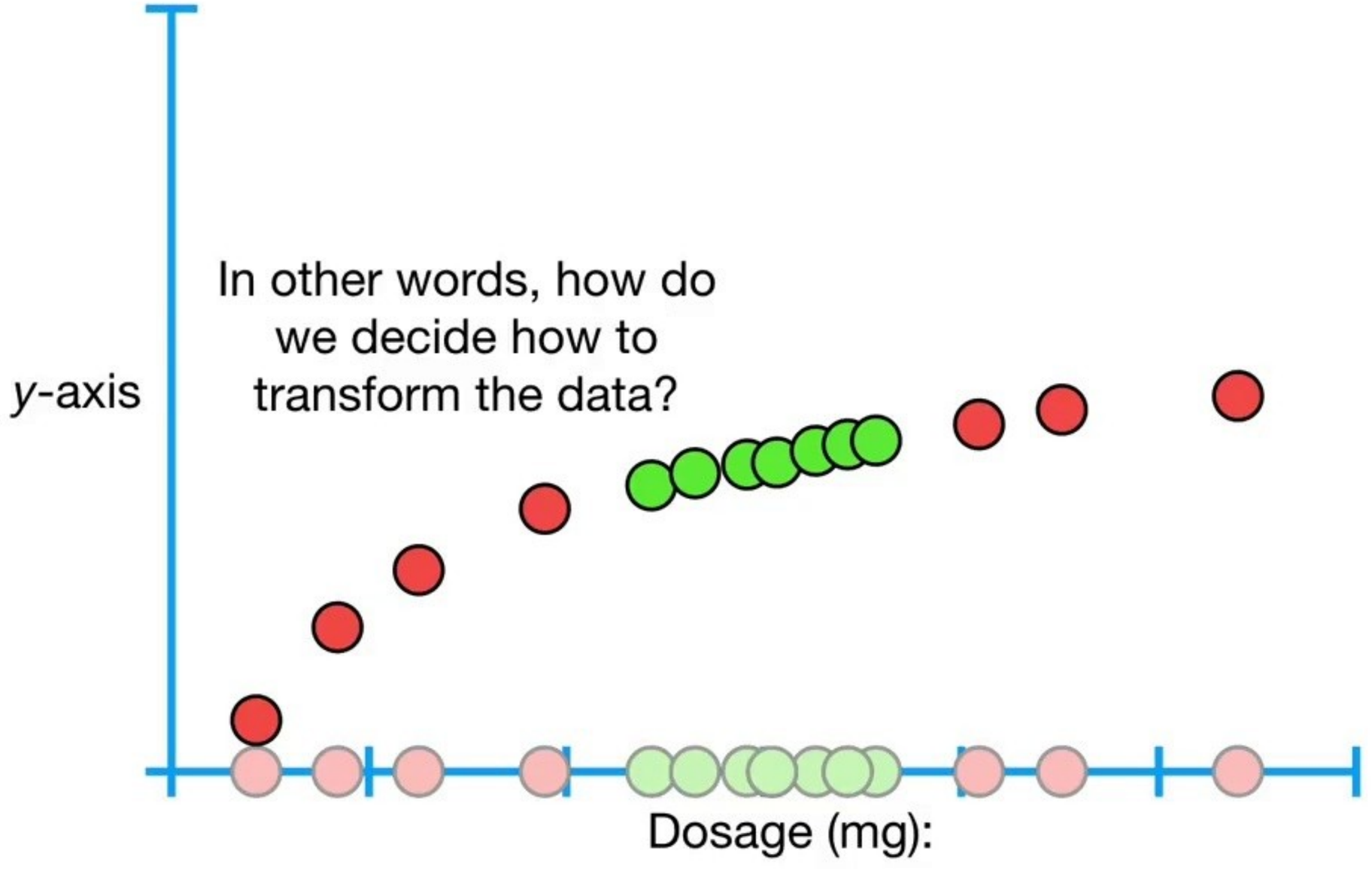

That's all there is to it.
y-axis
Dosage (mg):

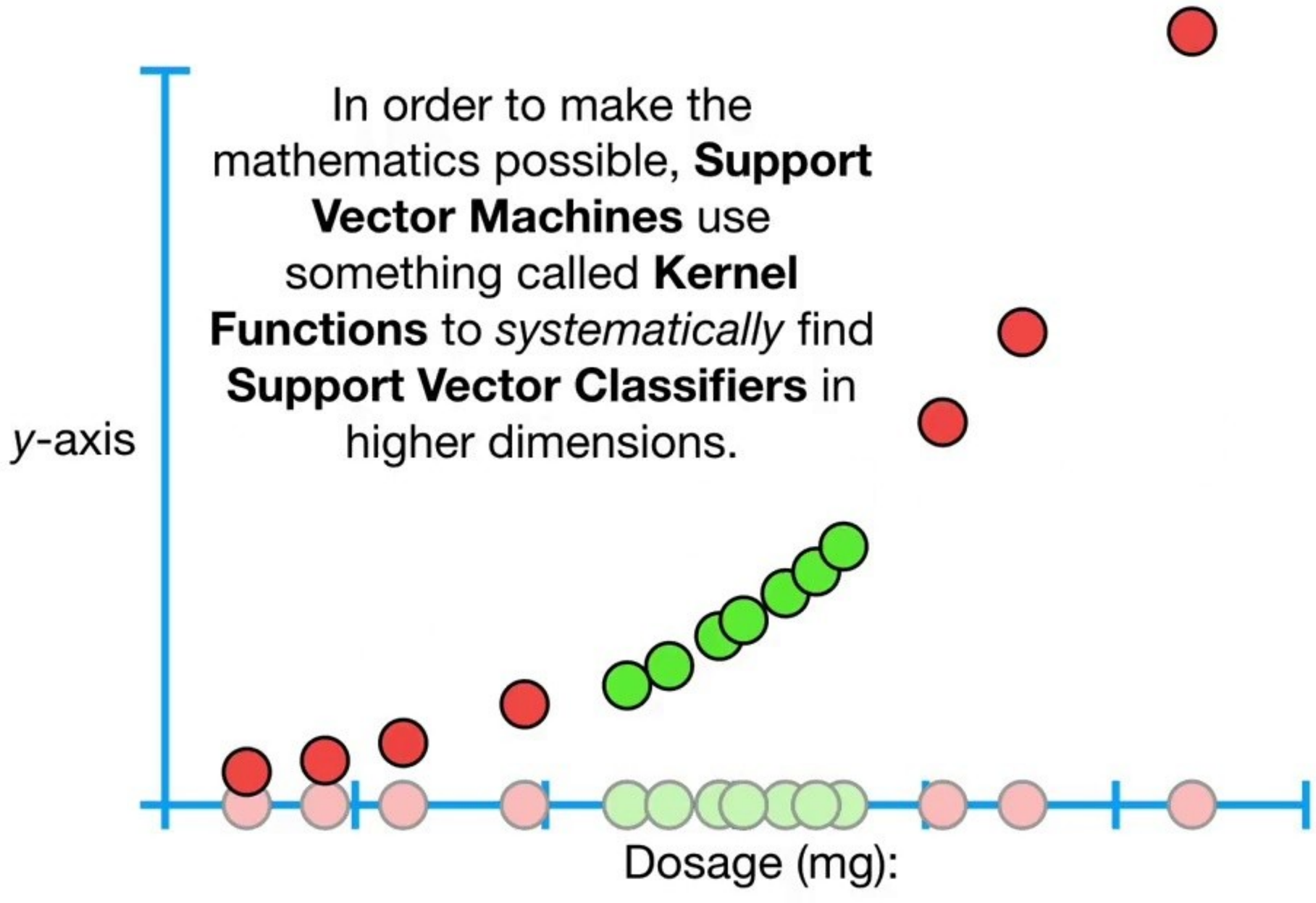
Going back to the original
1-Dimensional data…

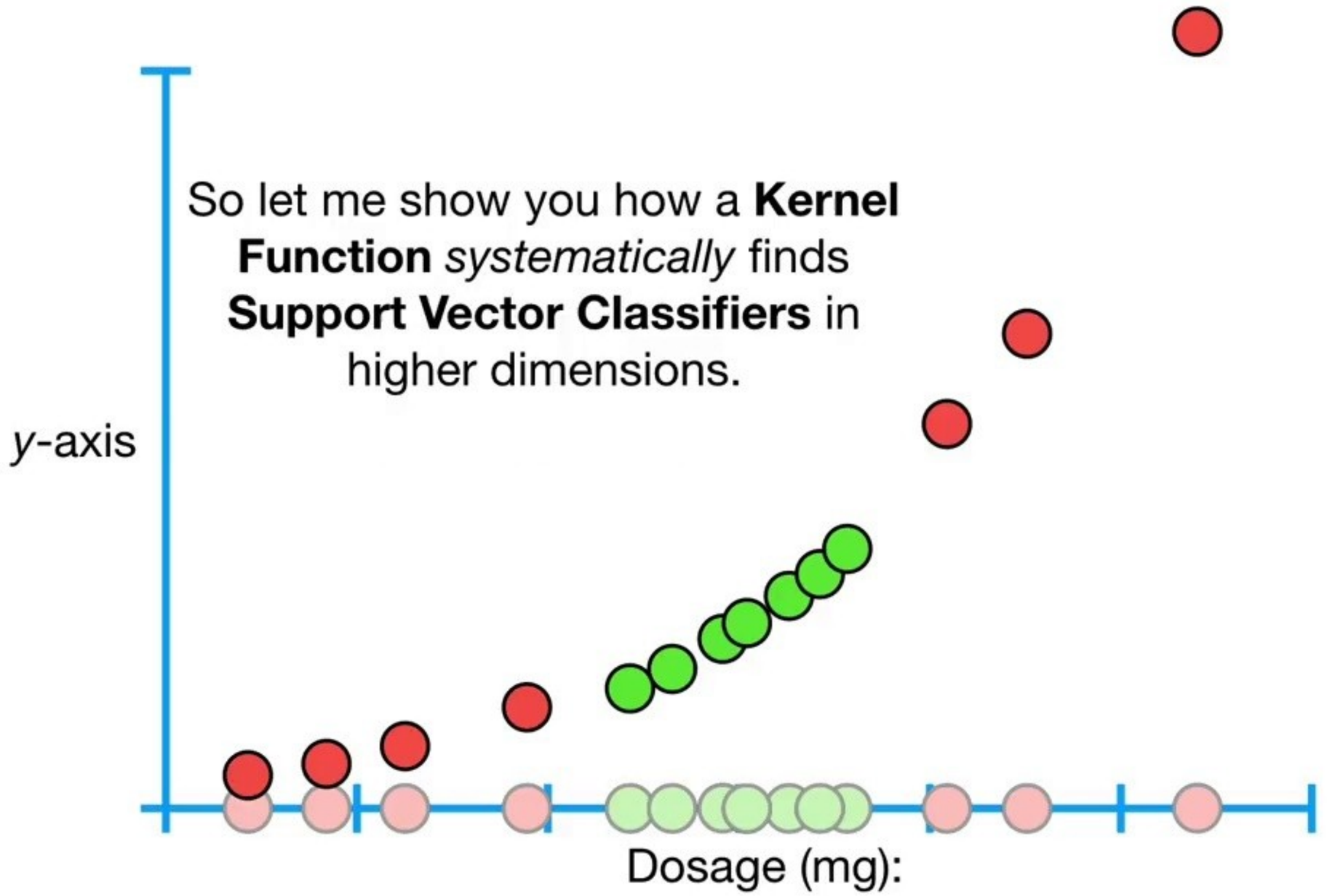

…you may be wondering why we decided to create **y-axis** coordinates with **Dosage²**.
y-axis
Dosage (mg):

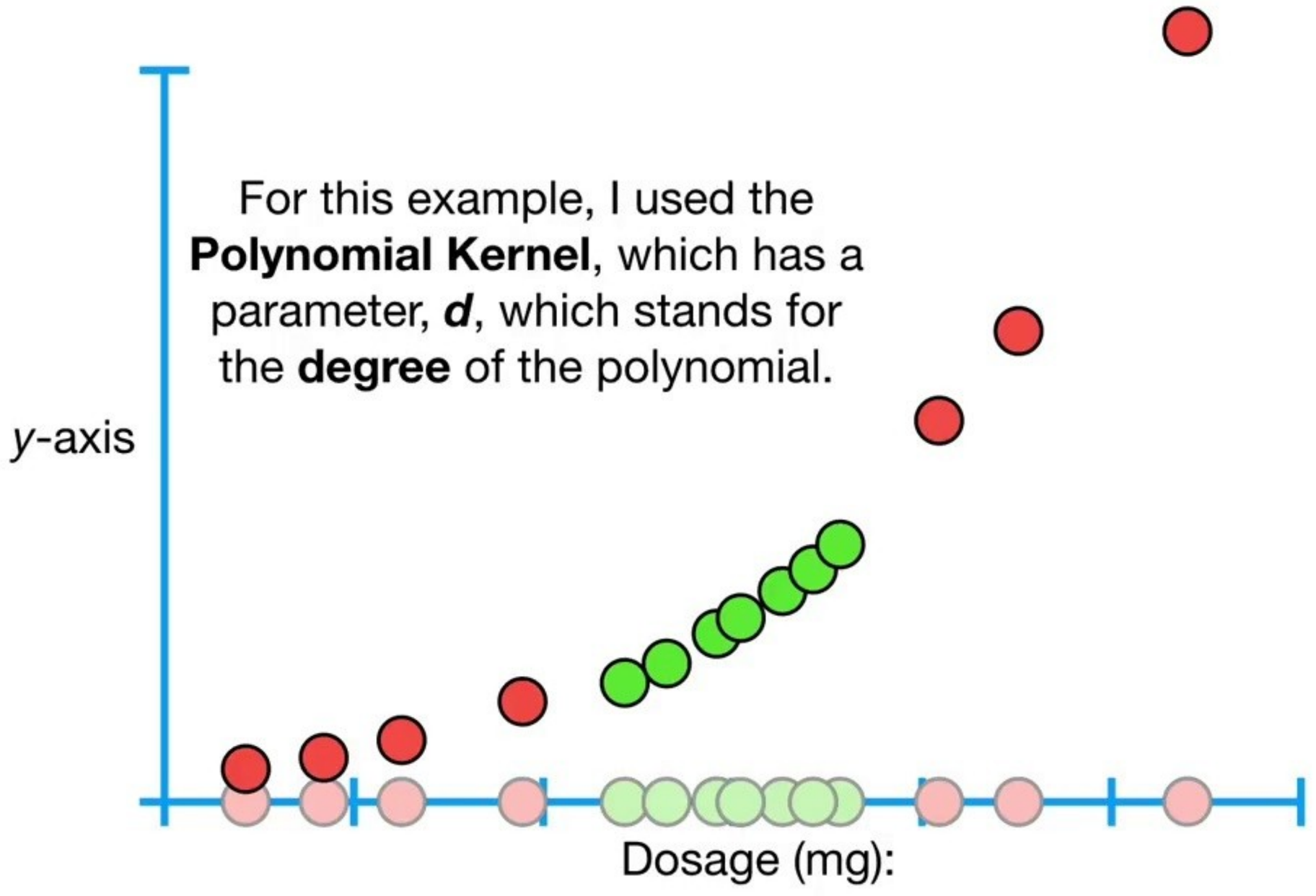

Why not **Dosage**^{3}?
y-axis
Dosage (mg):


…or $\frac{\pi}{4} \times \sqrt{\text{Dosage}}$?
y-axis
Dosage (mg):


In other words, how do we decide how to transform the data?
y-axis
Dosage (mg):

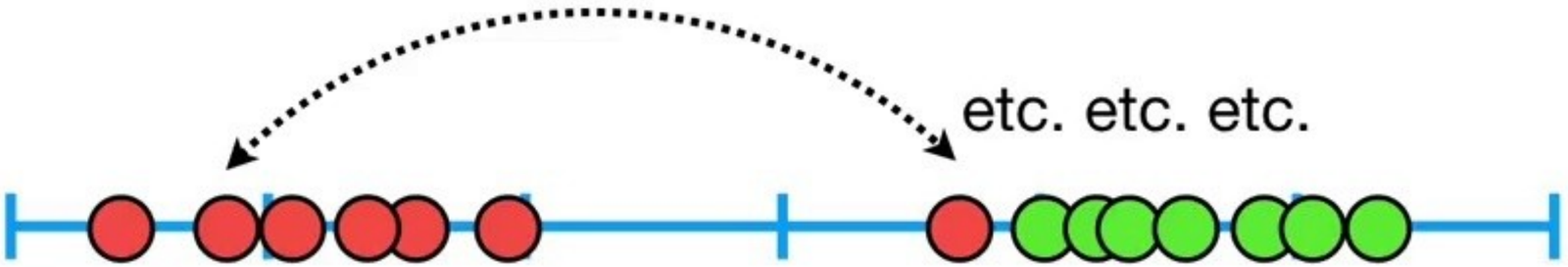

In order to make the mathematics possible, **Support Vector Machines** use something called **Kernel Functions** to *systematically* find **Support Vector Classifiers** in higher dimensions.
y-axis
Dosage (mg):


So let me show you how a **Kernel Function** *systematically* finds **Support Vector Classifiers** in higher dimensions.
y-axis
Dosage (mg):

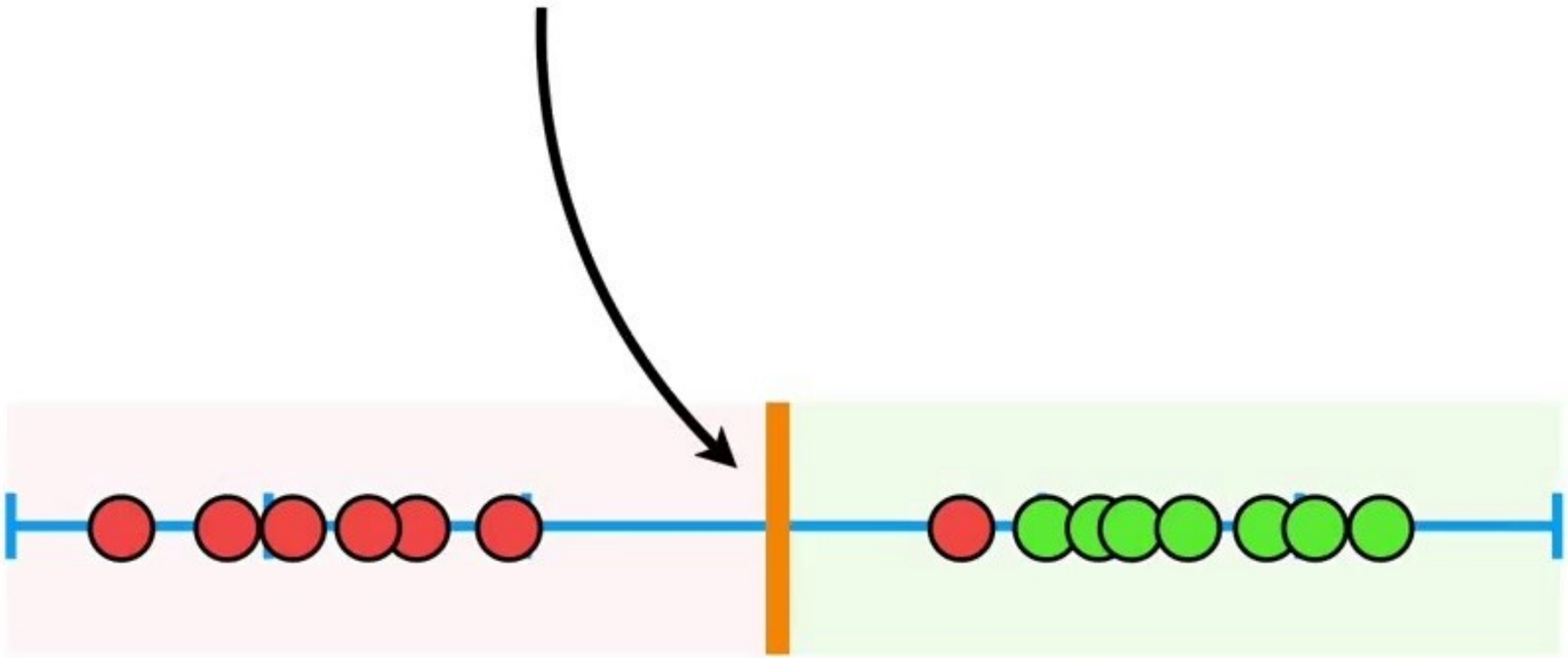

For this example, I used the
Polynomial Kernel, which has a
parameter, ***d***, which stands for
the **degree** of the polynomial.
y-axis
Dosage (mg):

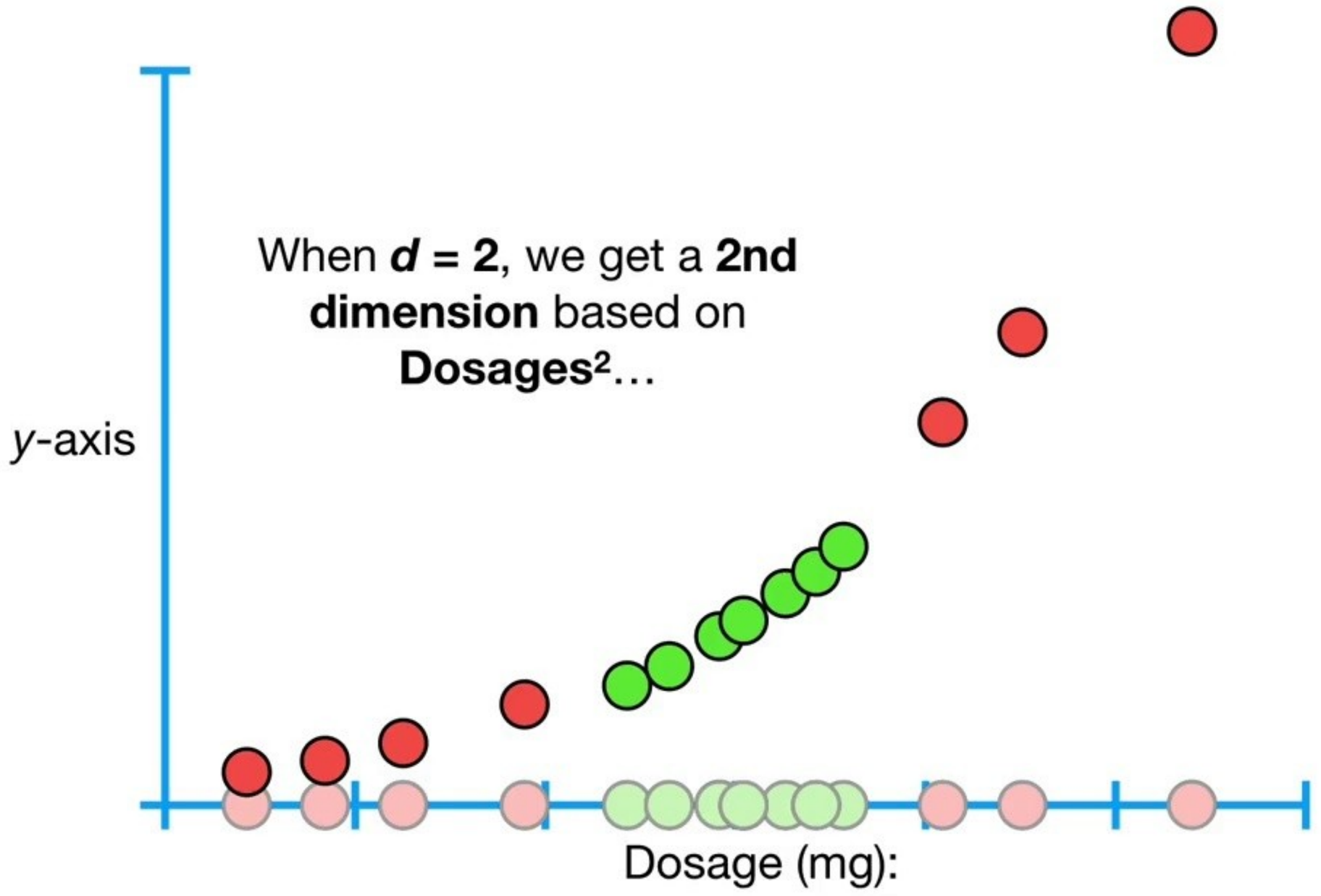
When ***d* = 1**, the **Polynomial Kernel** computes the relationships between each pair of observations in **1-Dimension**…

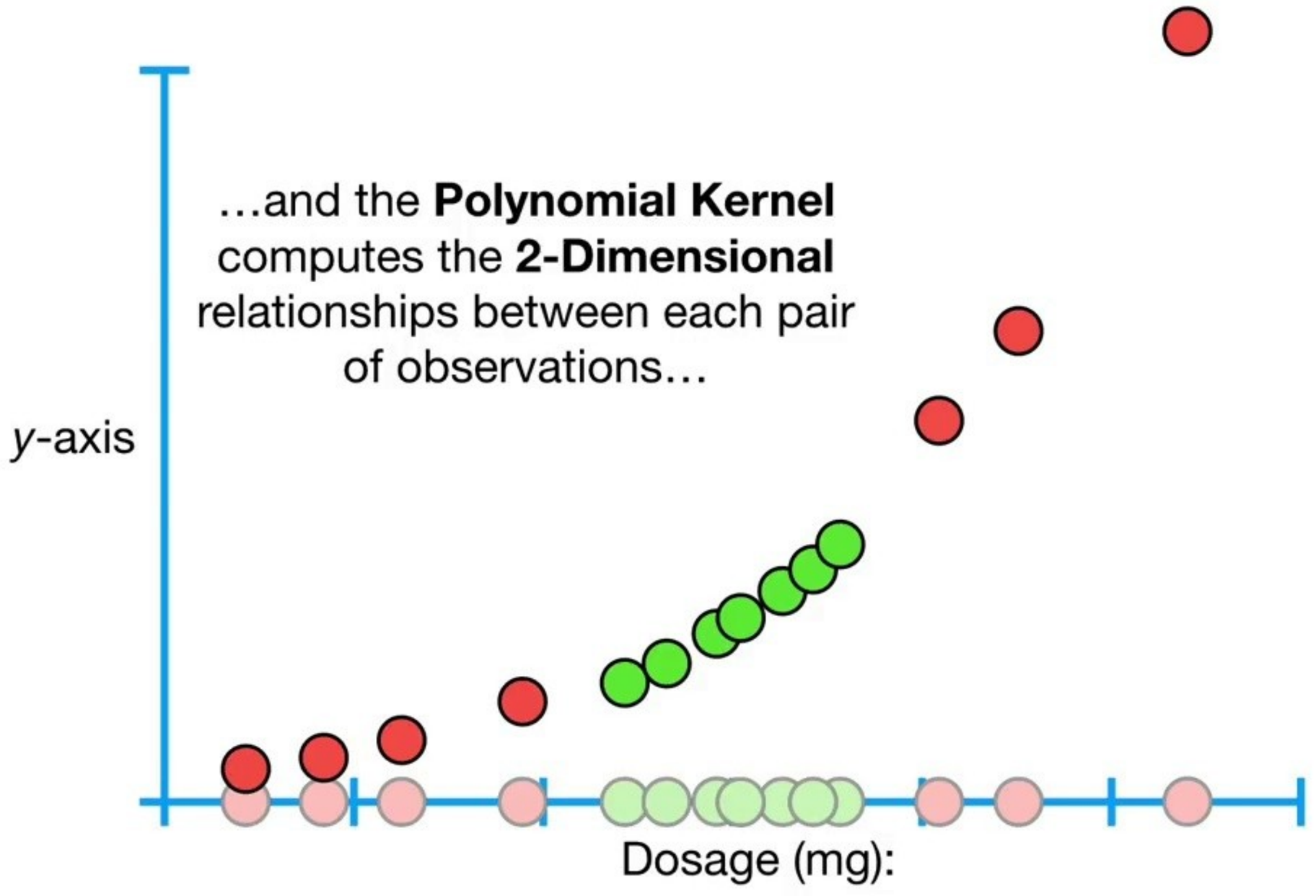
When ***d* = 1**, the **Polynomial Kernel** computes the relationships between each pair of observations in **1-Dimension**…

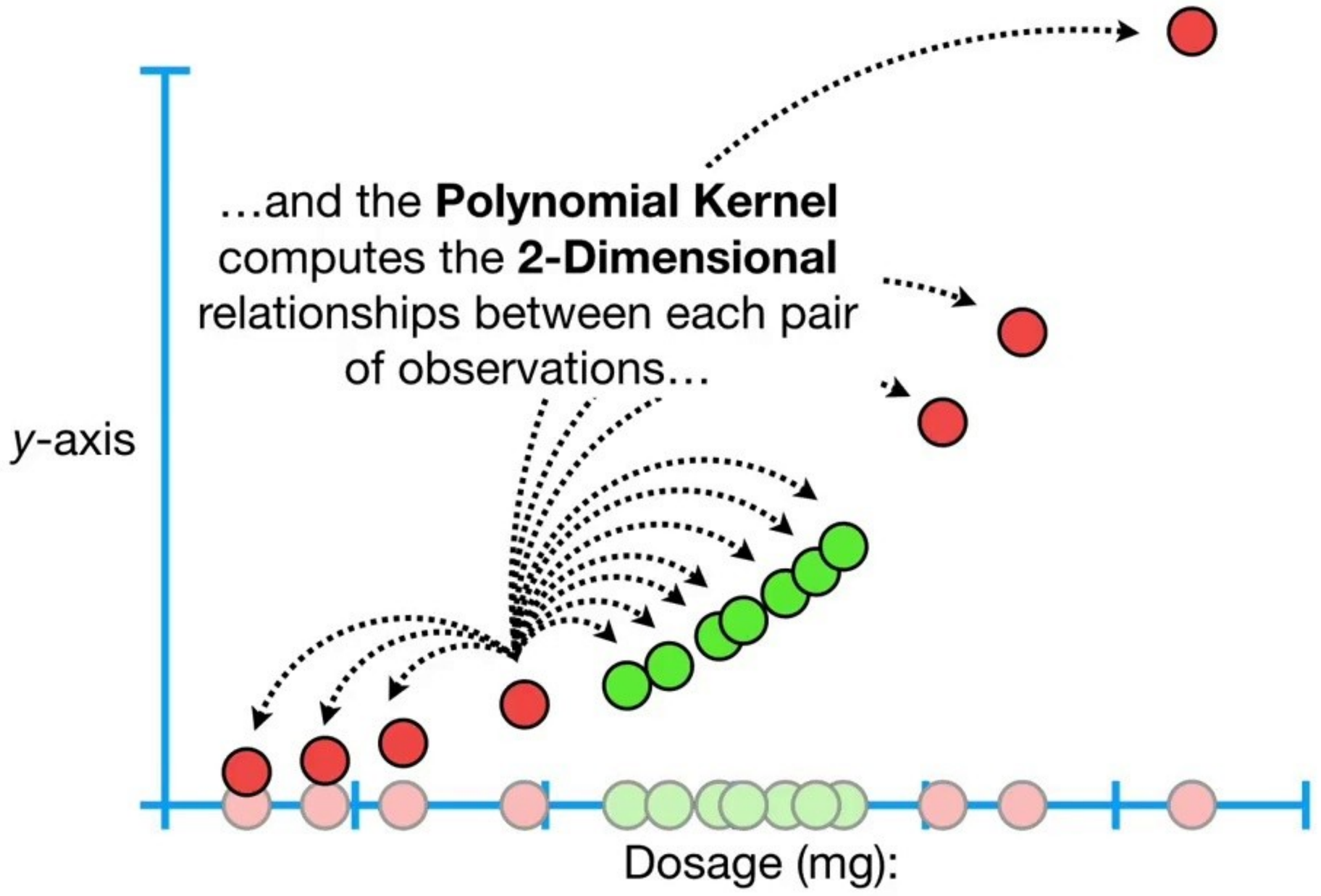


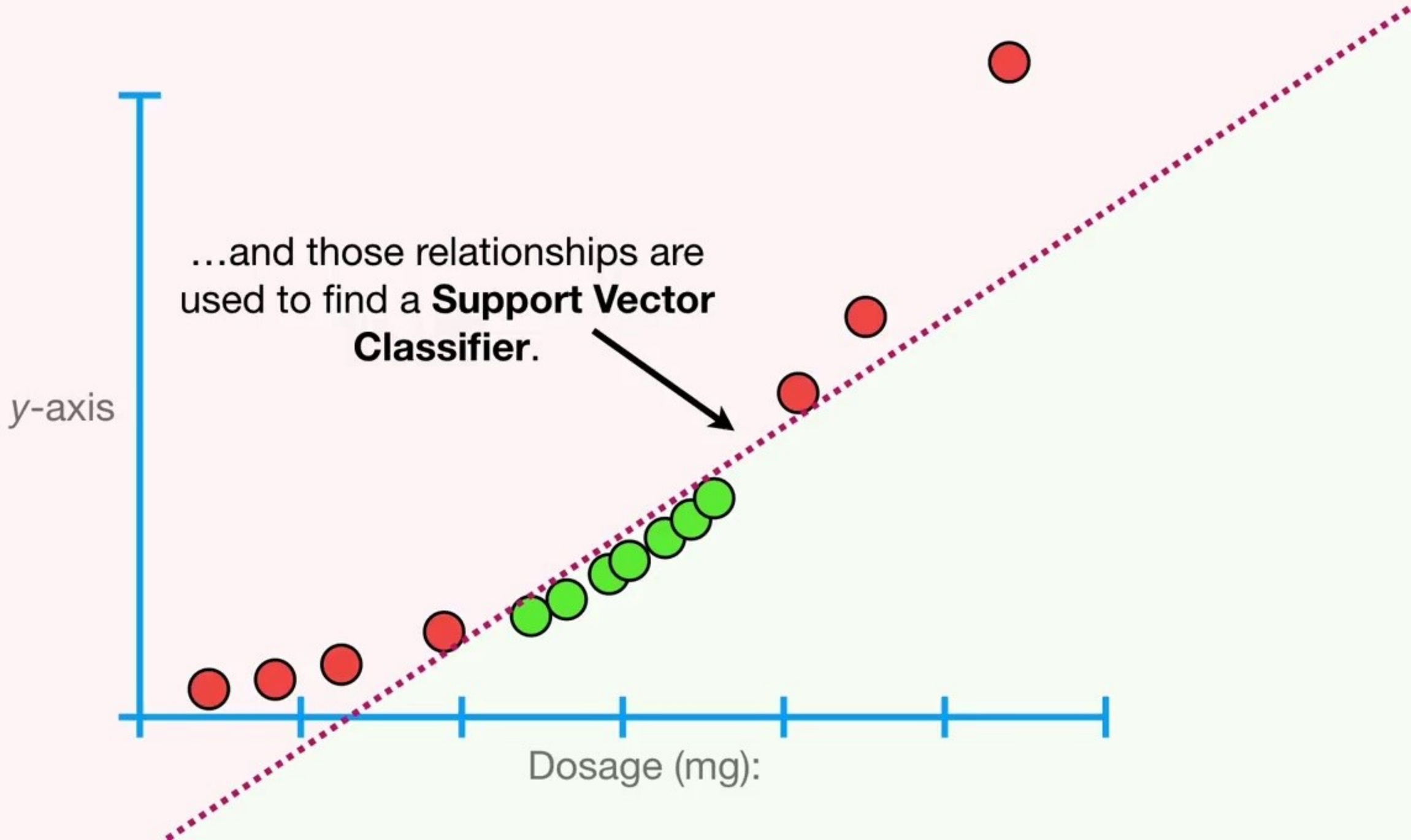
…and these relationships are used to find a **Support Vector Classifier**.

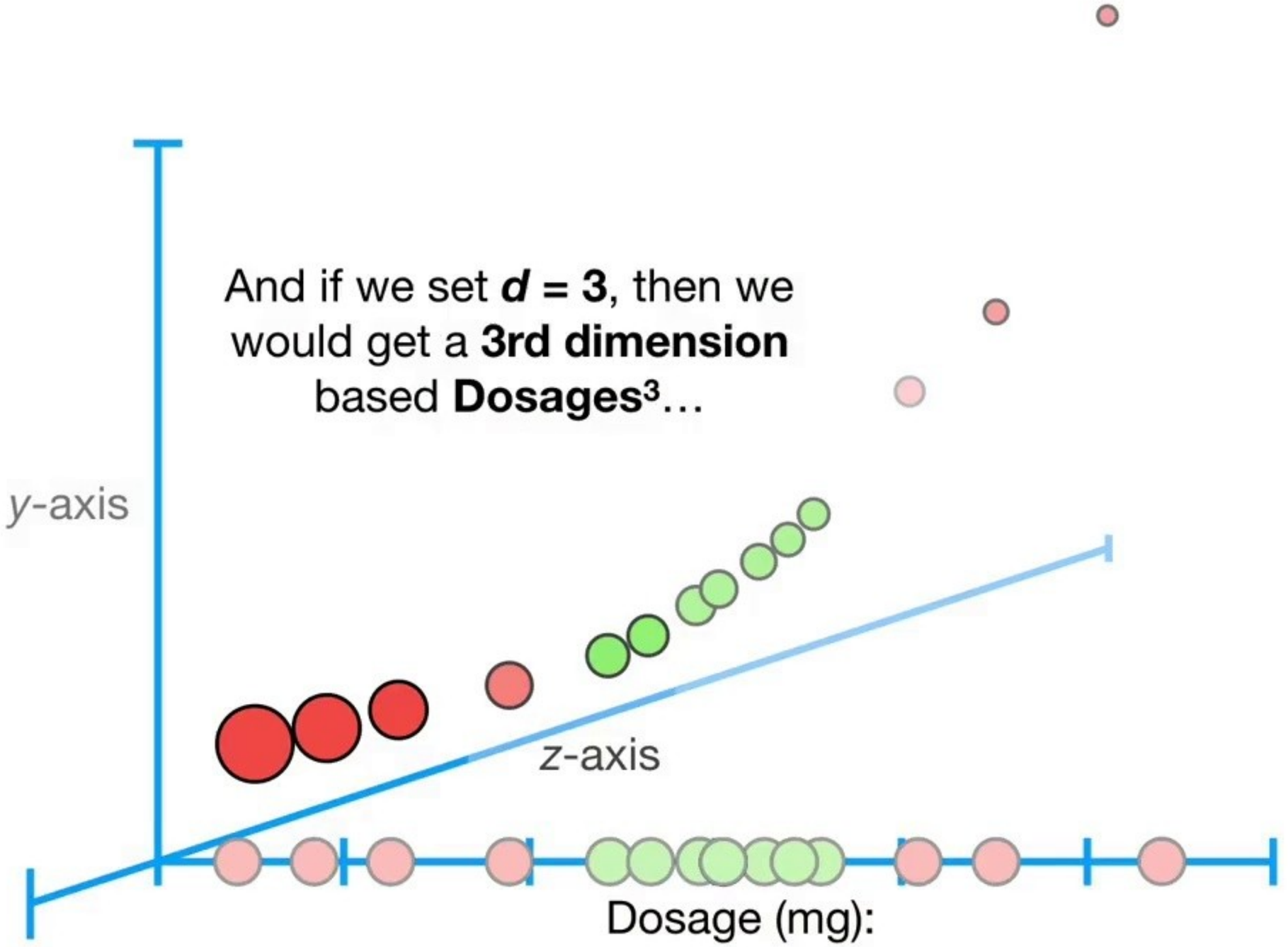


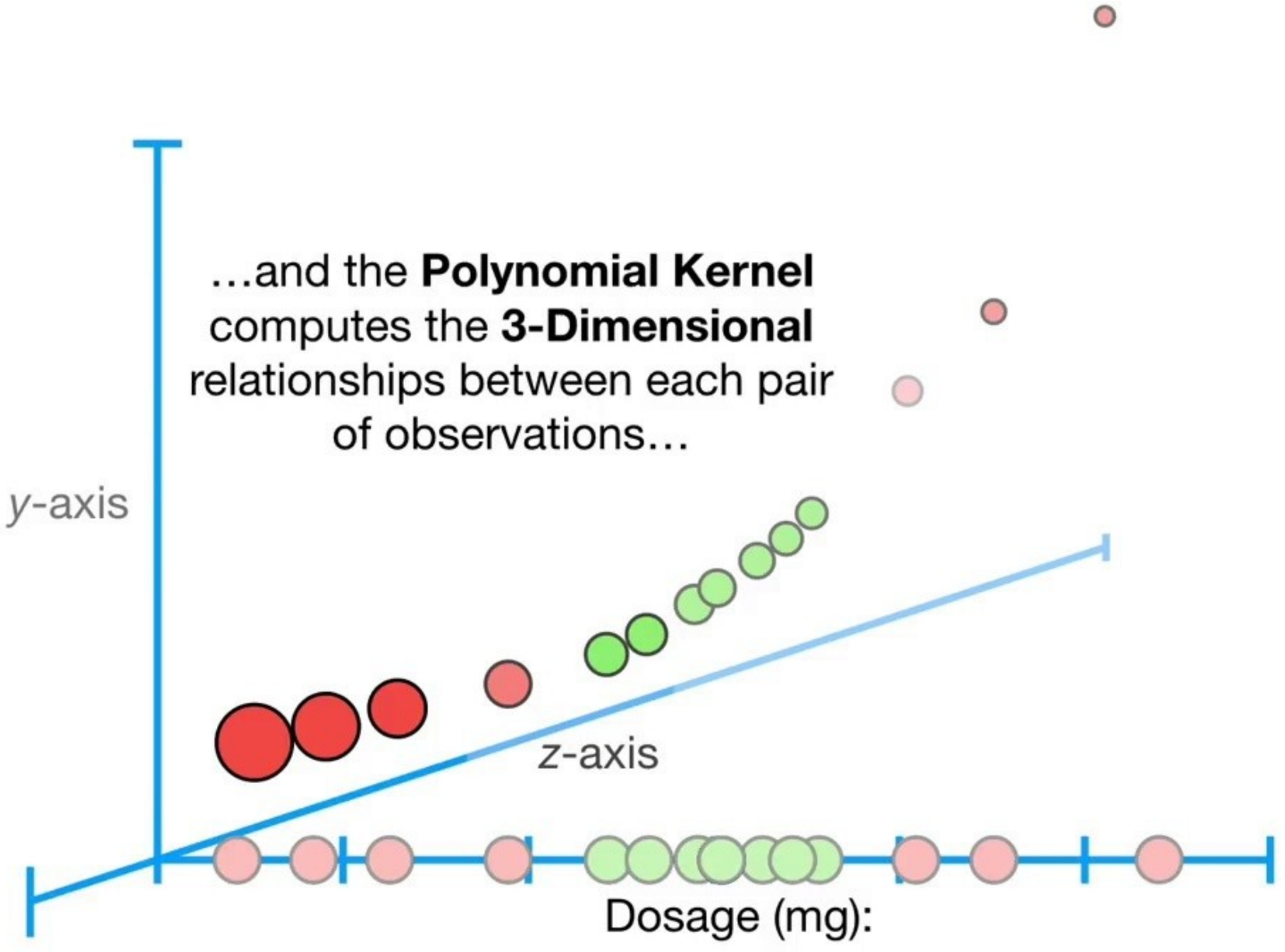

When **d = 2**, we get a **2nd dimension** based on **Dosages²**…
y-axis
Dosage (mg):

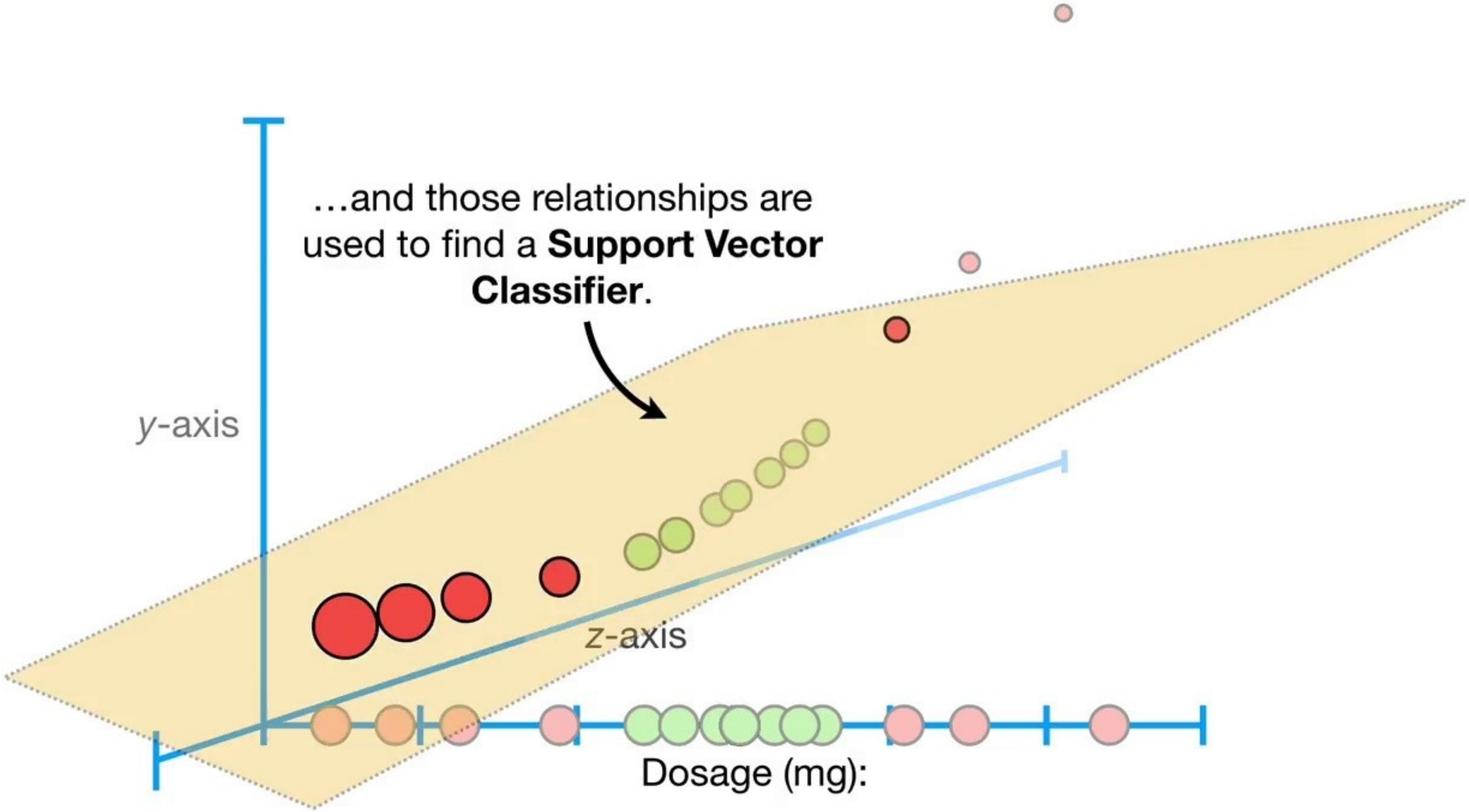

…and the **Polynomial Kernel** computes the **2-Dimensional** relationships between each pair of observations…
y-axis
Dosage (mg):


…and the **Polynomial Kernel** computes the **2-Dimensional** relationships between each pair of observations…
y-axis
Dosage (mg):


…and those relationships are used to find a **Support Vector Classifier**.
y-axis
Dosage (mg):


And if we set **d = 3**, then we would get a **3rd dimension** based **Dosages³**…
y-axis
z-axis
Dosage (mg):

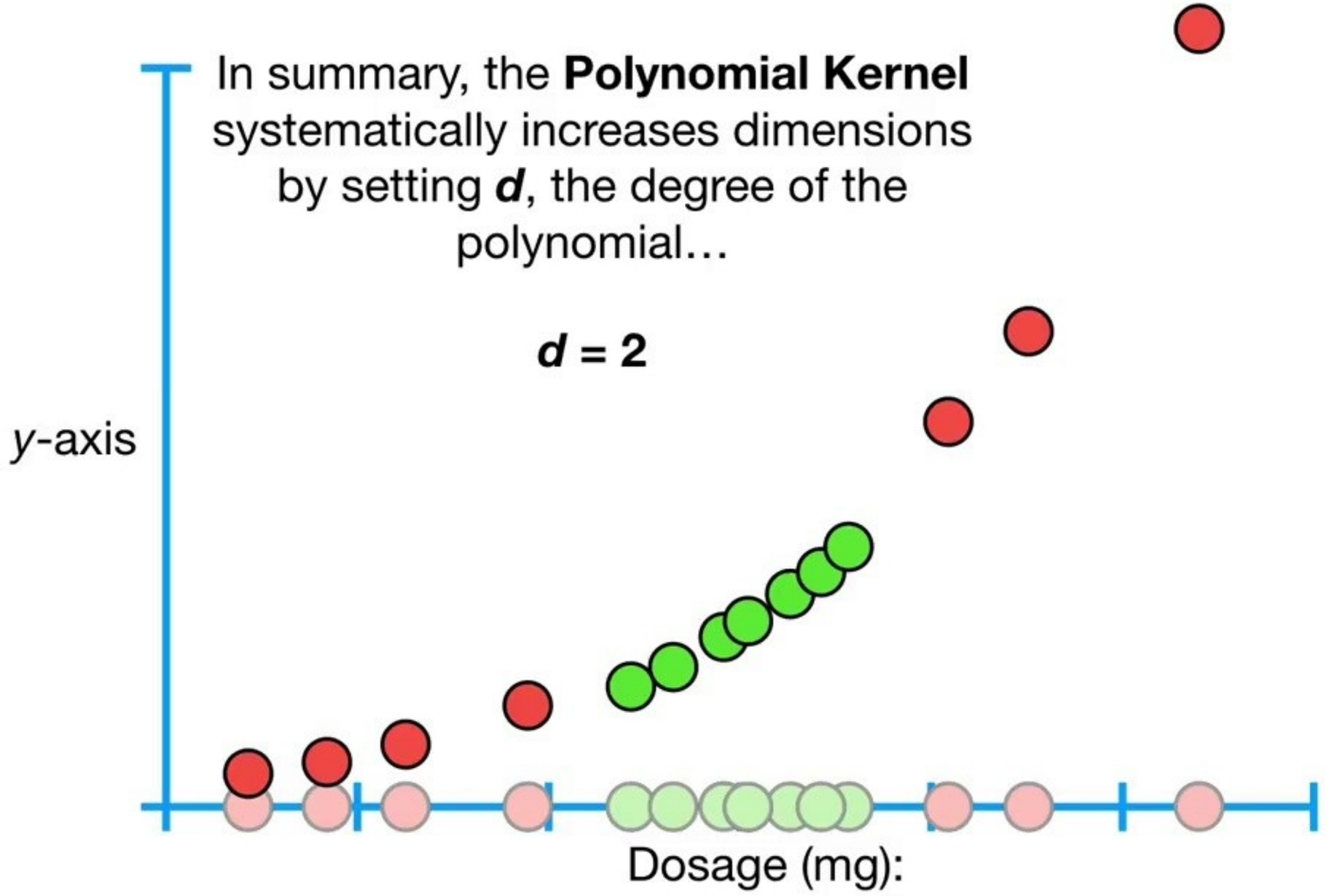

…and the **Polynomial Kernel** computes the **3-Dimensional** relationships between each pair of observations…
y-axis
z-axis
Dosage (mg):

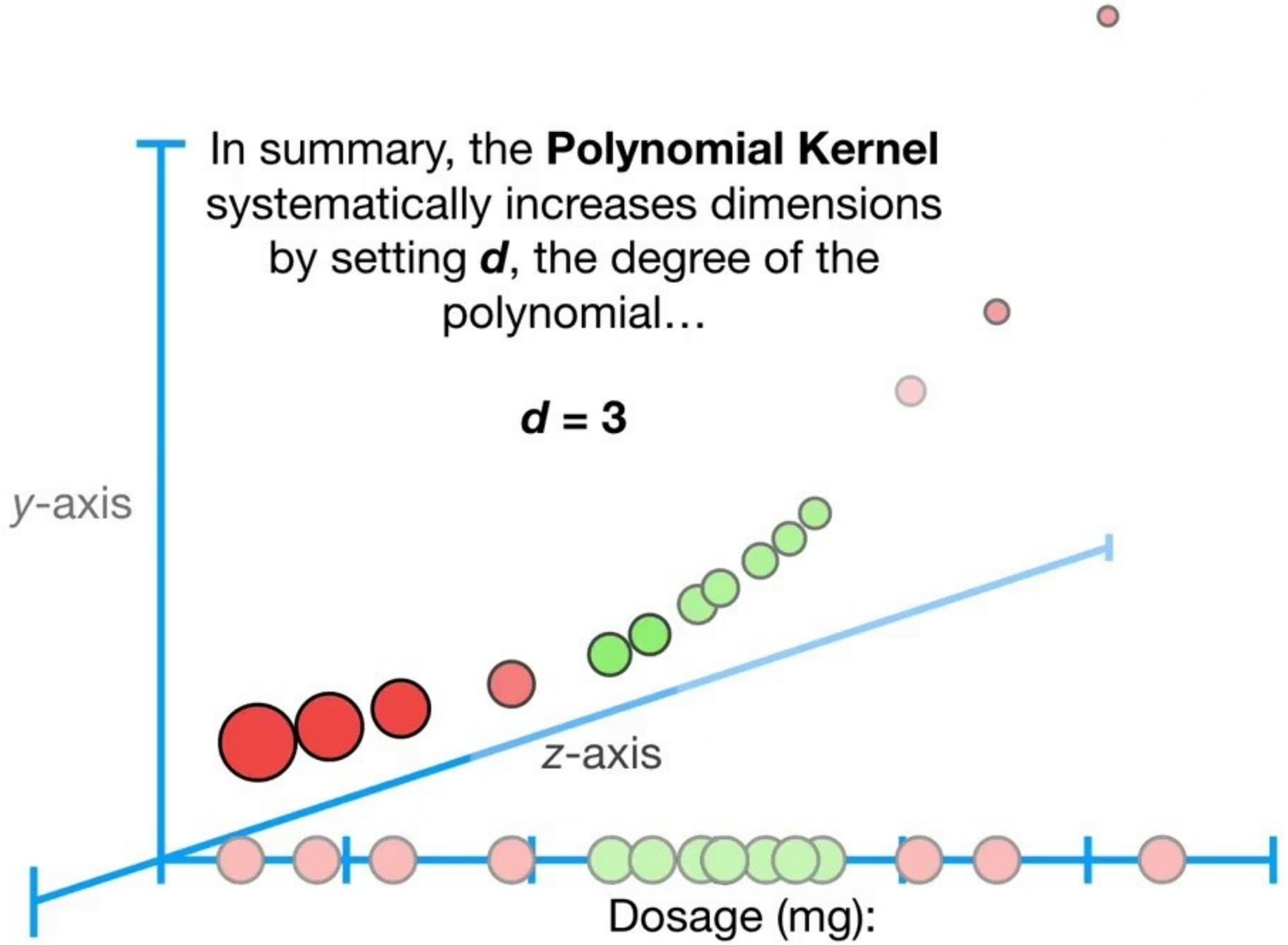

…and those relationships are used to find a **Support Vector Classifier**.
y-axis
z-axis
Dosage (mg):

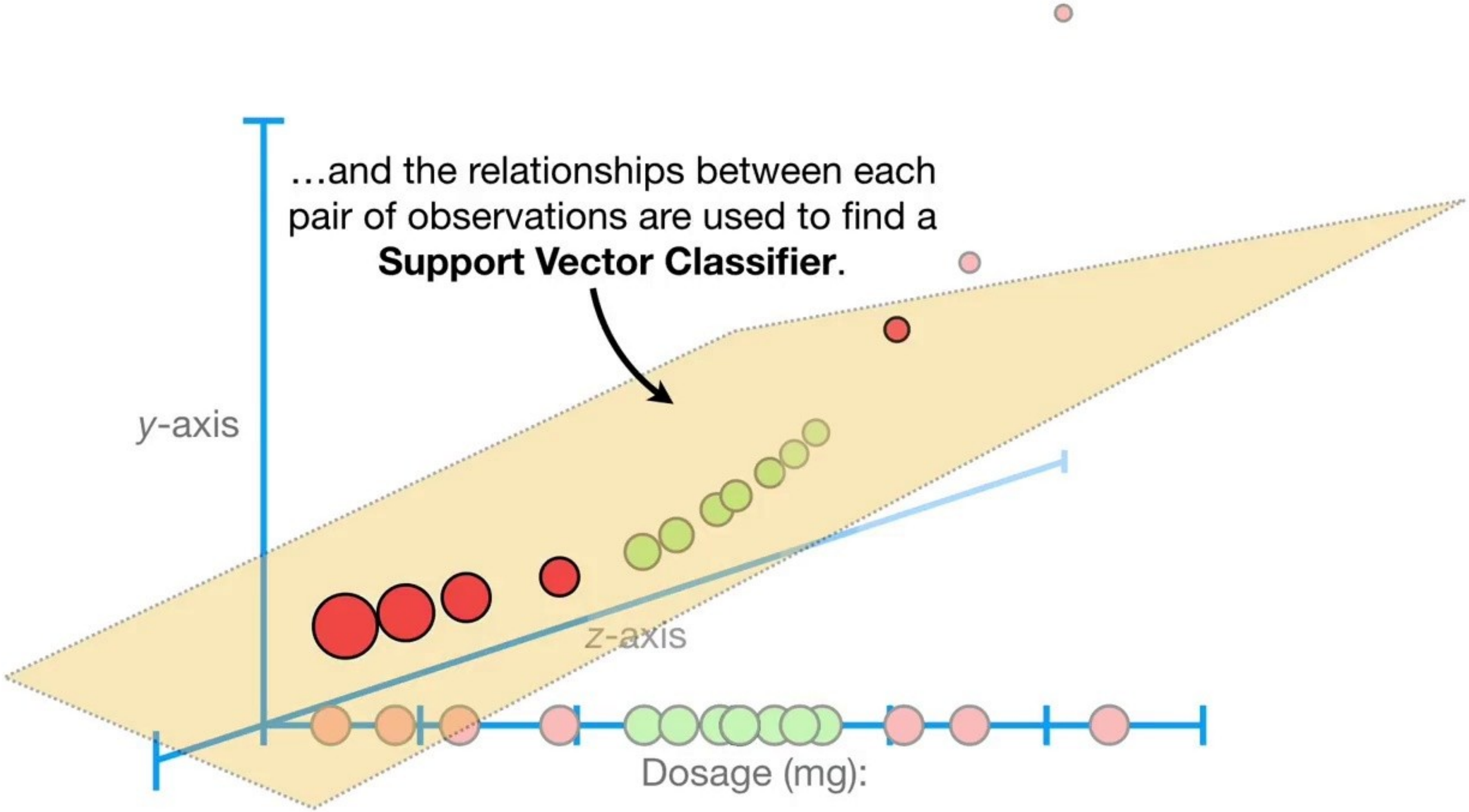
And when ***d* = 4 or more**, then we get even more dimensions to find a **Support Vector Classifier**.

In summary, the **Polynomial Kernel** systematically increases dimensions by setting ***d***, the degree of the polynomial…

***d* = 1**

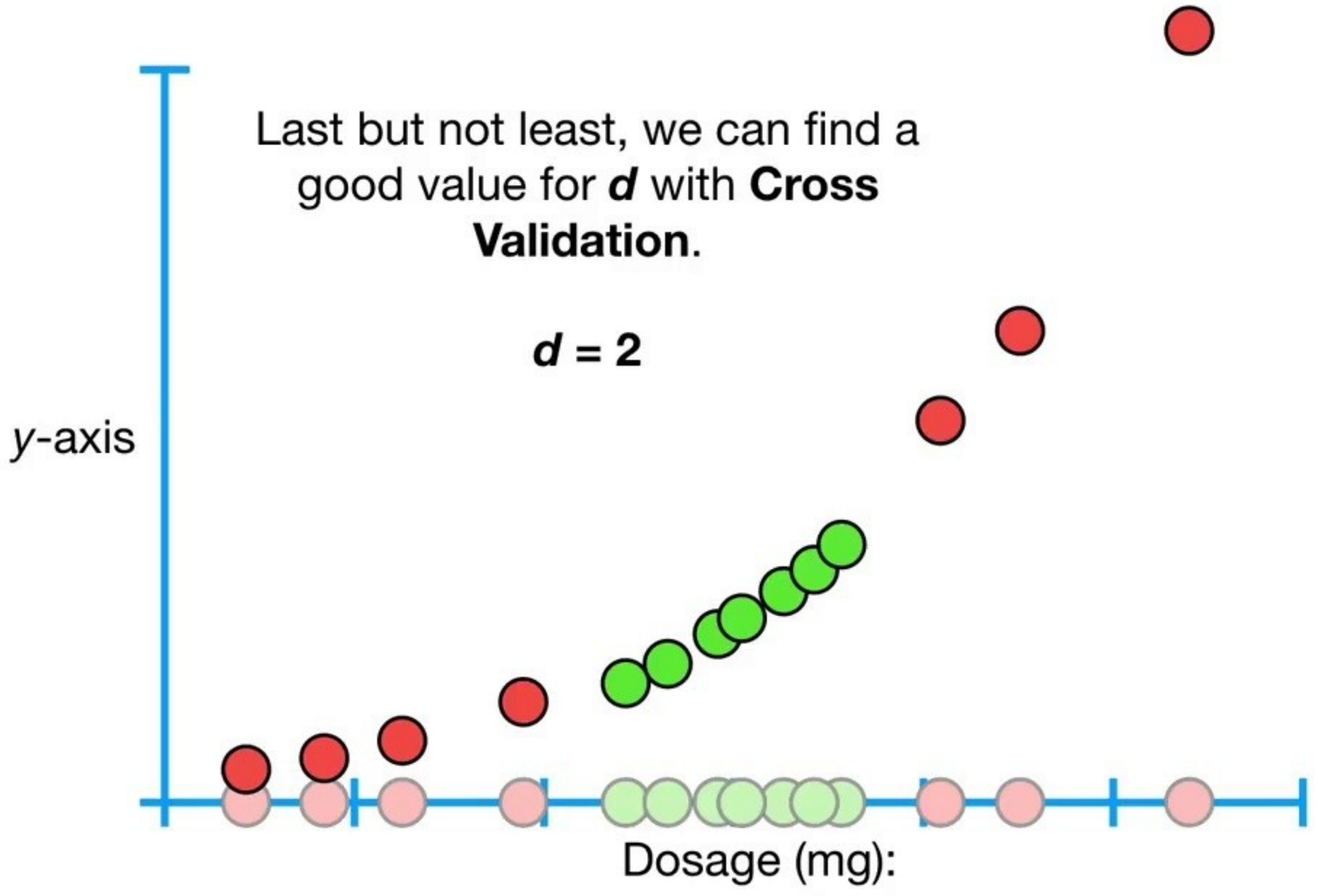

In summary, the **Polynomial Kernel** systematically increases dimensions by setting ***d***, the degree of the polynomial…
***d* = 2**
y-axis
Dosage (mg):

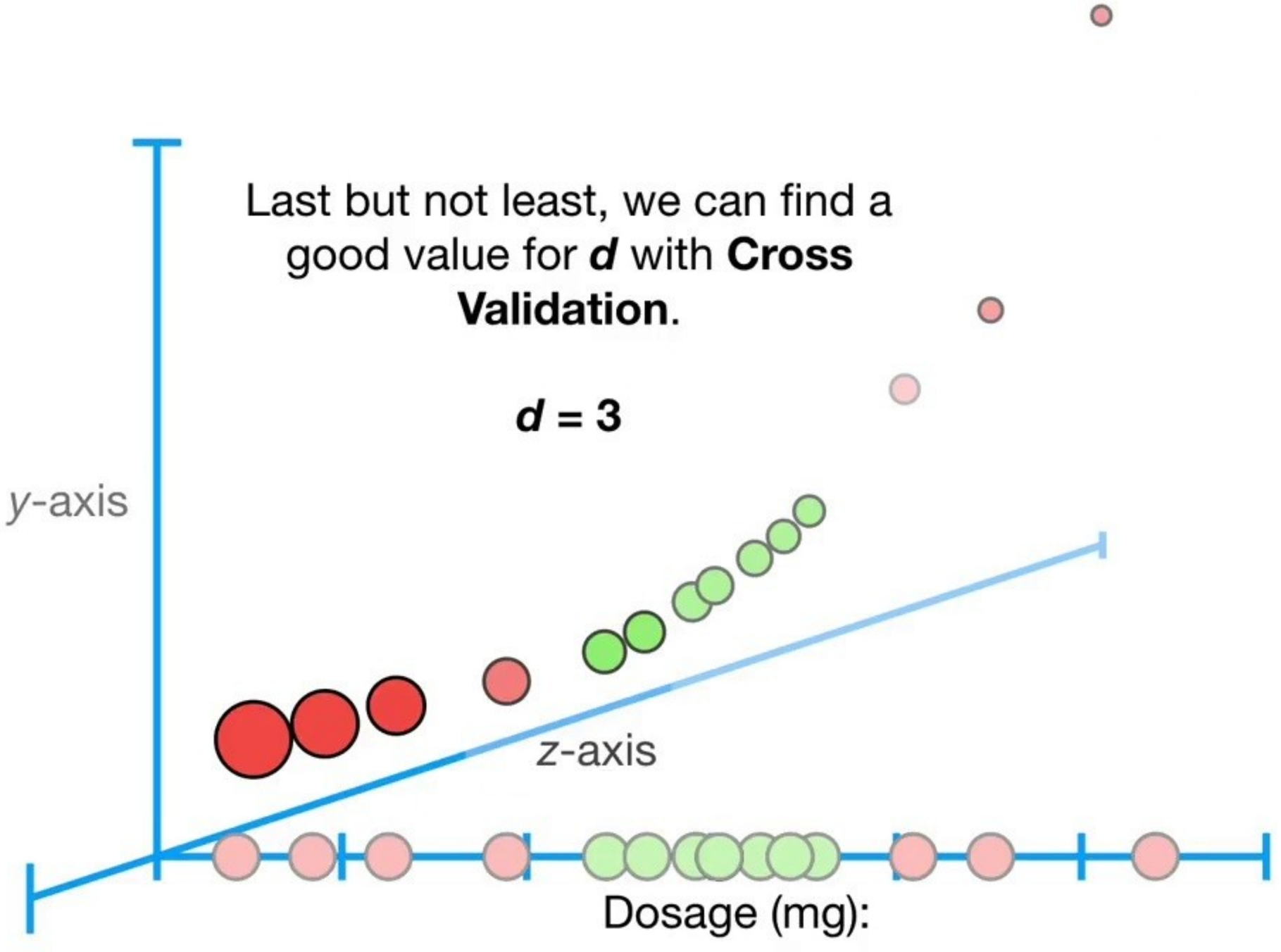

In summary, the **Polynomial Kernel** systematically increases dimensions by setting ***d***, the degree of the polynomial…
***d* = 3**
y-axis
z-axis
Dosage (mg):

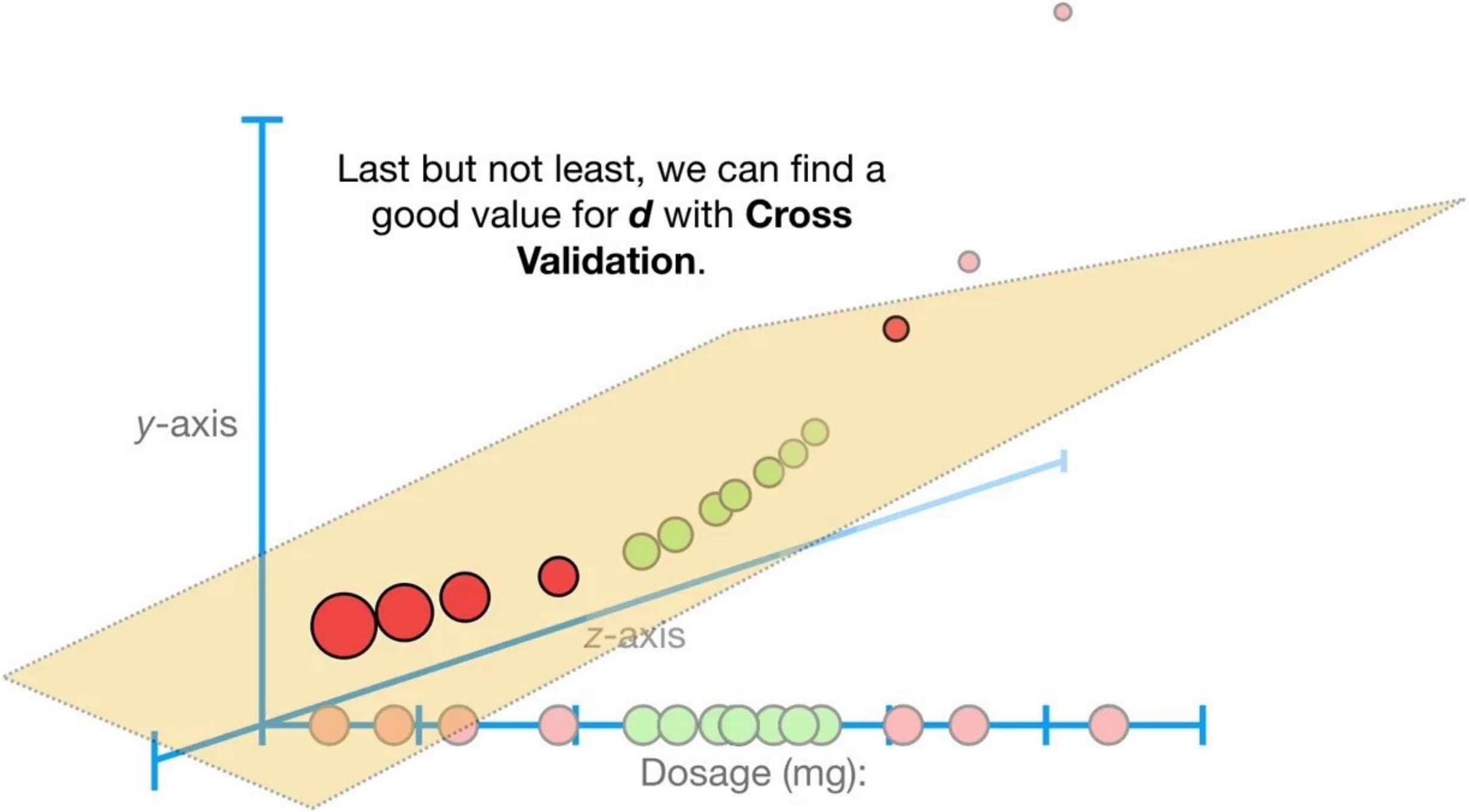

…and the relationships between each pair of observations are used to find a **Support Vector Classifier**.
y-axis
z-axis
Dosage (mg):

Last but not least, we can find a good value for ***d*** with **Cross Validation**.

***d* = 1**


Last but not least, we can find a good value for *d* with **Cross Validation**.
d = 2
y-axis
Dosage (mg):

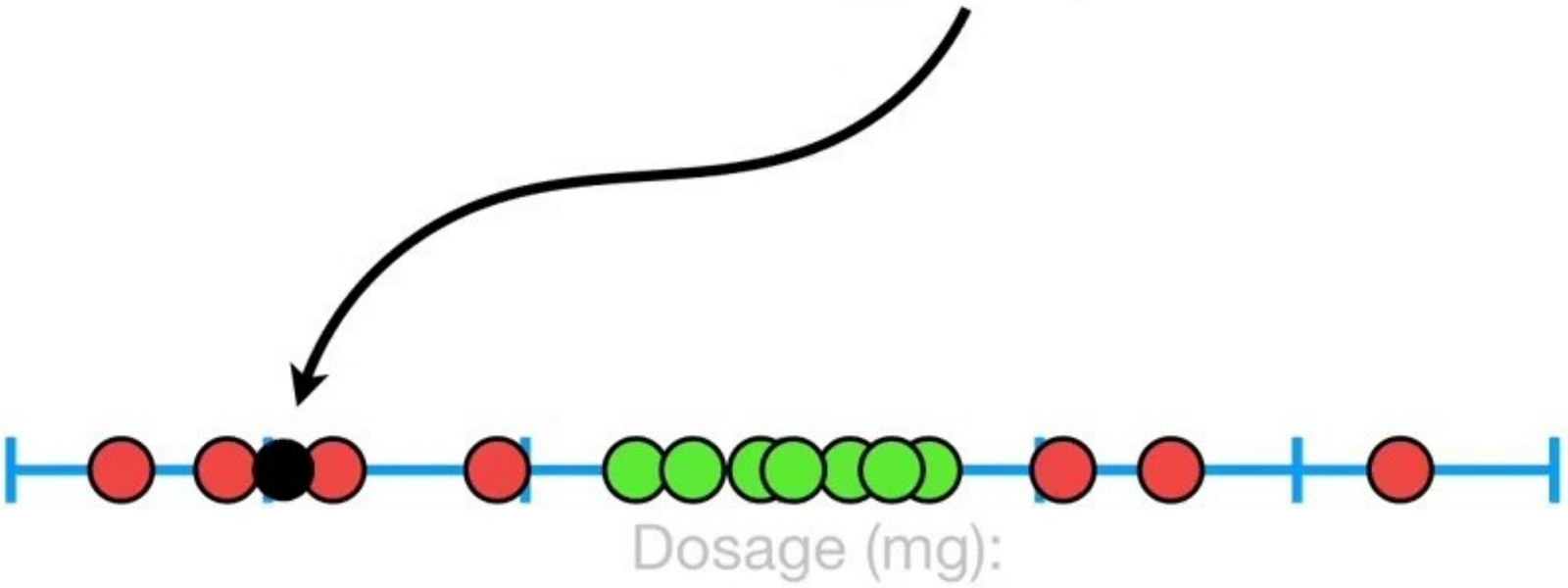

Last but not least, we can find a good value for d with Cross Validation.
d = 3
y-axis
z-axis
Dosage (mg):


Last but not least, we can find a good value for *d* with **Cross Validation**.
y-axis
z-axis
Dosage (mg):

Another very commonly used **Kernel** is the **Radial Kernel**, also known as the **Radial Basis Function (RBF) Kernel**.

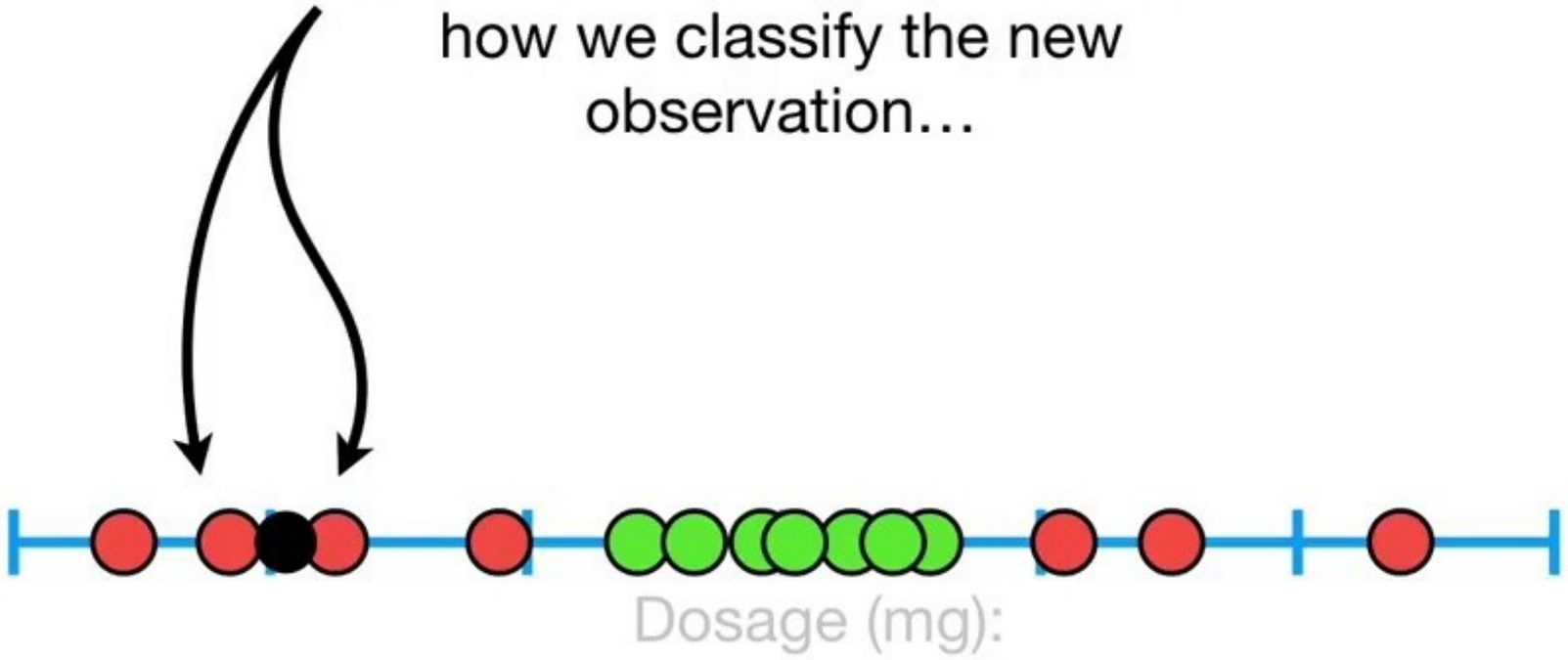
Unfortunately, the **Radial Kernel** finds **Support Vector Classifiers** in *infinite dimensions*, so I can't give you an example of what it does exactly.

However, when using it on a new observation like this…

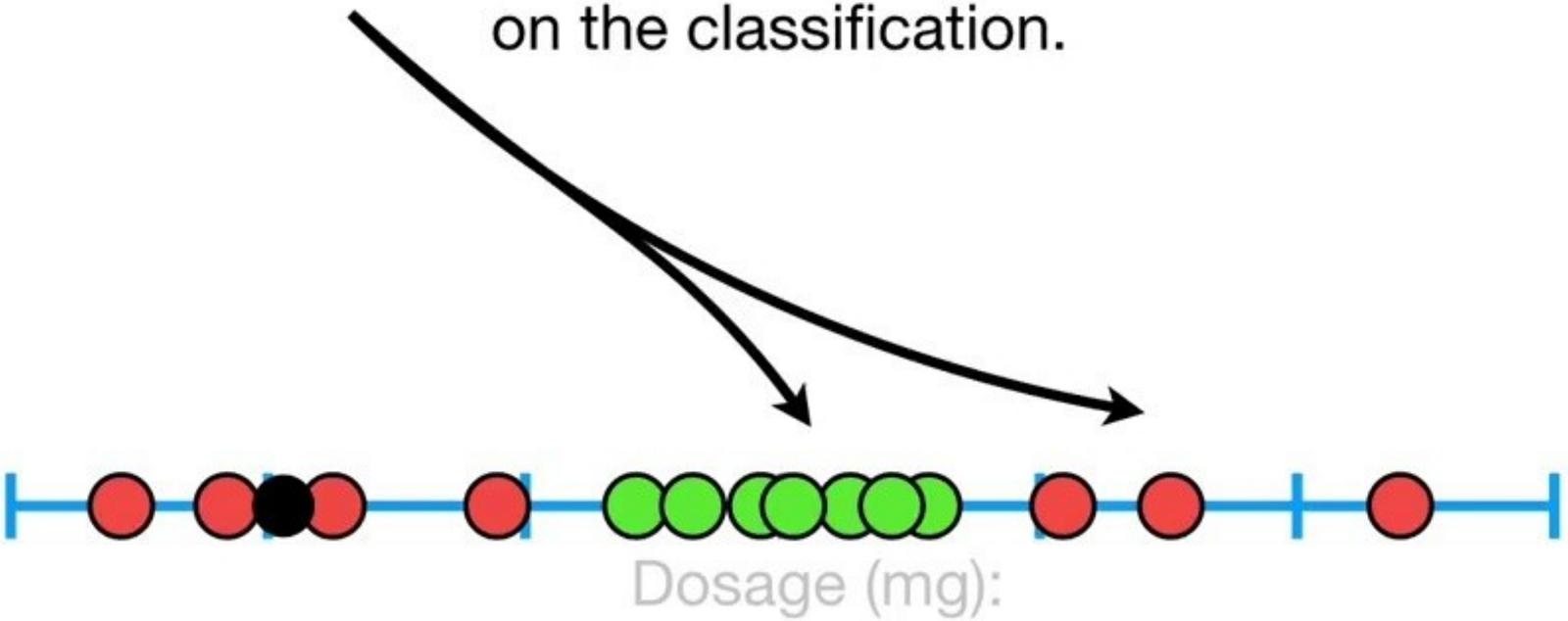


…the **Radial Kernel** behaves like a
Weighted Nearest Neighbor model.

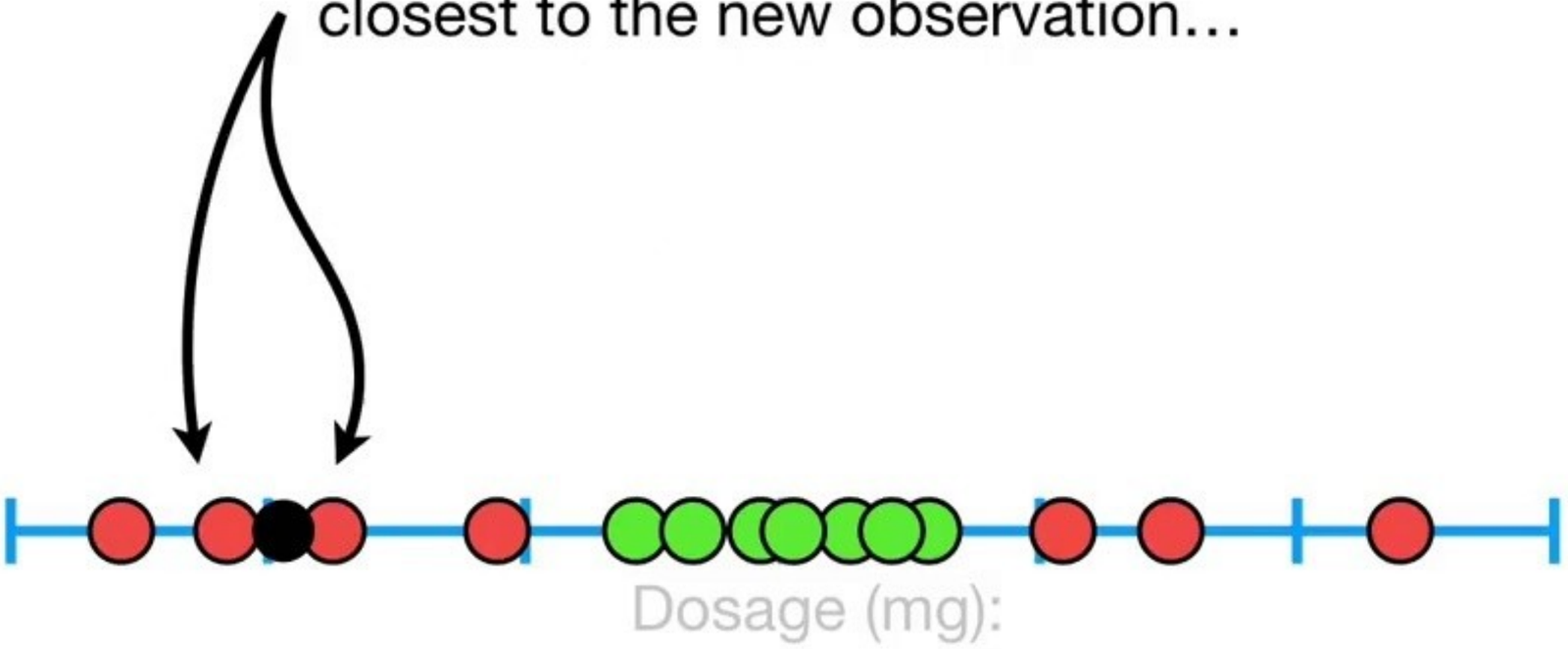
In other words, the closest observations (aka the nearest neighbors) have a lot of influence on how we classify the new observation…



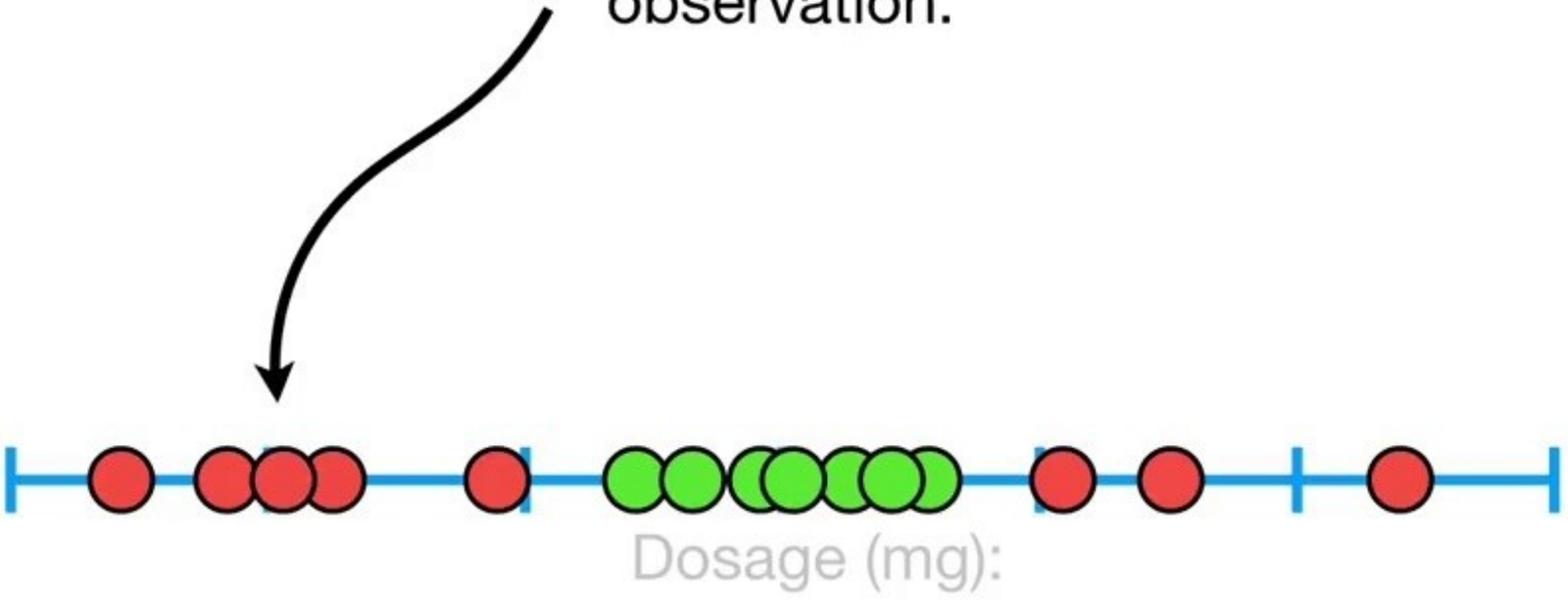
…and observations that are further away have relatively little influence on the classification.



So, since these observations are the closest to the new observation…

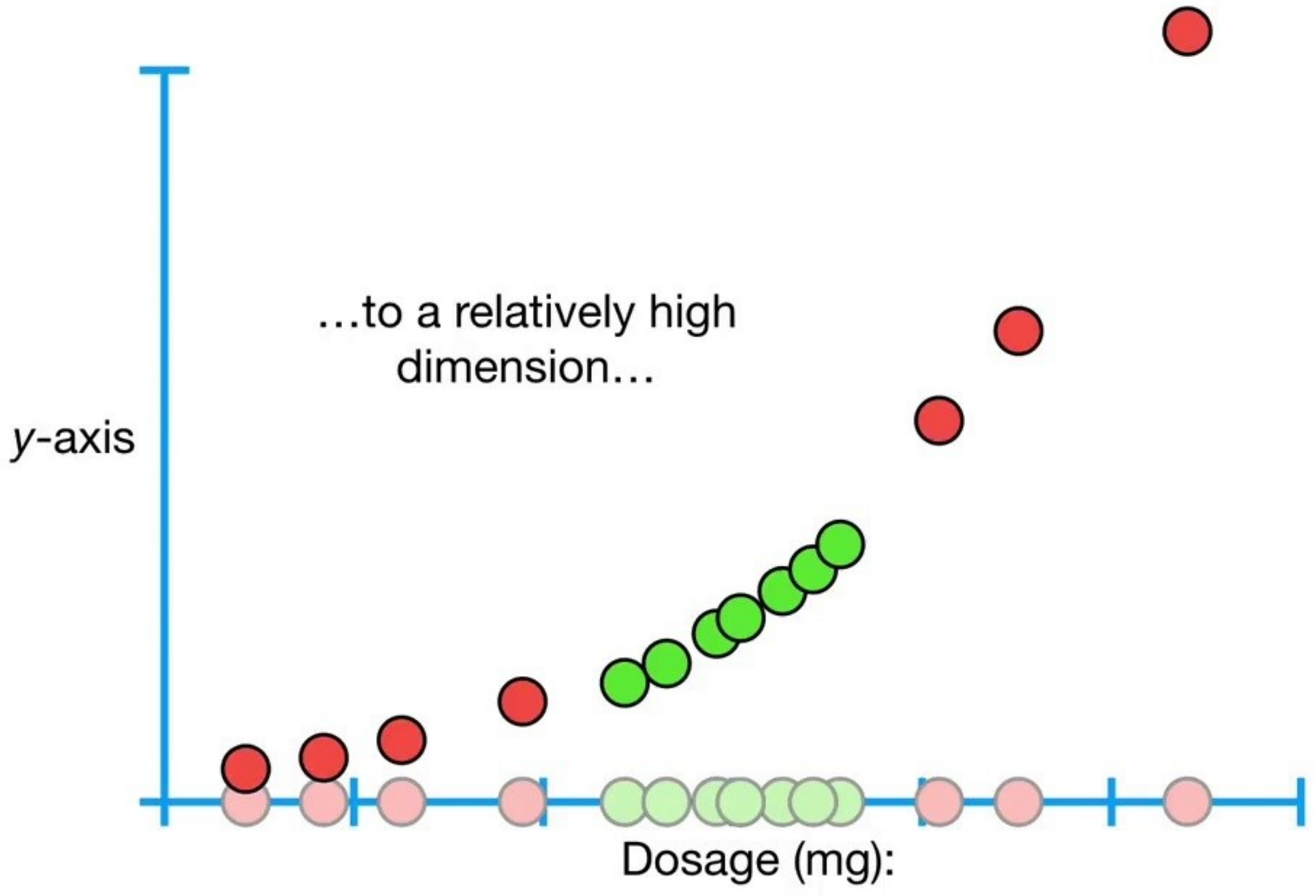


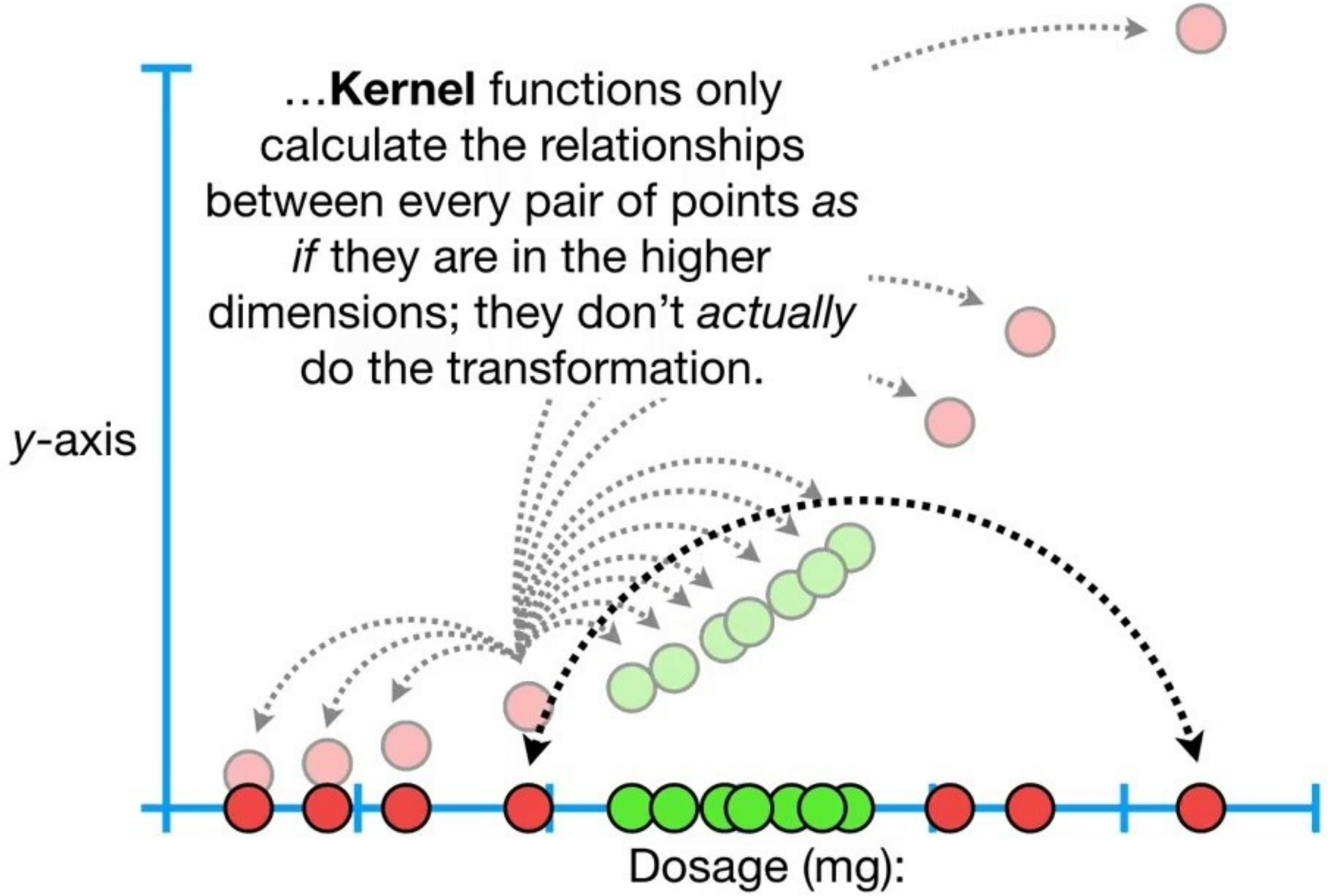
…the **Radial Kernel** uses their classification for the new observation.

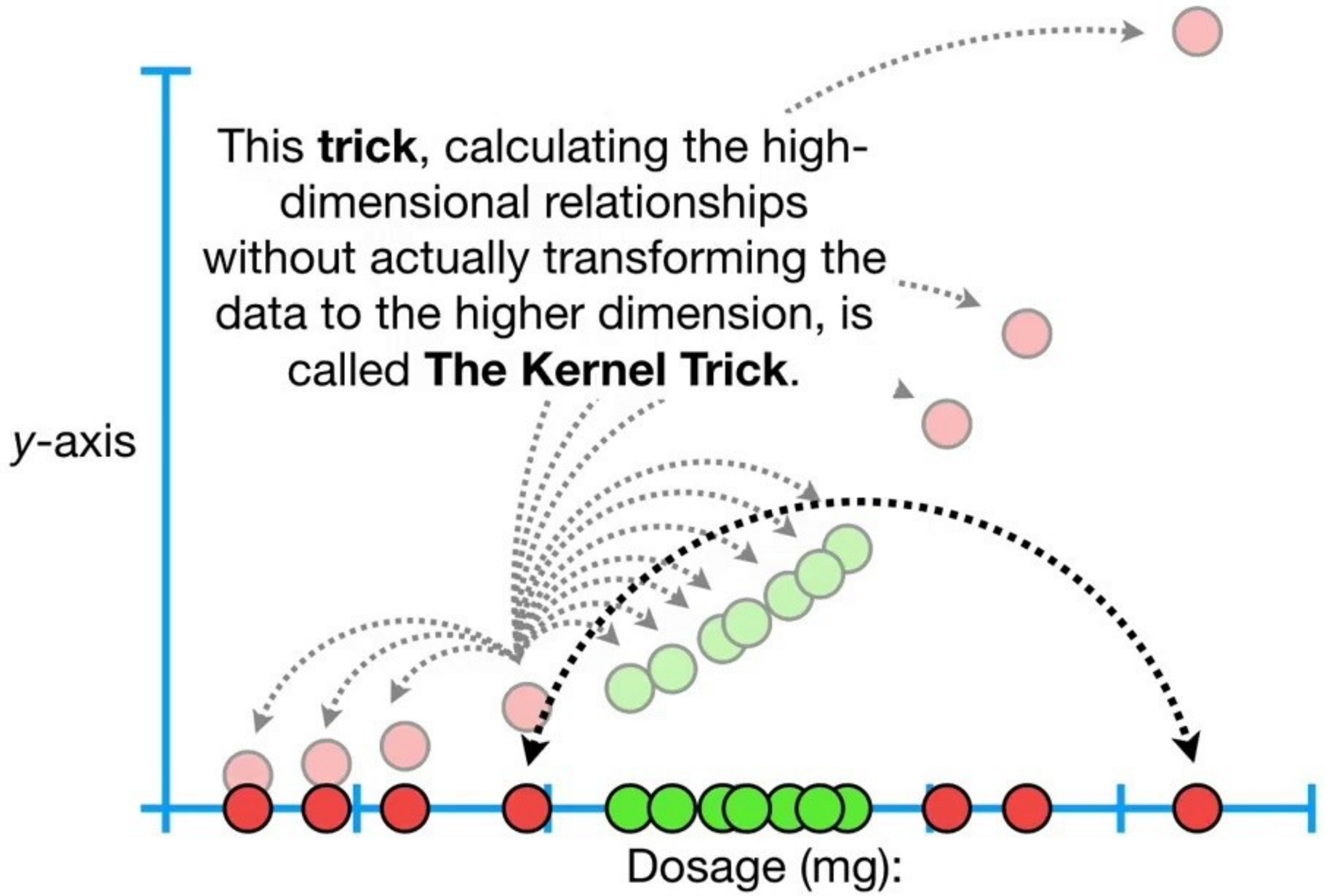


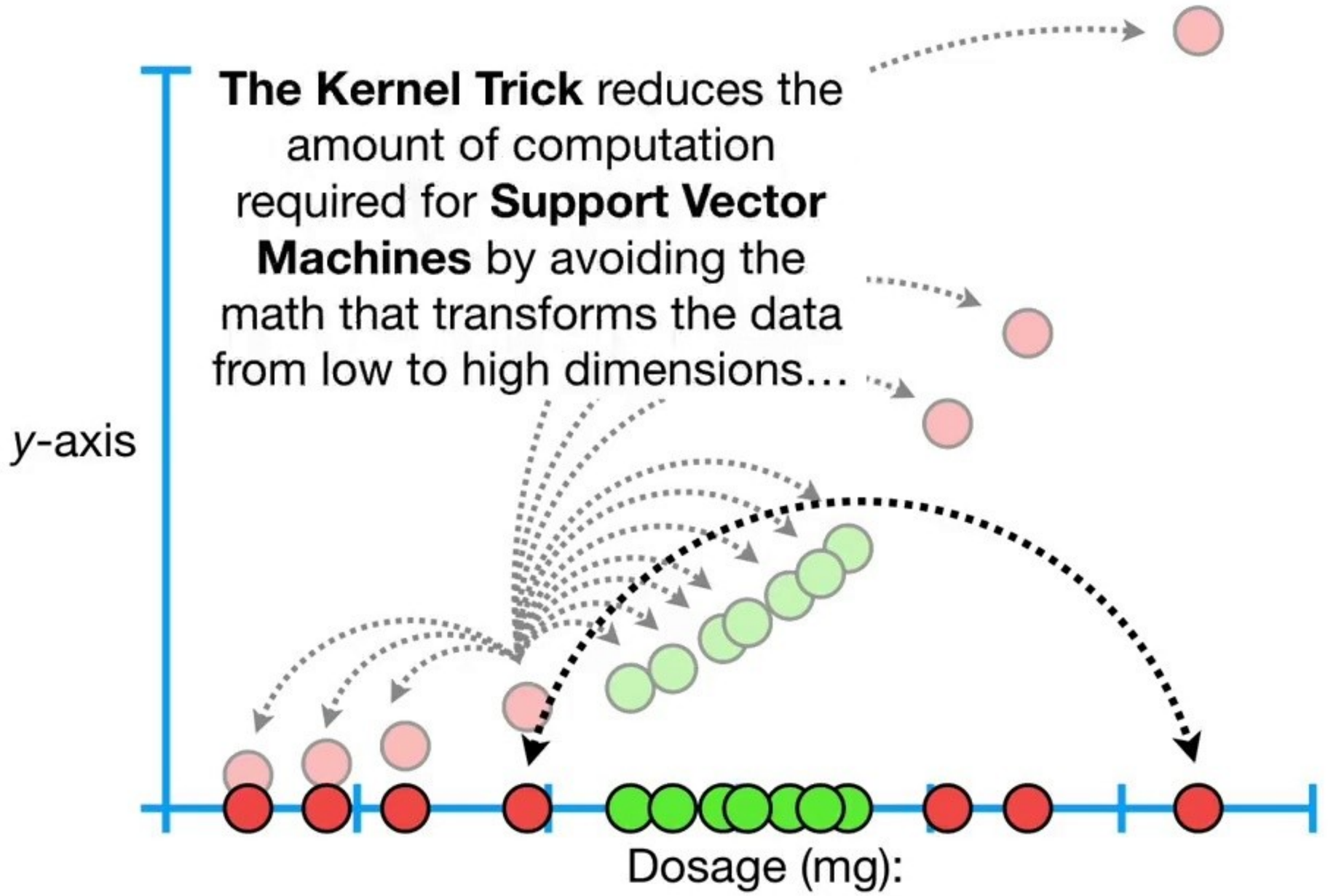
Now, for the sake of completeness, let me mention one last detail about **Kernels**.

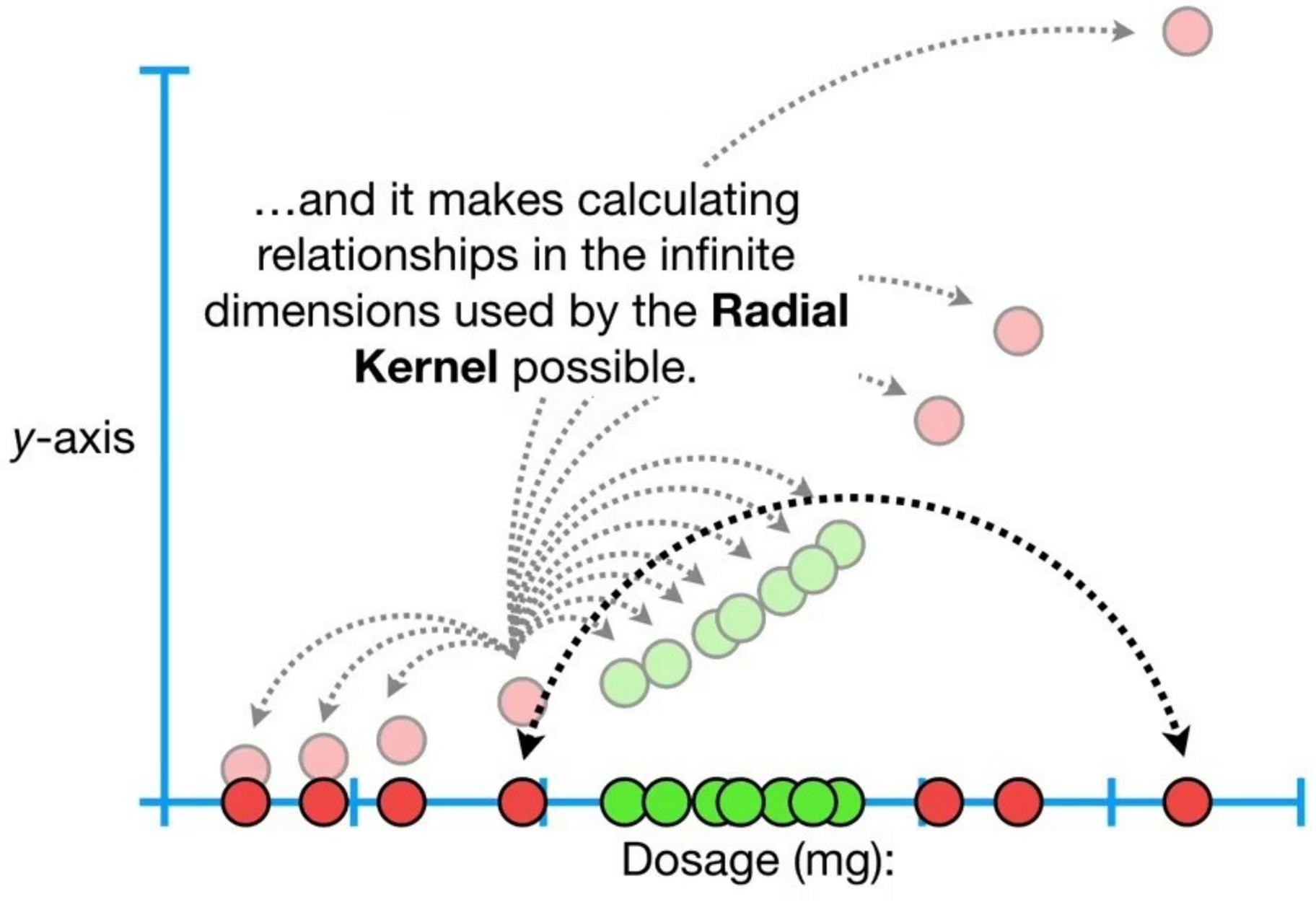
Although the examples I have given show the data being transformed from a relatively low dimension…


…to a relatively high
dimension…
y-axis
Dosage (mg):


…**Kernel** functions only calculate the relationships between every pair of points *as if* they are in the higher dimensions; they don't *actually* do the transformation.
y-axis
Dosage (mg):

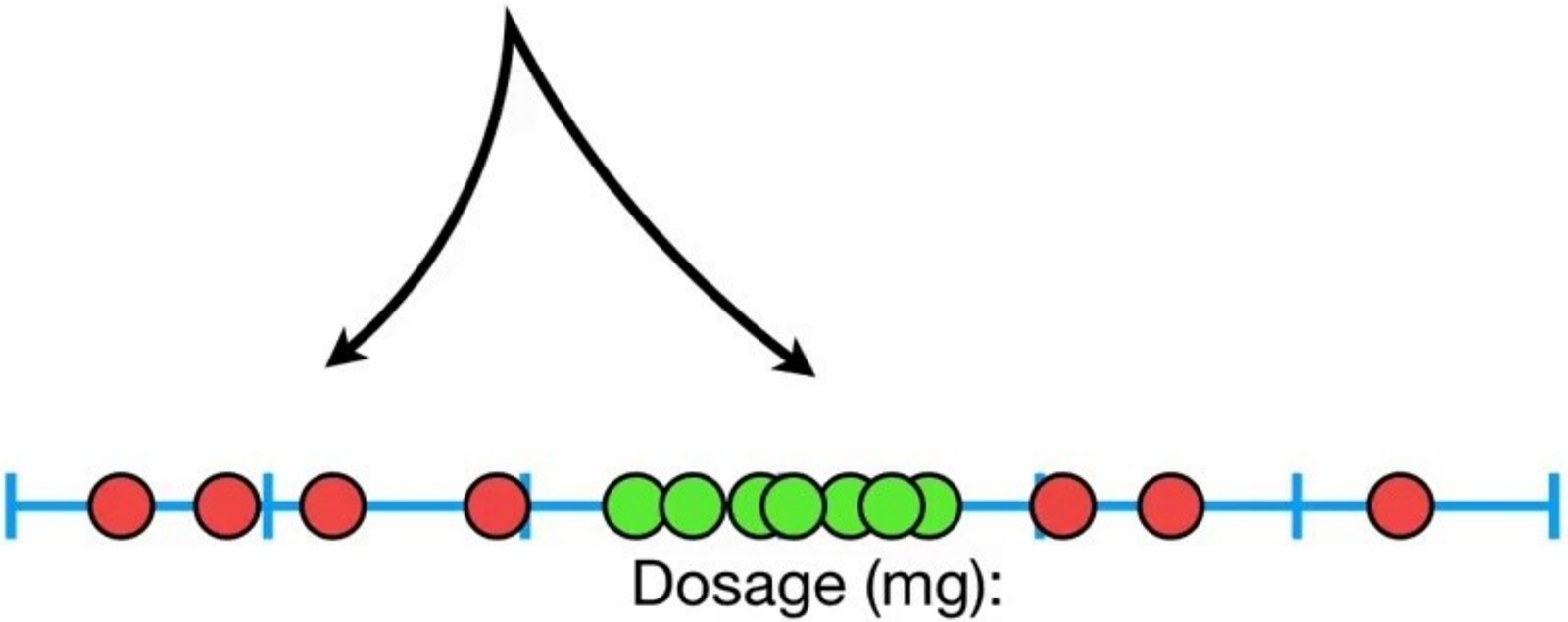

This **trick**, calculating the high-dimensional relationships without actually transforming the data to the higher dimension, is called **The Kernel Trick**.
y-axis
Dosage (mg):

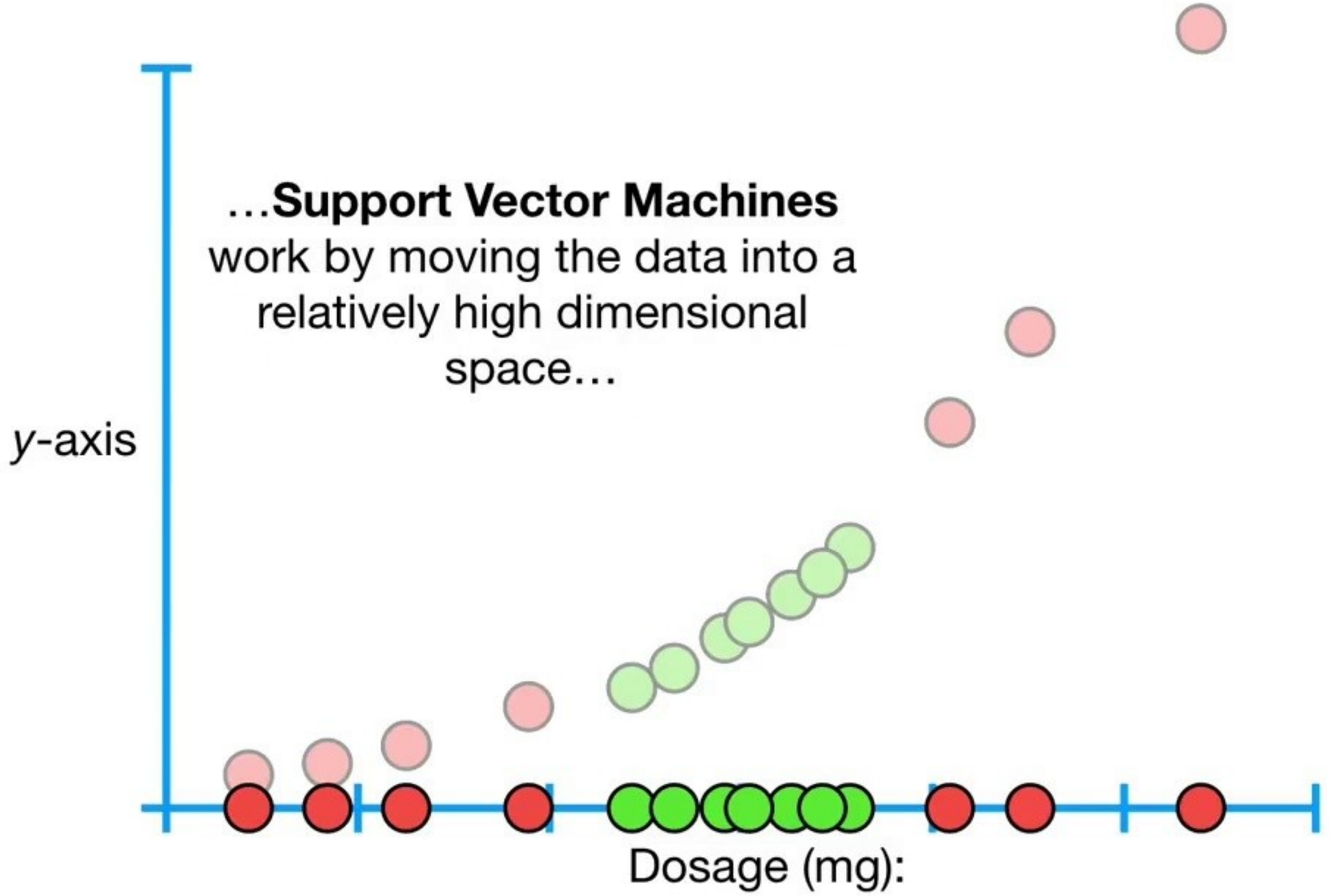

The Kernel Trick reduces the amount of computation required for **Support Vector Machines** by avoiding the math that transforms the data from low to high dimensions…
y-axis
Dosage (mg):

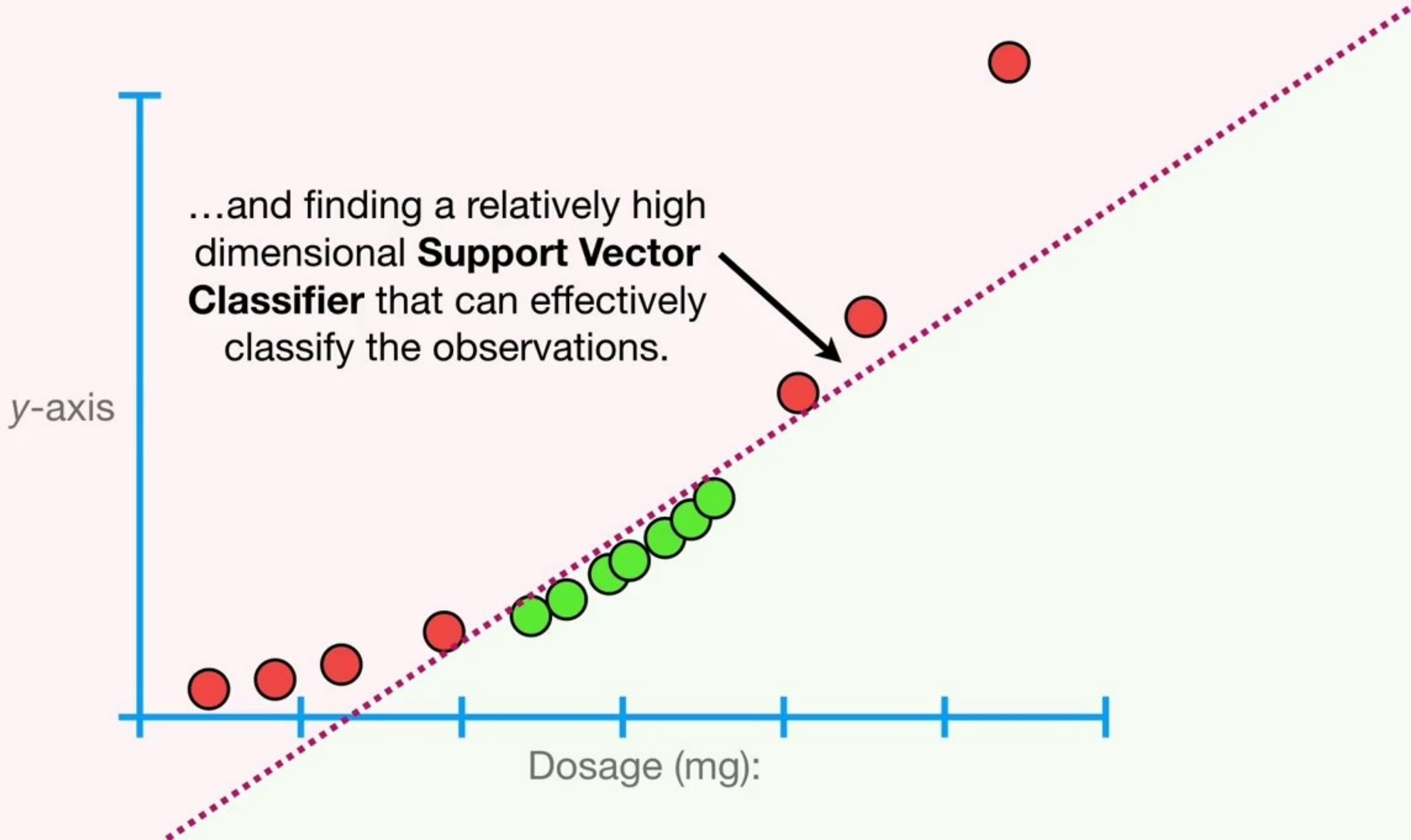

…and it makes calculating relationships in the infinite dimensions used by the **Radial Kernel** possible.
y-axis
Dosage (mg):

However, regardless of how the relationships are calculated, the concepts are the same.

When we have **2** categories, but no obvious linear classifier that separates them in a nice way…




…**Support Vector Machines**
work by moving the data into a
relatively high dimensional
space…
y-axis
Dosage (mg):


…and finding a relatively high dimensional **Support Vector Classifier** that can effectively classify the observations.
y-axis
Dosage (mg):