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# Supervised and Unsupervised Learning

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PSU

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PSU Astrostats Summer School

# Unsupervised

- Clustering
- Feature selection
- Dimensionality Reduction

# vs Supervised Learning

- Classification
- Regression
- Forecasting

# How to fit a model using M00

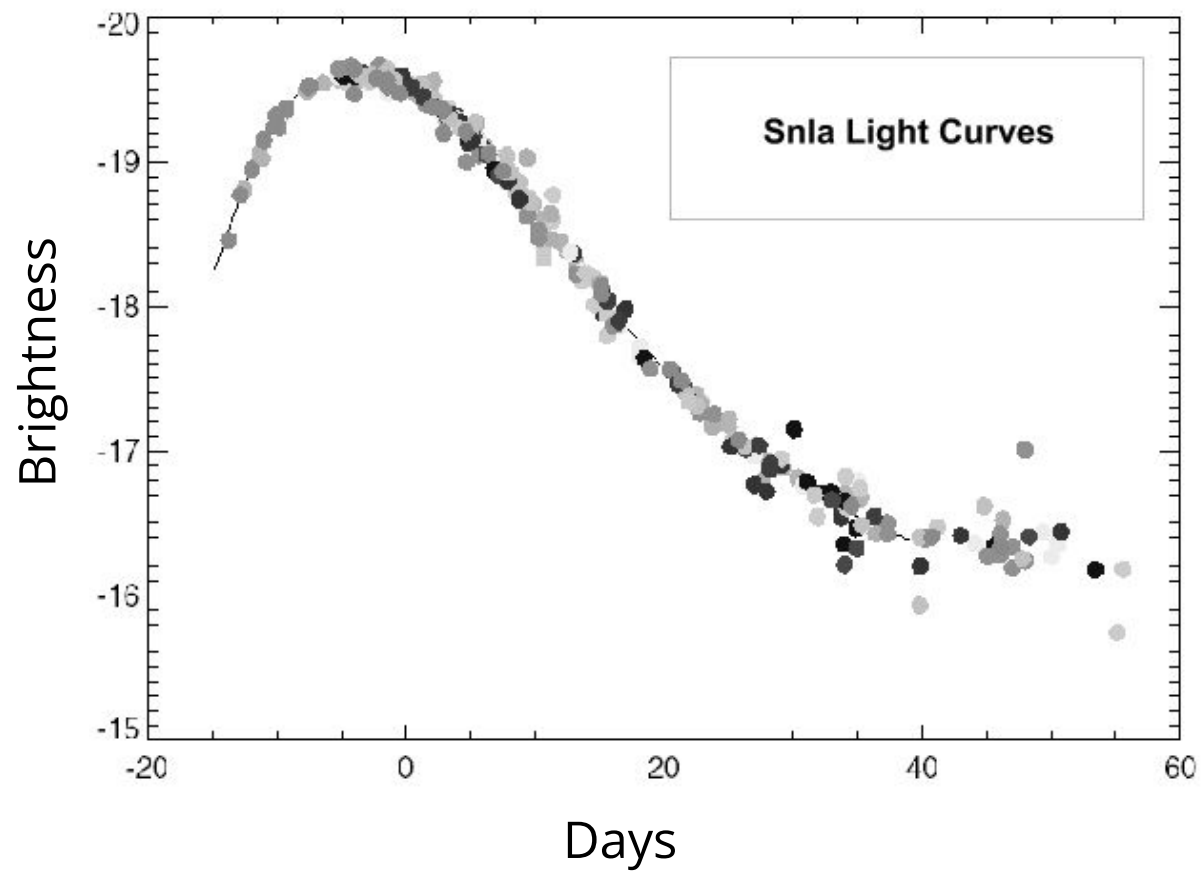
1. **Model** to fit the data (e.g. physics).
2. **Objective Function** (or 'loss/cost function') which is a metric that you will choose to quantify how well the model fits the data (e.g. chi-squared).
3. **Optimization Method** which you will use to find the best model (e.g. gradient descent).

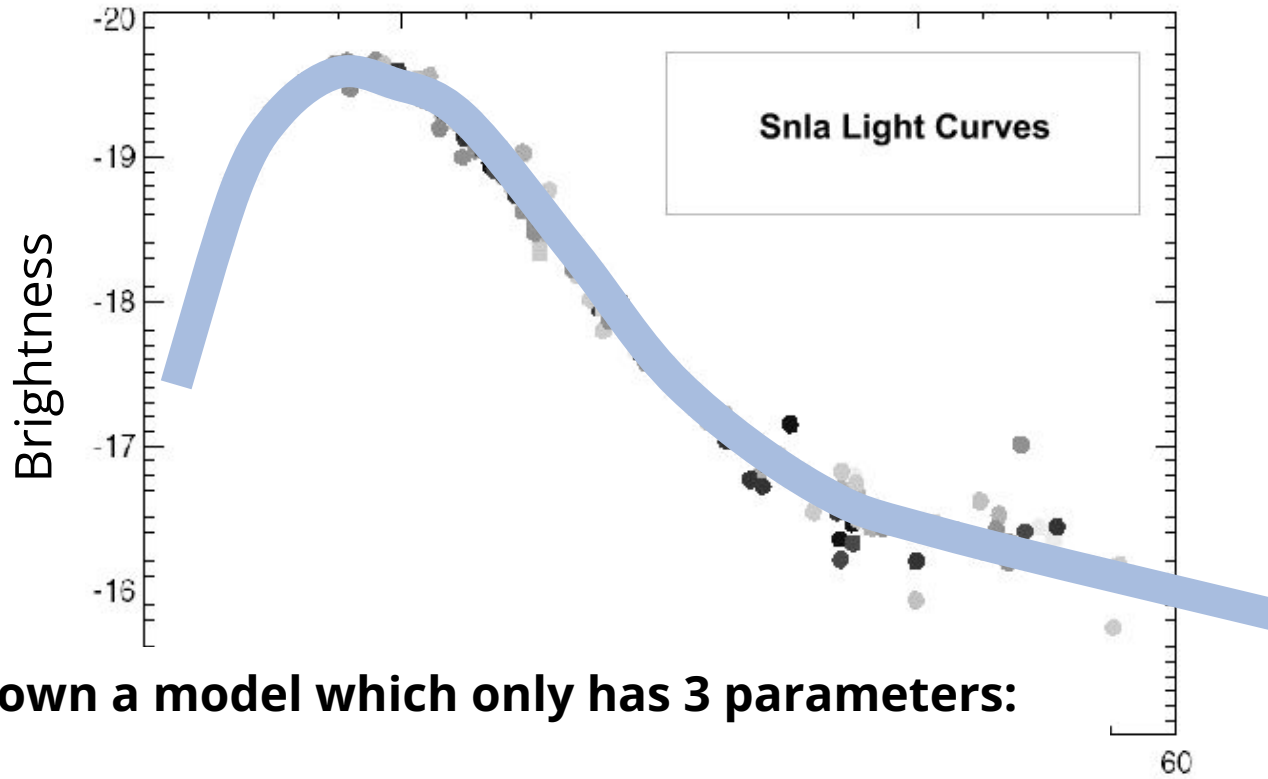
# Unsupervised Learning

Learning **structures** within our data

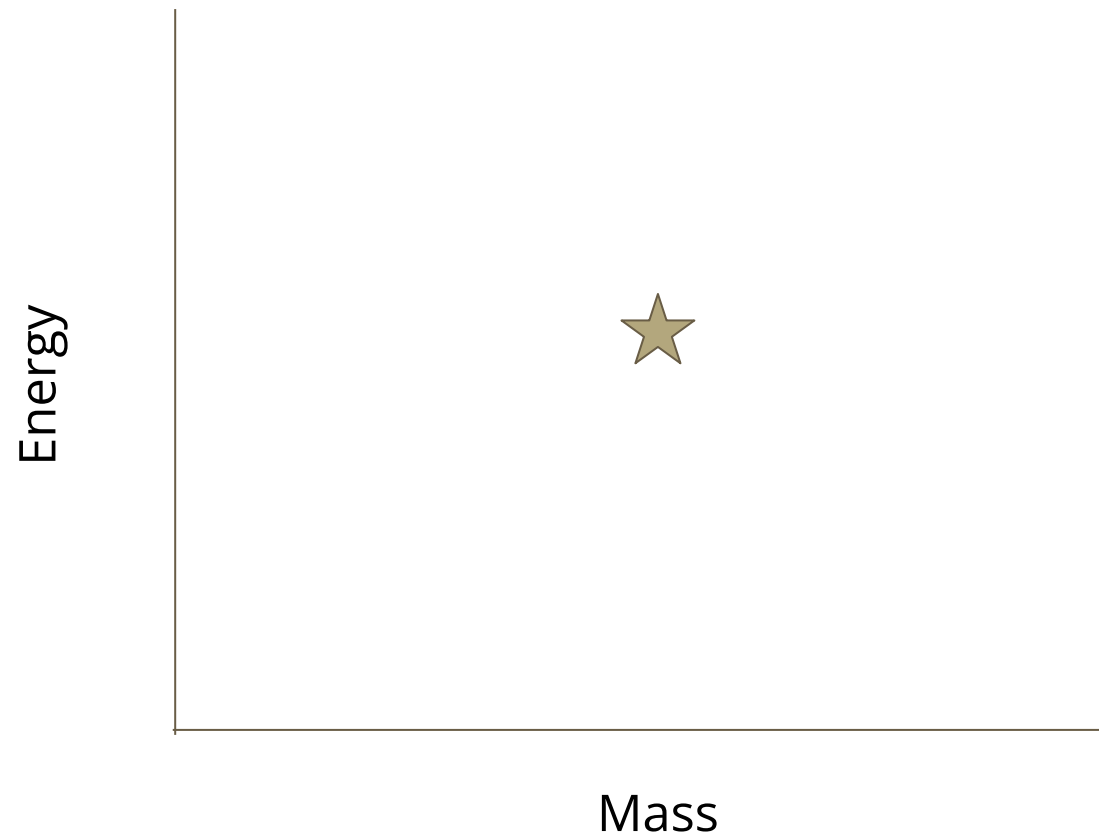
First, let's focus on **reducing dimensionality**

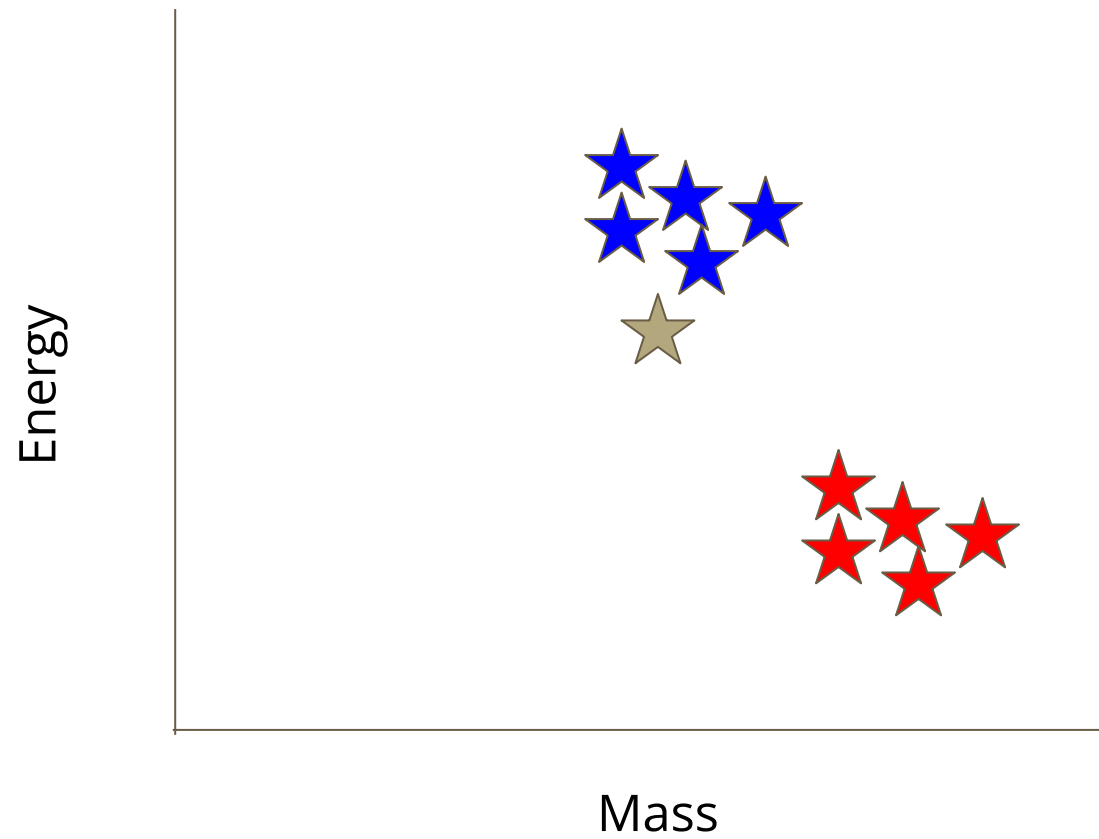
Then, we'll focus on **clustering**





**I can write down a model which only has 3 parameters:**  
**Energy,**  
**Mass,**  
**Amount of radioactive material**



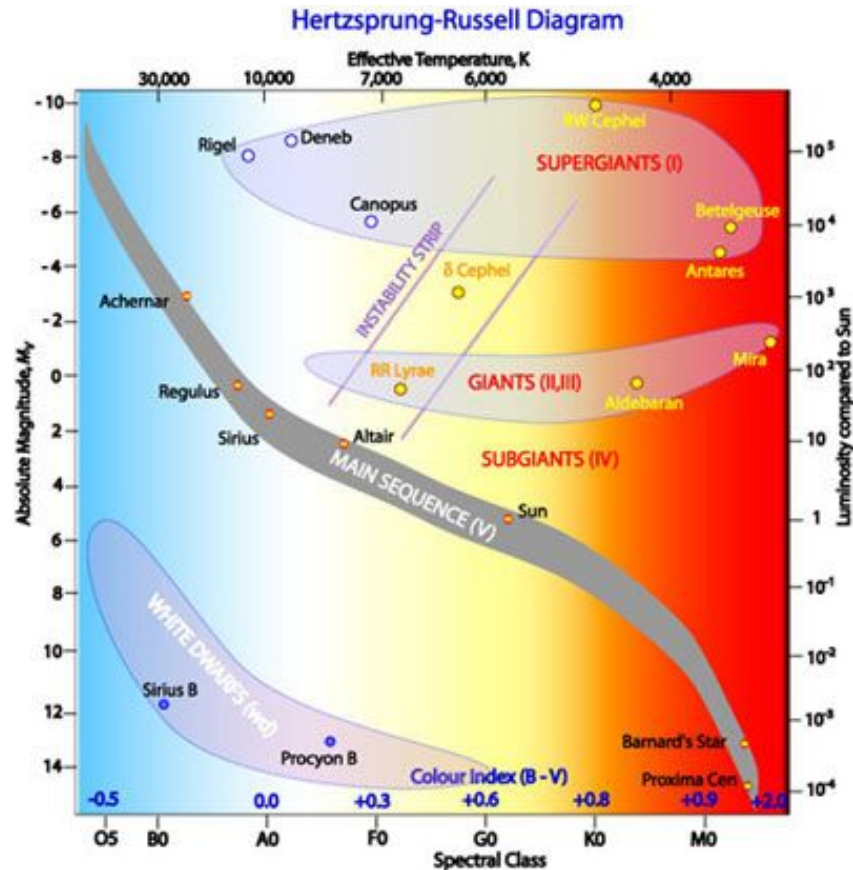




Let's call this space a "latent" space. Why "latent"?

How is this different (if at all) from physical model parameters (e.g., mass and energy)?

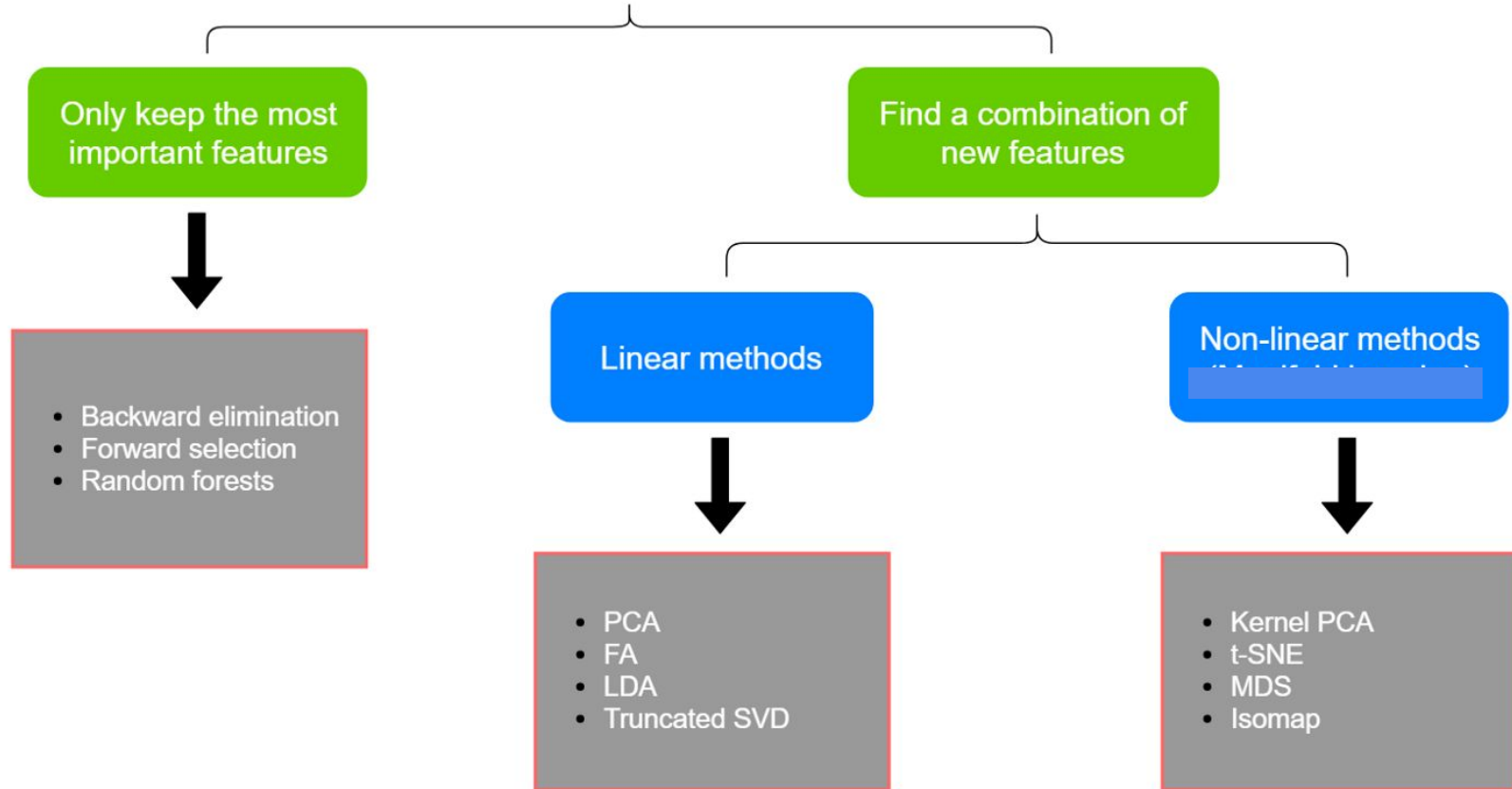
# Why do we care about latent spaces?



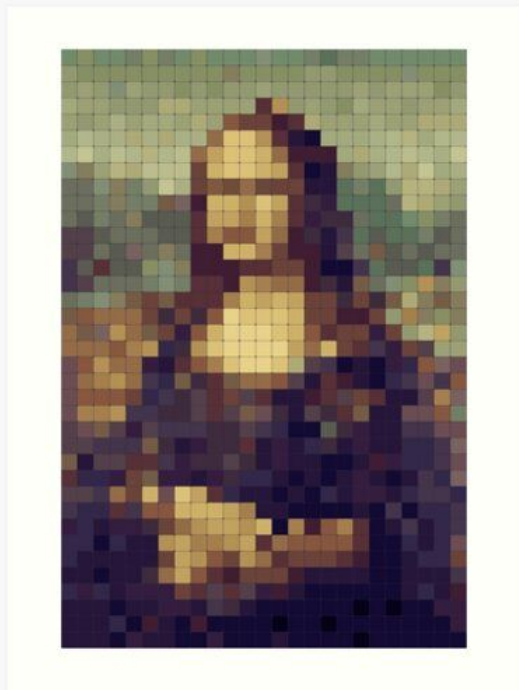
# Once our data is in a low-dimensional space, we can complete a number of tasks:

1. Better feature selection for classification
2. Anomaly detection
3. Data simulations
4. Physical interpretability

# Dimensionality reduction methods

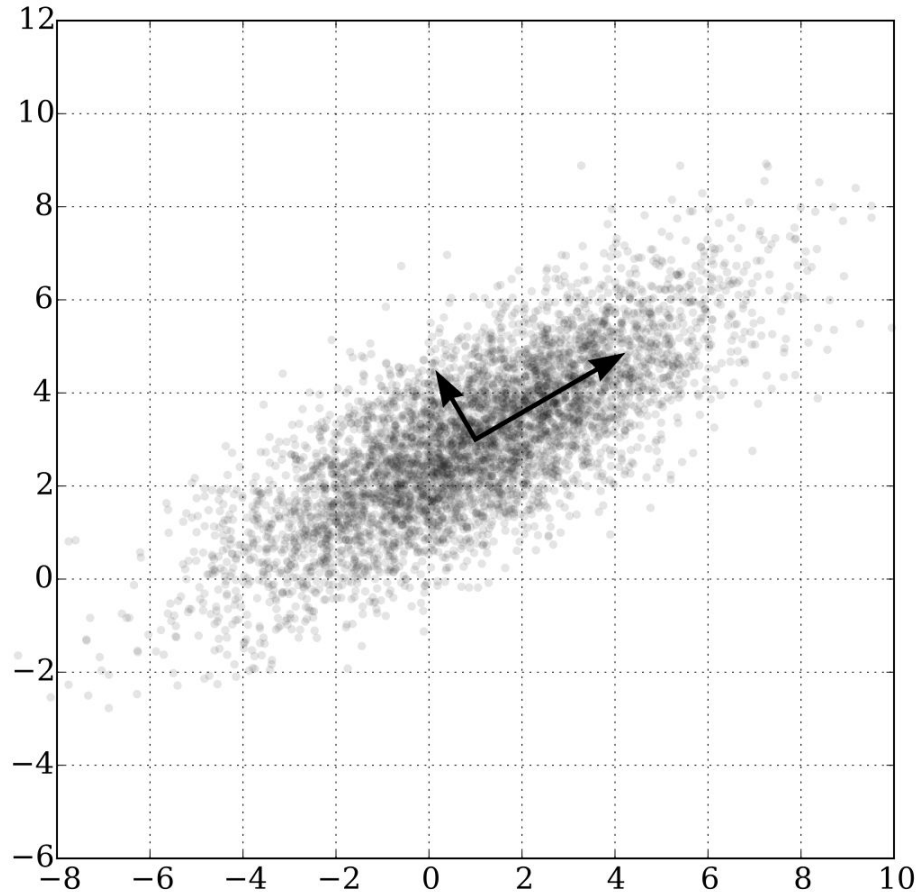


**Removing information can be an effective way to remove dimensionality**

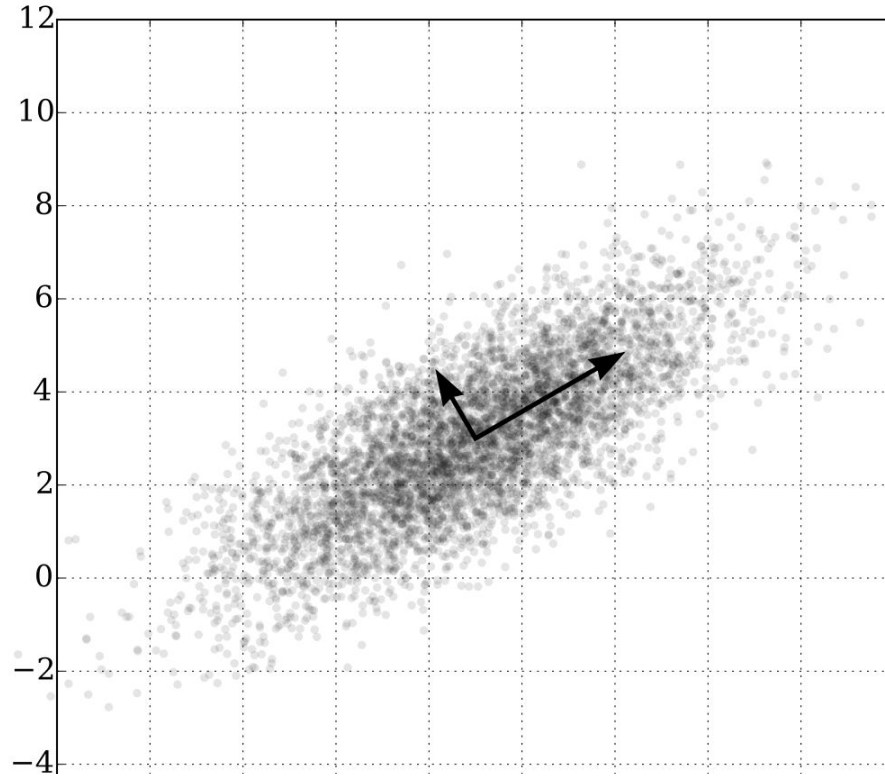


**How can we create a low-dimensional representation  
without directly fitting a physical model?**

The simplest solution is to break down data into **basis vectors**



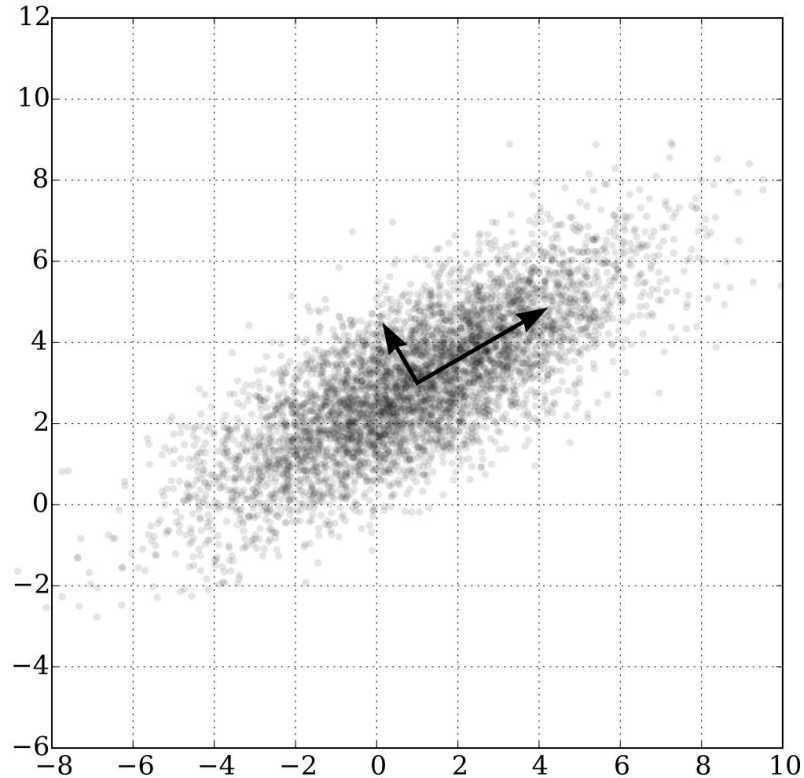
The simplest solution is to break down data into **basis vectors**



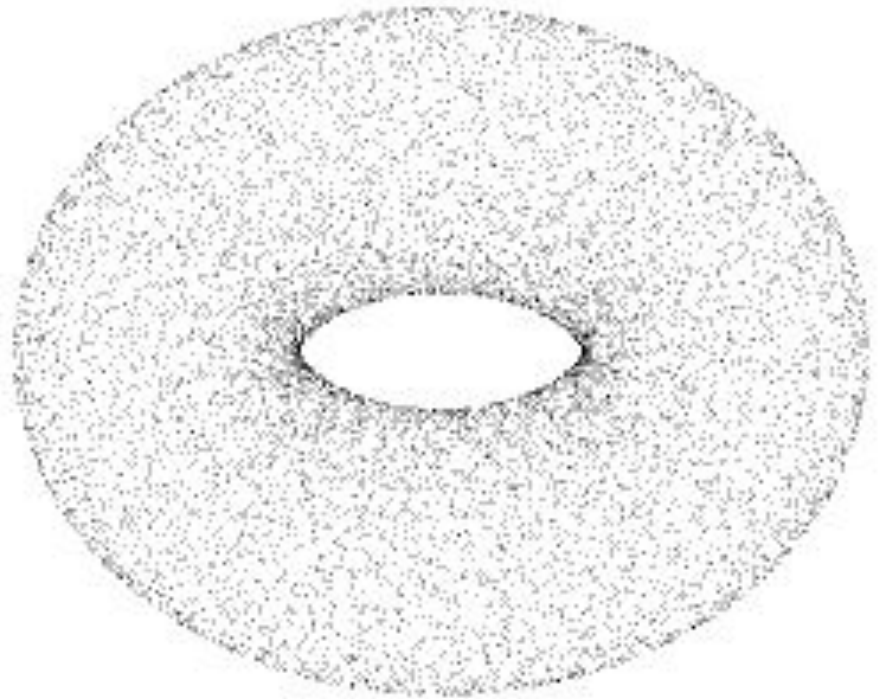
*An eigenbasis is one with orthogonal, normalized vectors*



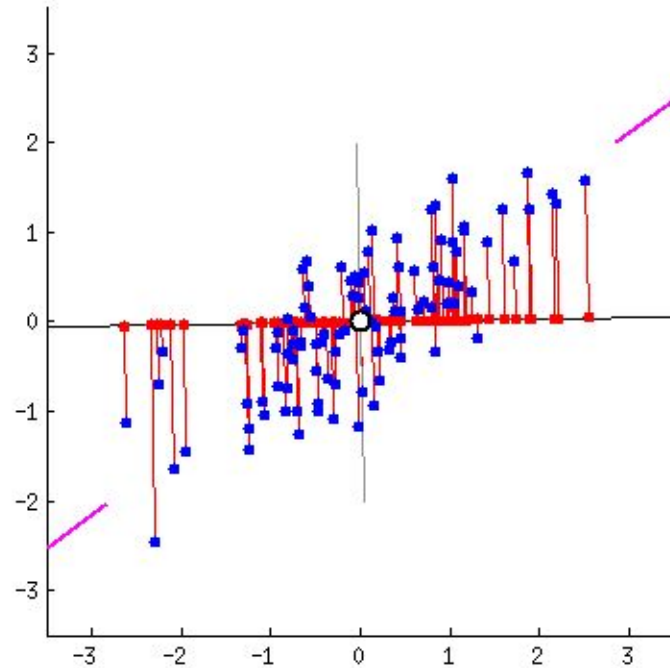
In this 2D example, every point is exactly described by the sum of two eigenvectors



In higher dimensions,  
2 detectors may  
describe 'most' of the  
variance within our  
data



Each observed datapoint can be projected onto a basis vector

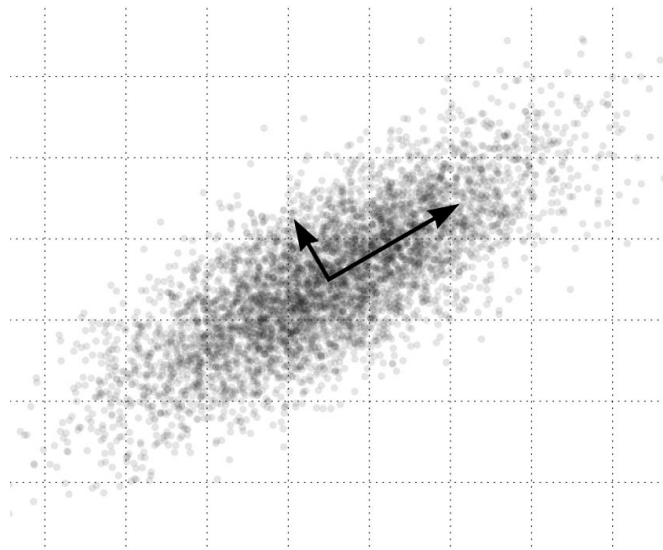


# Principal Component Analysis (roughly) has the following steps:

- Find the eigenvectors of the dataset

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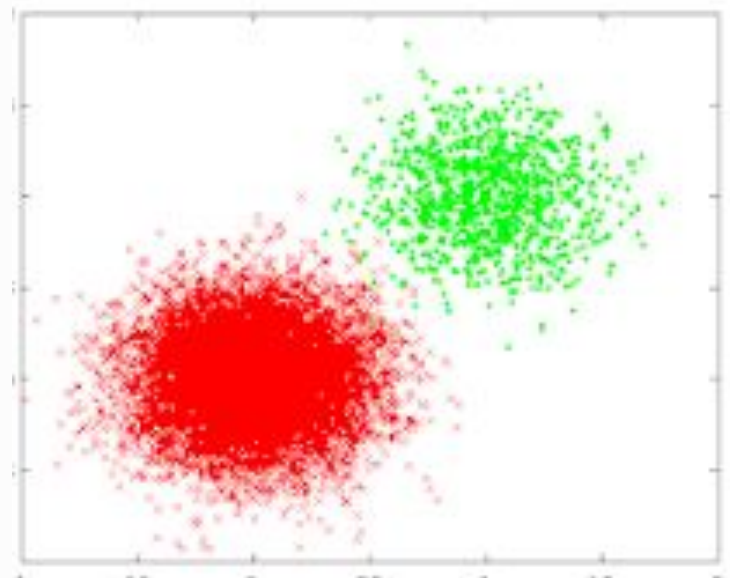
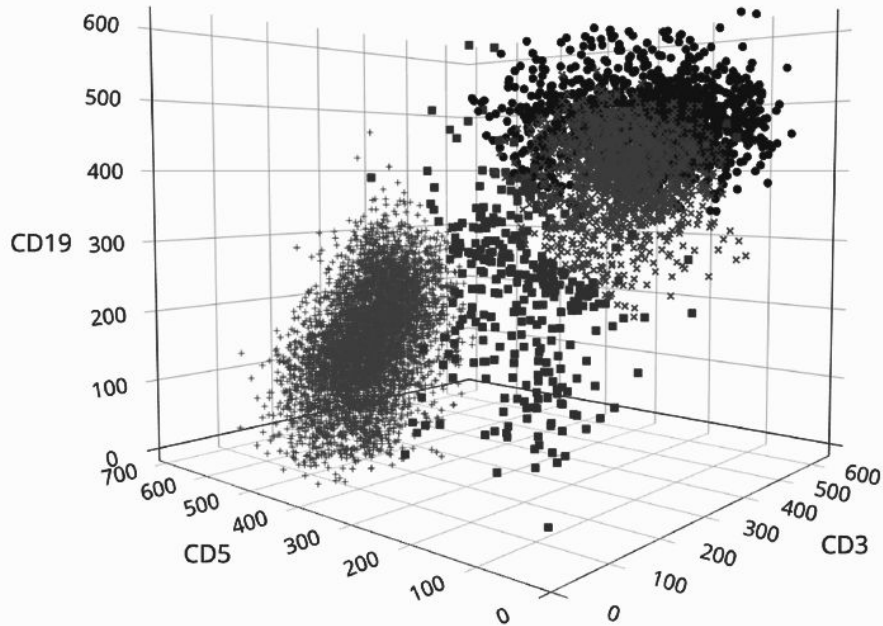
- Find the eigenvectors of the dataset
- Sort the eigenvectors by explained variance
  - Which ones explain the majority of the scatter within the data?



# Principal Component Analysis (roughly) has the following steps:

- Find the eigenvectors of the dataset
- Sort the eigenvectors by explained variance
- Project the data onto each basis, tracking the weights
  - For  $N$ -dimensional data, each point should be exactly described with  $N$ -vectors. So we want to grab the  $M$  vectors which describe most of the variance in our data, with  $M < N$

PCA transforms our high-dimensional observed space, to a low-dimension **latent space**



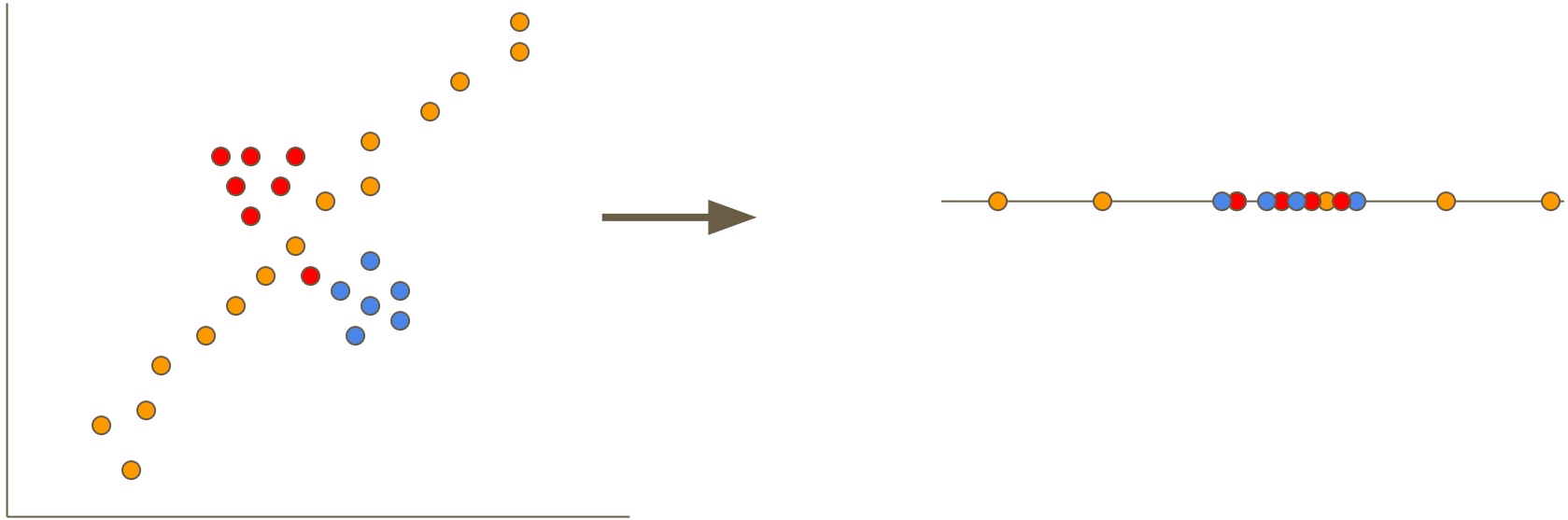
# What if my data is high dimensional?

It can be computational expensive to find *every* eigenvector if our data-space is high-dimensional. Instead, we can iteratively find the top  $k$  eigenvectors using the **power iteration method**:

1. Given  $M=X^TX$ , select a random vector  $v_0$
2. For  $i = 1, 2, \dots$ , let  $v_i = Mv_{i-1}$ .
3. If  $v_i / |v_i| \approx v_{i-1} / |v_{i-1}|$ , then return  $v_i / |v_i|$  as an approximation for the first component ( $w_1$ )
4. Project our data orthogonally to  $w_1$ . Repeat steps 1-3 to find the next PCA component. Repeat for  $k$  components



# PCA is limited by its linear nature



# Group chat - discuss the following questions

1. What does it mean to have a 'linear' transformation of our data?
2. Can you give an example of a non-linear transformation in astronomical data?

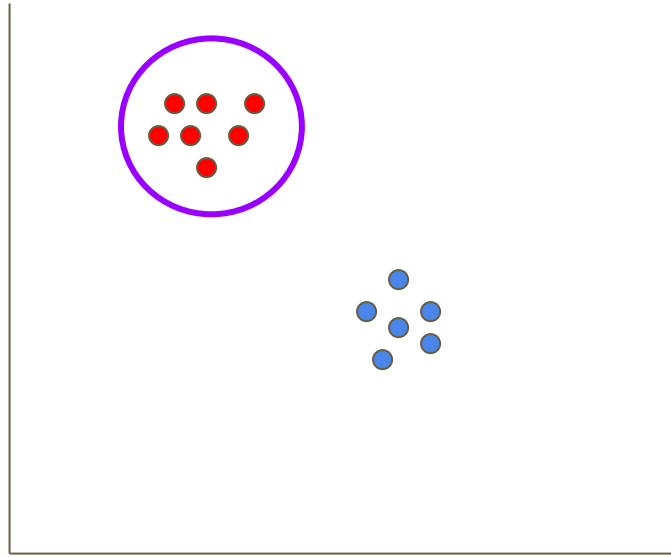
**PCA is limited in its linear assumption, but other, more sophisticated, methods exist as well**

**(e.g., t-sne, UMAP)**

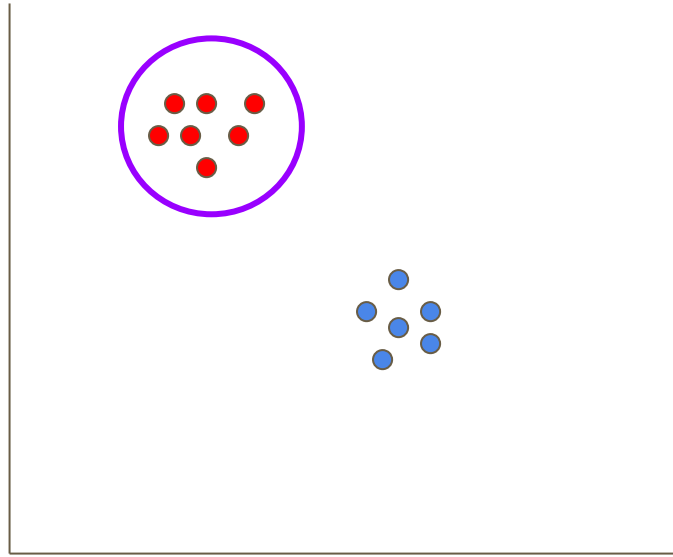
**t-distributed stochastic neighbor embedding**  
**(t-SNE or “tee-snee”)**

**t-distributed stochastic  
neighbor embedding**

# Neighbor embedding: quantify which observations are similar

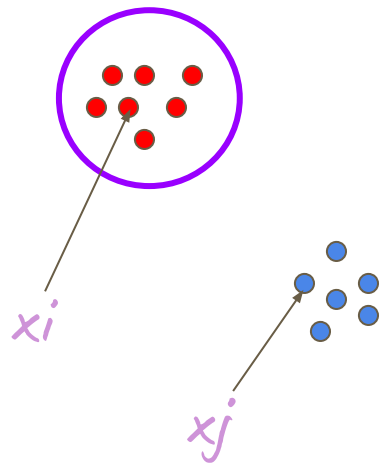


Define a distance metric (e.g., Euclidean distance)



$$d_{i,j}^2 = ||x_i - x_j||^2$$

Think of this distance as being proportional to the chance that observations are “neighbors”

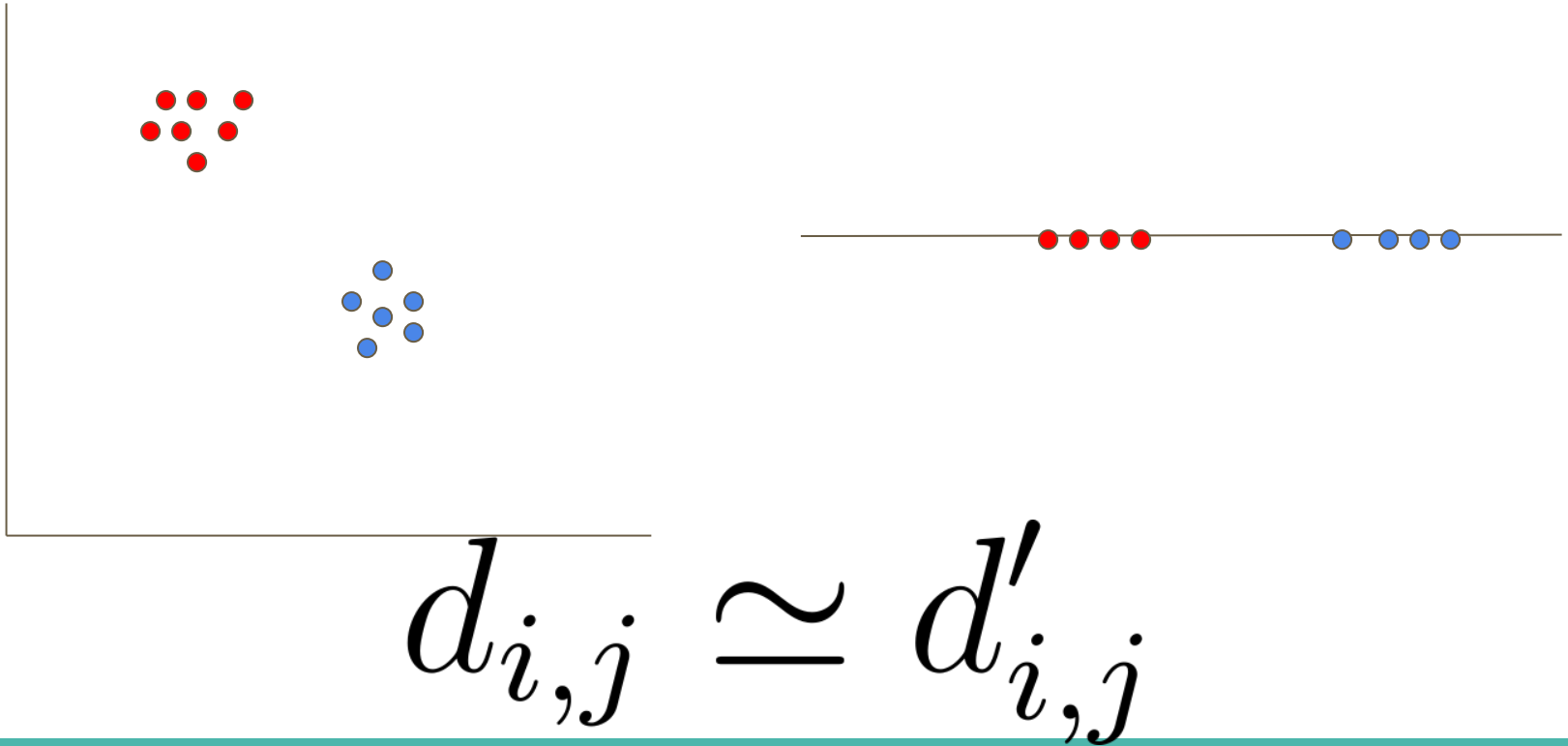


$$p_{i|j} \propto \exp \left( - \frac{||x_i - x_j||^2}{2\sigma_j^2} \right)$$

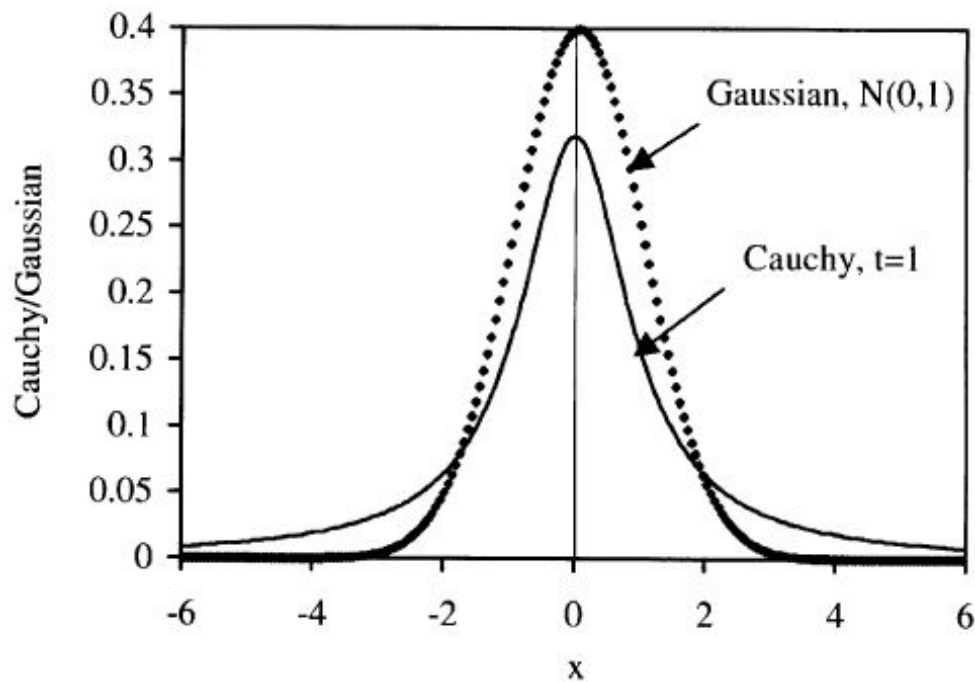
Free parameter to tune



t-SNE aims to learn an embedding which preserves distance measures in the latent space



There are cases in which we *can't* achieve this embedding perfectly, but to help, we will use a Student **t-distribution**



Intuition: Try to match distances for neighbors, but the distance between neighborhoods can be fudgy

In observed space:

$$p(x_i | x_j)$$

In observed space:

$$p(x_i | x_j)$$

In latent space:

$$q(x'_i | x'_j)$$

In observed space:

$$p(x_i | x_j)$$

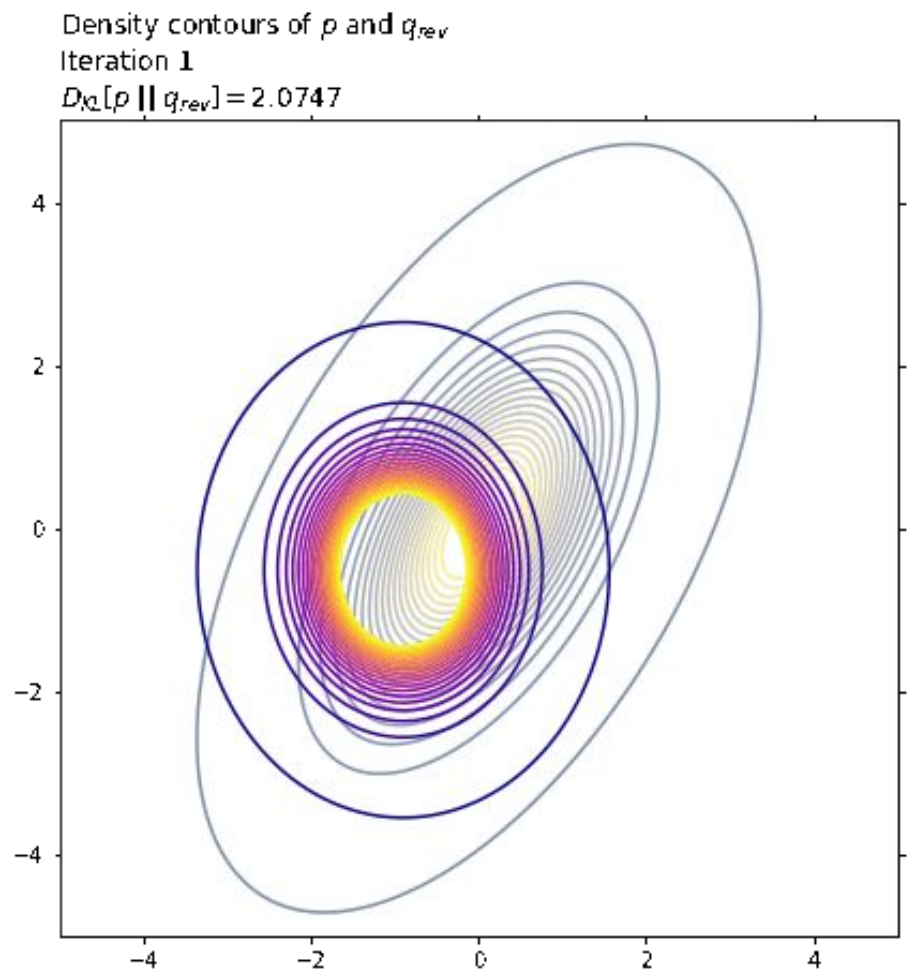
In latent space:

$$q(x'_i | x'_j)$$

We want to minimize the difference  
between these distributions

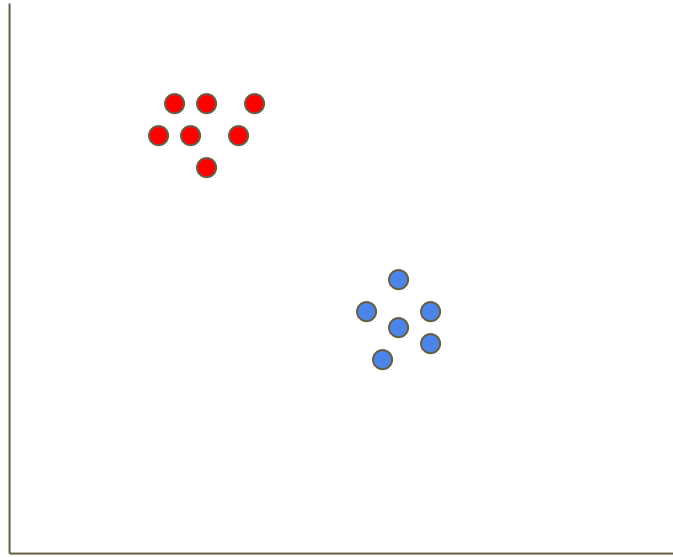
**KL divergence of  $KL(p||q)$**   
**tries to match the**  
**probability distributions**  
**of  $p(x_i|x_j)$  and  $q(x'_i|x'_j)$**

**We will minimize the KL**  
**divergence using**  
**gradient descent**



**t-distributed stochastic  
neighbor embedding**

Randomly choose points while optimizing distance metrics....

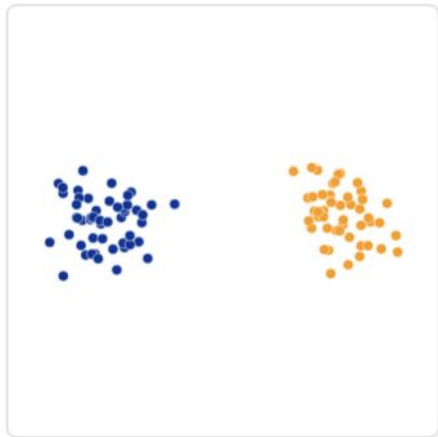


So while PCA is deterministic, t-SNE is a stochastic method

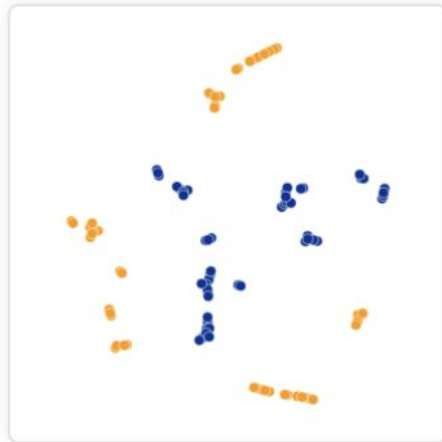


# “Perplexity” is important!

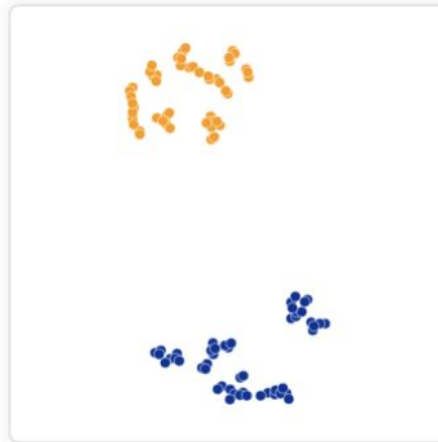
Perplexity ~ number of points expect in each cluster, a hyperparameter



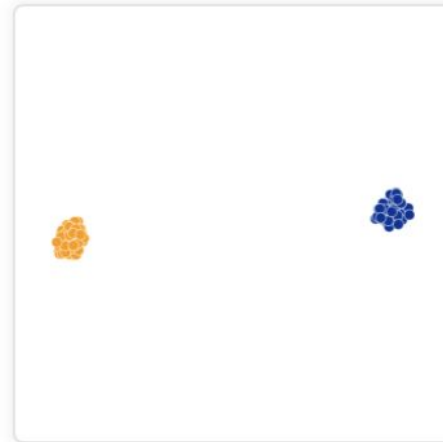
*Original*



Perplexity: 2  
Step: 5,000



Perplexity: 5  
Step: 5,000



Perplexity: 30  
Step: 5,000

# Pros and Cons of each method

## PCA

**Computationally fast**

**Simple interpretations  
of latent spaces**

**Limited expressiveness  
due to linearity**

## t-sne

**Preservation of local  
structure**

**Performs especially  
well in 2D cases**

**Extremely expensive**  
**Complex interpretation**

# Clustering

We will explore three algorithms: Gaussian mixture models, K-means and DBScan

M(odel):

O(objective function):

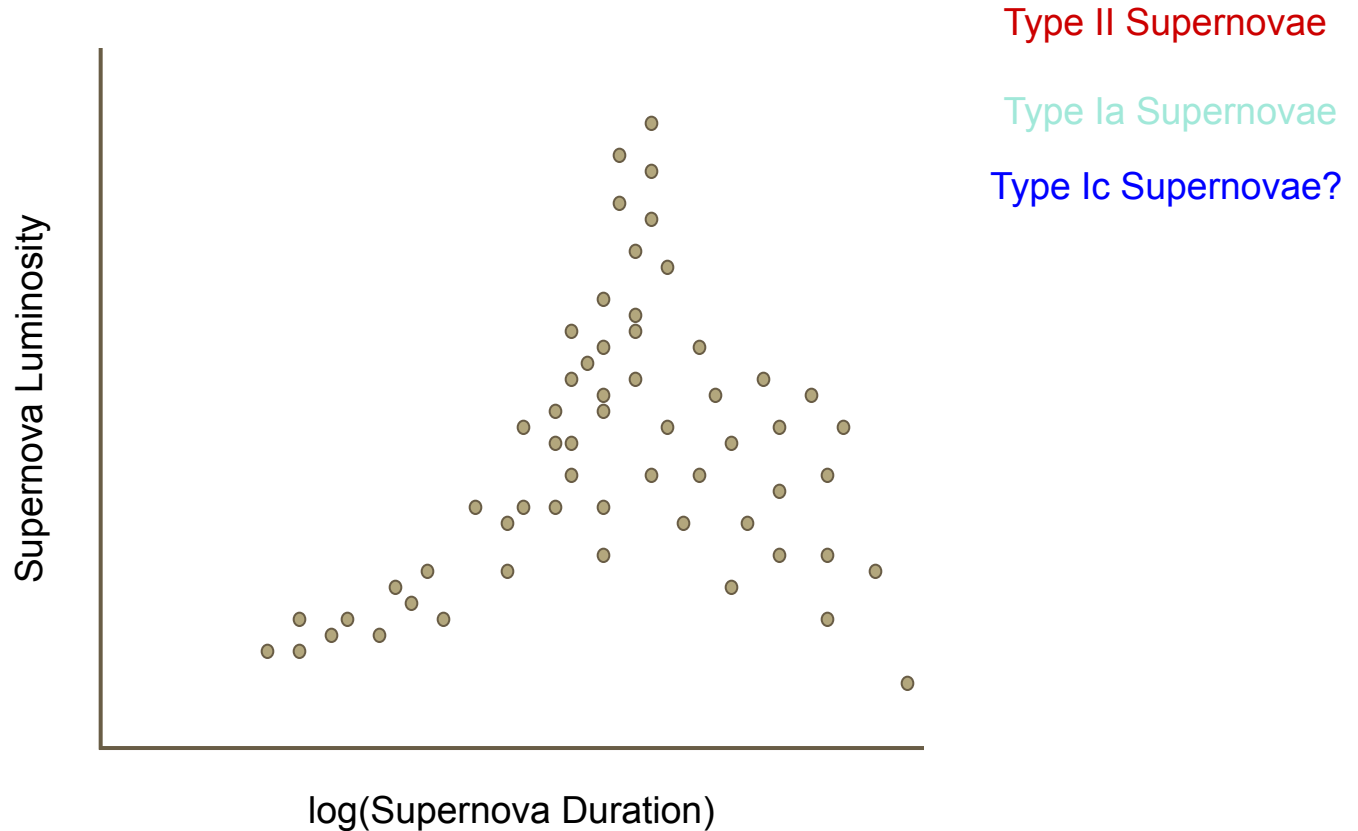
O(optimization):



# K-means

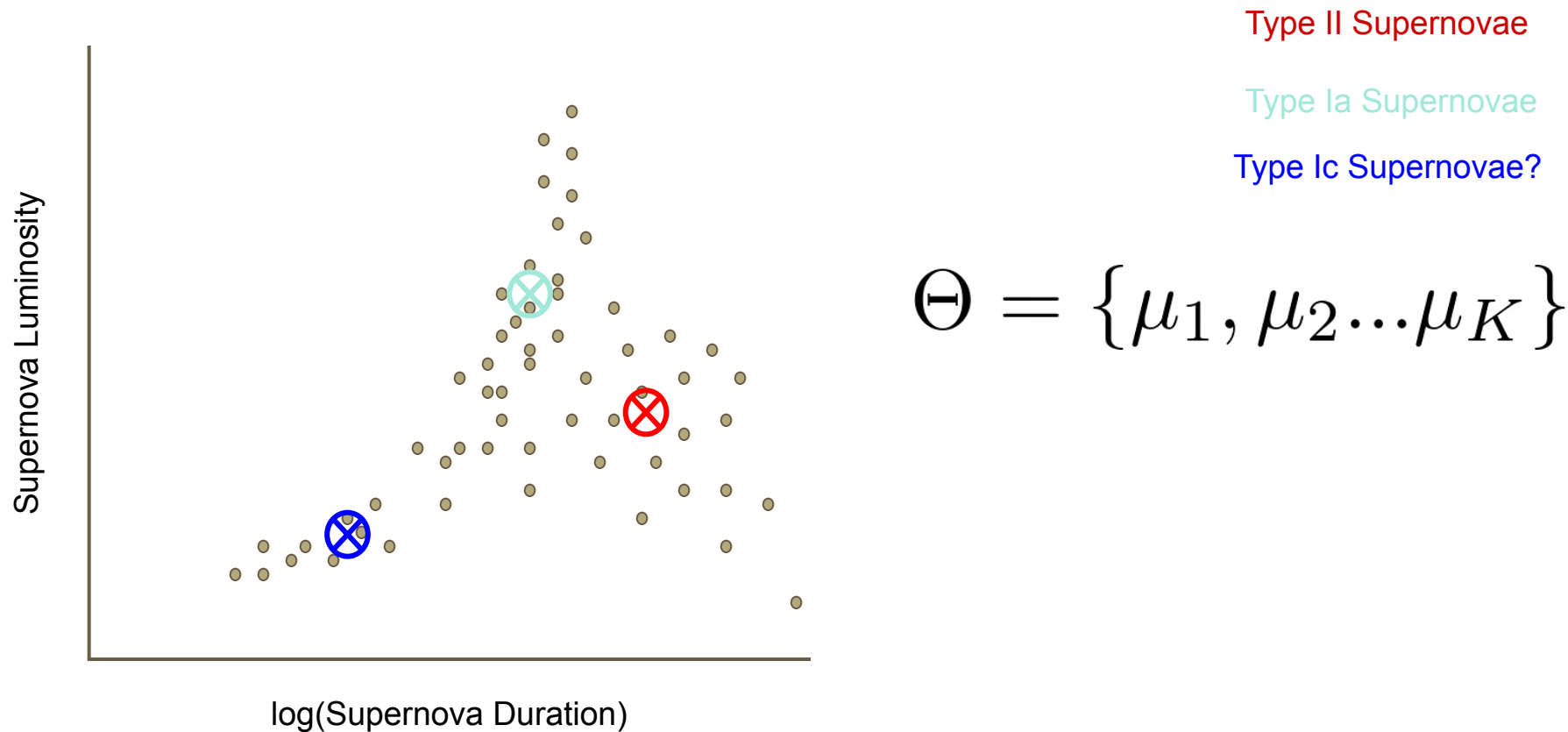
M(odel):

K-clusters, of any shape. K must be chosen by the user.



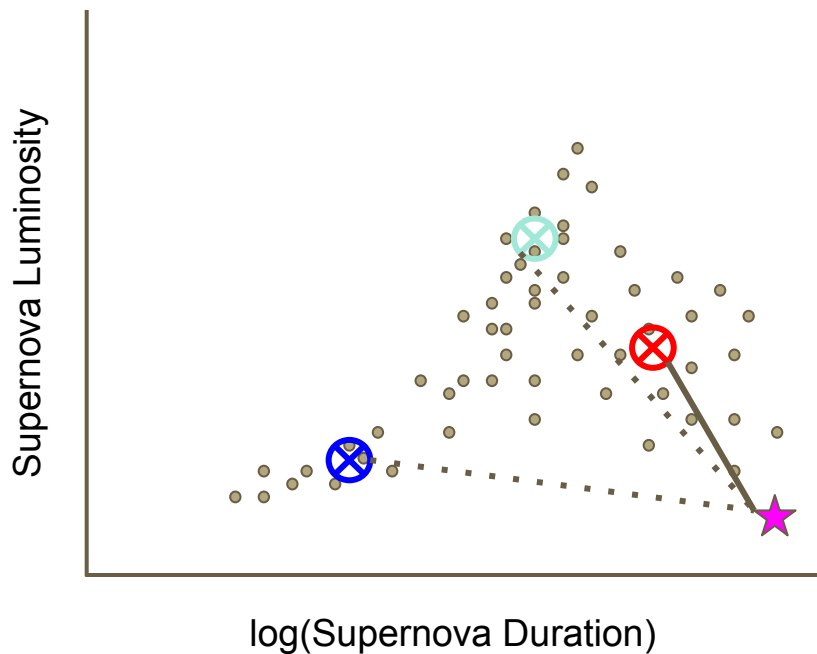
M(odel):

Each centroid has 1 free parameters: the mean  $\mu_k$



M(odel): Each observation comes from 1 of  $K$  clusters  $\Theta = \{\mu_1, \mu_2 \dots \mu_K\}$

O(bjective function):



$$\sum_{i=1}^N \min_{c_k \in C} (||x_i - \mu_k||^2)$$

*This is called "inertia"*



Model: Each observation comes from 1 of K clusters  $\Theta = \{\mu_1, \mu_2 \dots \mu_K\}$

Objective function:

$$\sum_{i=1}^N \min_{c_k \in C} (||x_i - \mu_k||^2)$$

Optimization: gradient descent?

M(odel): Each observation comes from 1 of K clusters  $\Theta = \{\mu_1, \mu_2 \dots \mu_K\}$

O(objective function):  $\sum_{i=1}^N \min_{c_k \in C} (\|x_i - \mu_k\|^2)$

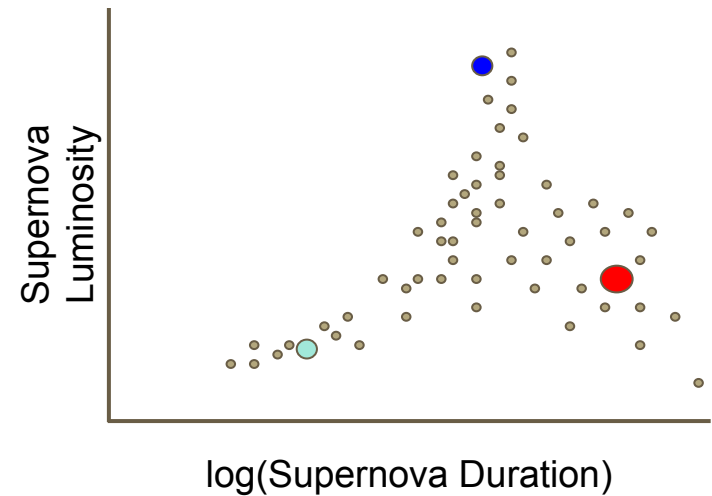


O(optimization): gradient descent?

*How do I take the gradient of a “minimum” function??*

# O(ptimeimization): Expectation-maximization!

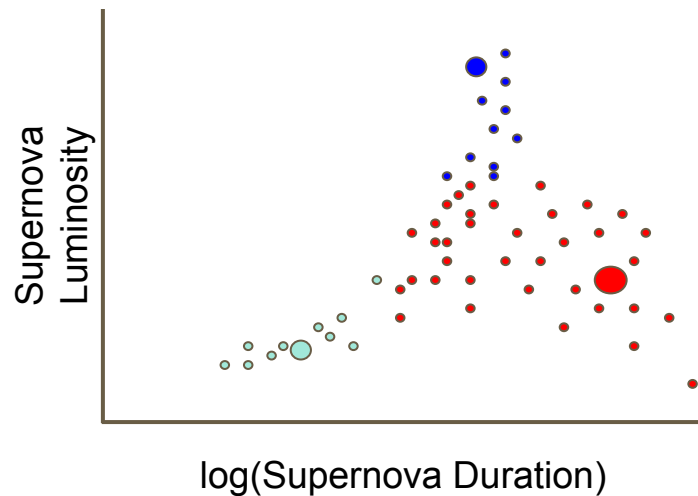
Step 0: Randomly choose K data points and call those your centers



# O(ptimeimization): Expectation-maximization!

Step 0: Randomly choose K data points and call those your centers

Step 1 (Expectation): Assign each observed datapoint to a cluster



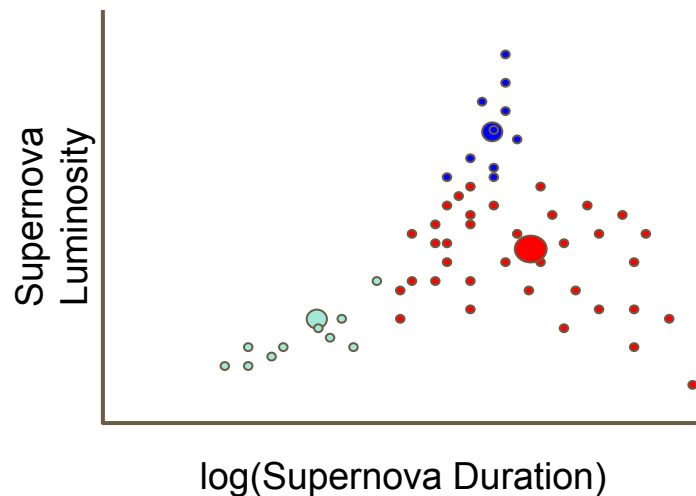
# O(ptimeimization): Expectation-maximization!

Step 0: Randomly choose K data points and call those your centers

Step 1 (Expectation): Assign each observed datapoint to a cluster

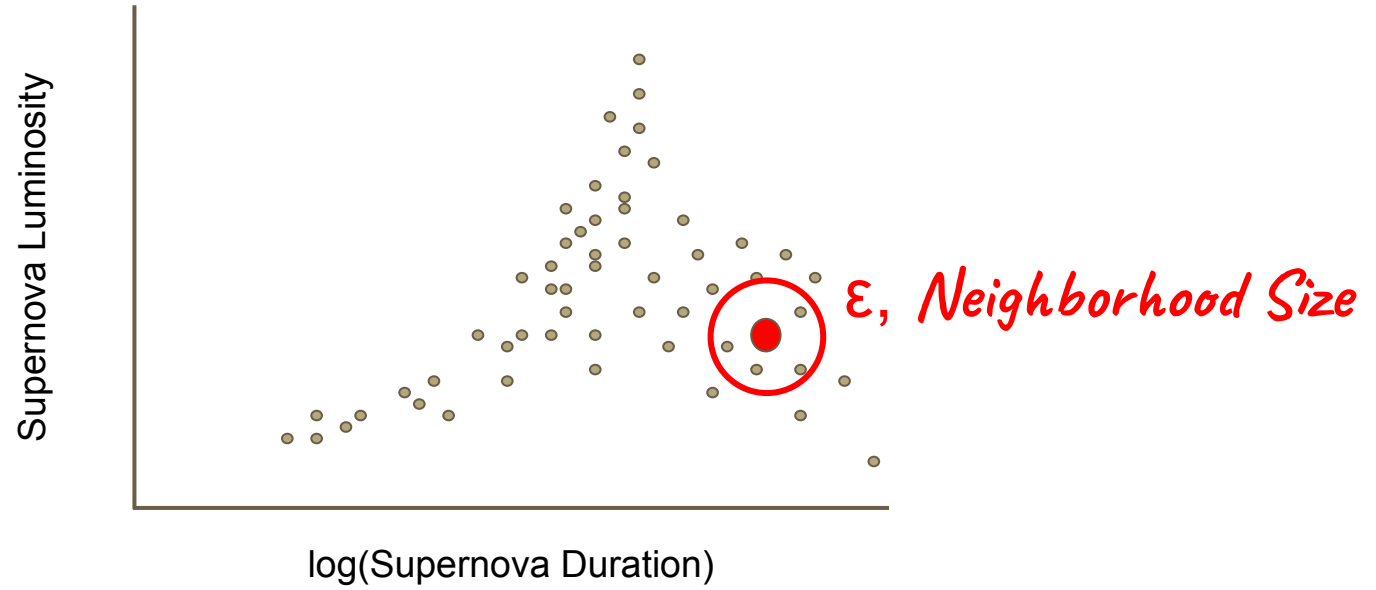
Step 2 (Maximization): Choose new centers of each cluster

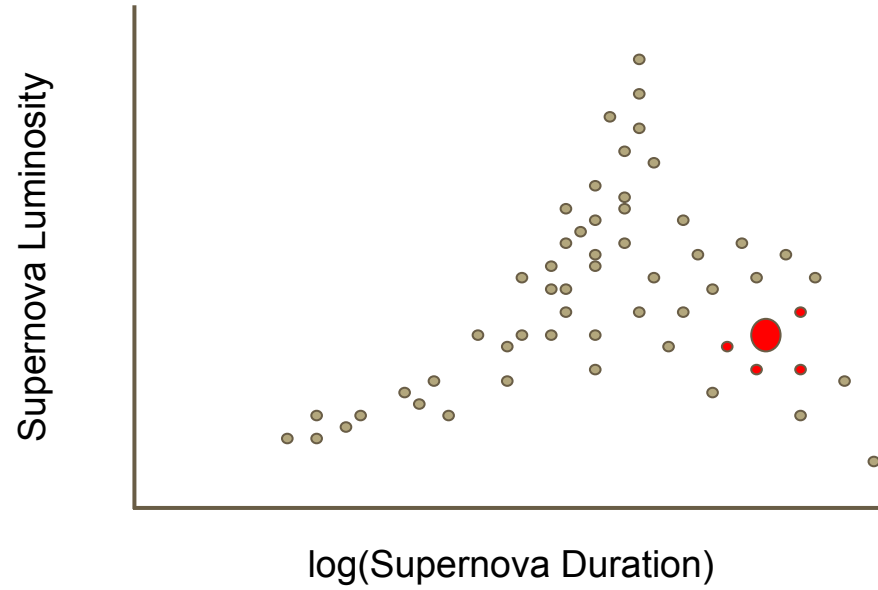
Repeat steps 1/2 until convergence



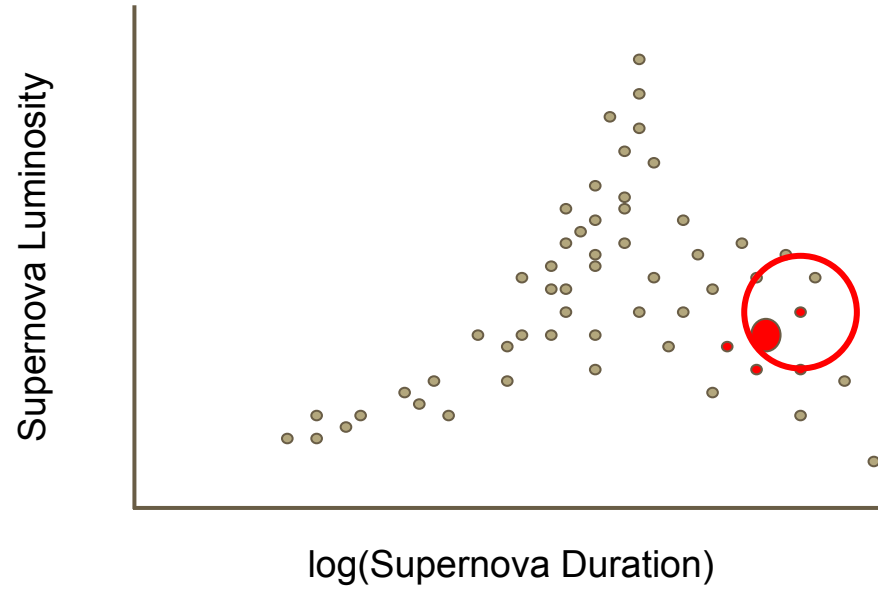
# **DB-SCAN**

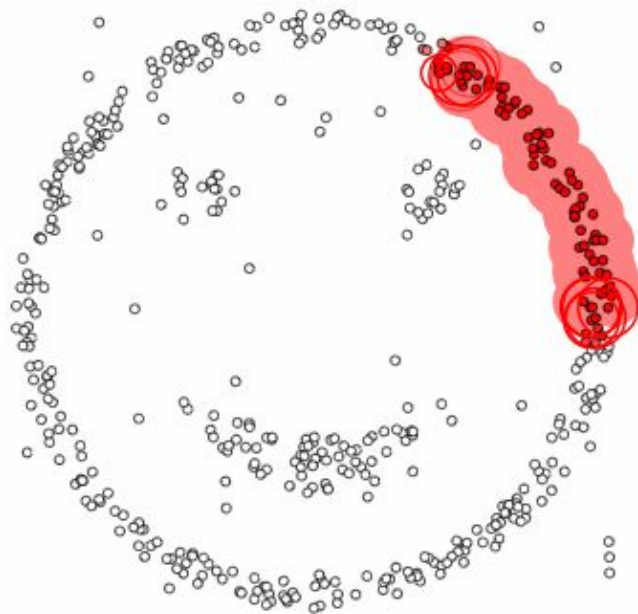
**(An extremely abbreviated description)**











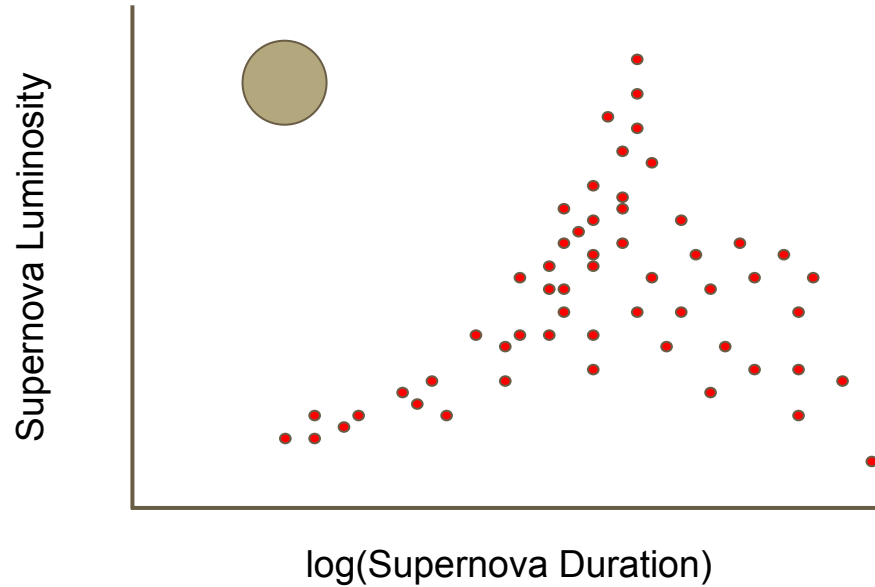
epsilon = 1.00  
minPoints = 4

Restart

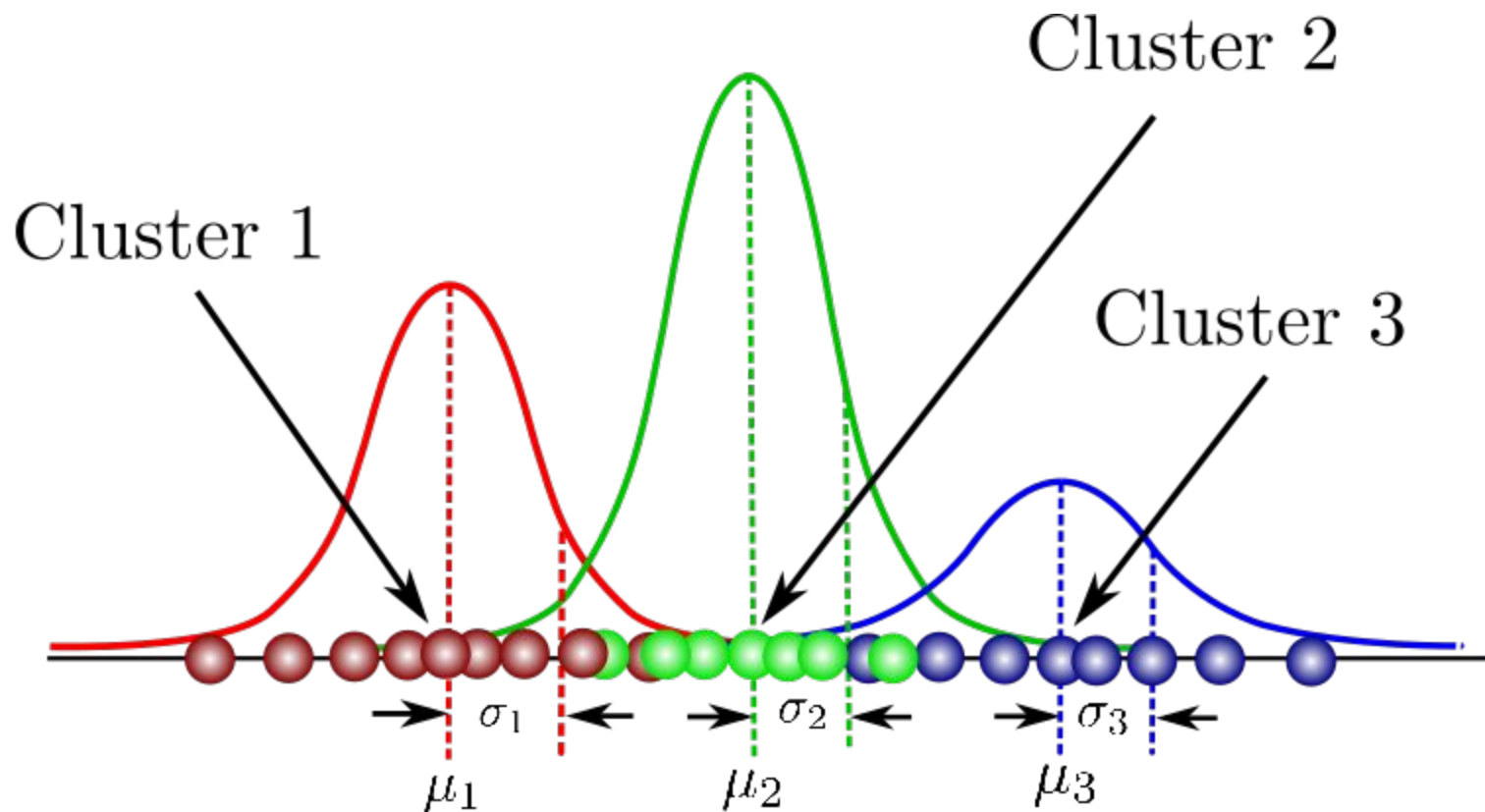


Pause

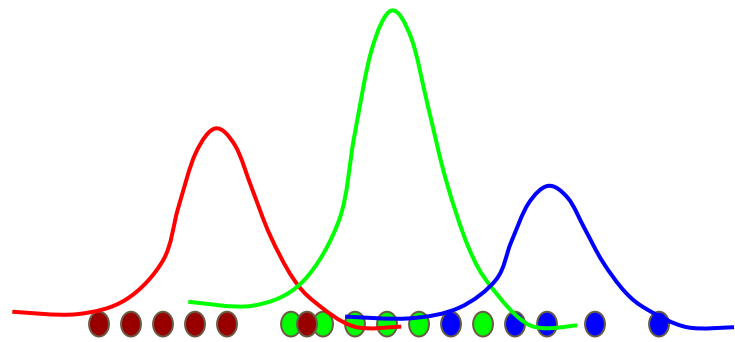
If some points cannot be reached, they will not be clustered  
and considered an outlier!



# Gaussian Mixture Models

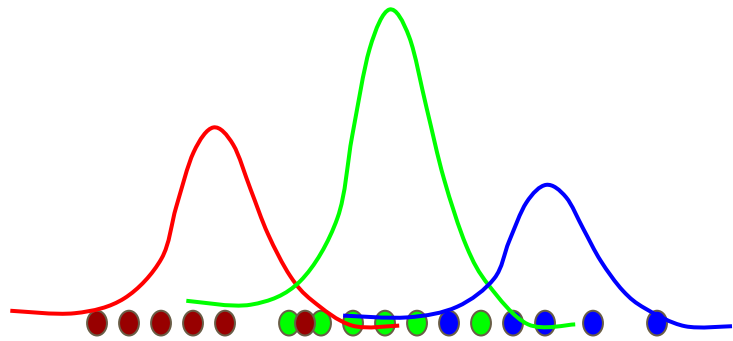


Example: I measure the masses of different degenerate objects, including BHs and NSs. Now, with a new mass measurement, what is the probability that it is a NS?



$$p(x|\Theta) = \sum_{k=1}^K \alpha_k p_k(x|\mu_k, \sigma_k)$$

$$\Theta = \{\alpha_1, \mu_1, \sigma_1, \dots, \alpha_k, \mu_k, \sigma_k\}$$




*Mixture weights, this of this as the fraction of events which should fall in each component*

$$p(x|\Theta) = \sum_{k=1}^K \alpha_k p_k(x|\mu_k, \sigma_k)$$

*Mixture components*

*Membership weights, or the probability that  $x_i$   
comes from the  $k$ th component*


$$w_{i,k} = \frac{\alpha_k p_k(x_i | \mu_k, \sigma_k)}{\sum_{m=1}^K \alpha_k p_m(x_i | \mu_m, \sigma_m)}$$



Note, we're looking at the 1D case, but this is easily extended into N-dimensions

$$p_k(x|\mu_k, \Sigma_k) = \frac{\exp(-\frac{1}{2}(x - \mu_k)^T \Sigma_k^{-1}(x - \mu_k))}{(2\pi)^{d/2} |\Sigma_k|^{1/2}}$$

**M(odel):**

**O(bjective function):**

**O(ptimization):**

**M(odel): A mixture of Gaussians**

**O(bjective function):**

**O(ptimization):**

# Model: A mixture of Gaussians

Objective function)

Log-likelihood! :

$$\sum_{i=1}^N \log(p(x_i | \Theta))$$

Optimization):

# M(odel): A mixture of Gaussians

Objective function)

Log-likelihood! :

$$\sum_{i=1}^N \left( \log \sum_{k=1}^K \alpha_k p_k(x_i | \mu_k, \sigma_k) \right)$$

Optimization): gradient descent?

# Optimization, why not gradient descent?

*Positive, semidefinite*

$$p_k(x|\mu_k, \Sigma_k) = \frac{\exp(-\frac{1}{2}(x - \mu_k)^T \Sigma_k^{-1}(x - \mu_k))}{(2\pi)^{d/2} |\Sigma_k|^{1/2}}$$

*And mixture weights must sum to 1!*

$$\sum_{i=1}^N \left( \log \sum_{k=1}^K \alpha_k p_k(x_i|\mu_k, \sigma_k) \right)$$

*AND I have to take the derivative  
of a sum in a log 🤯*

# Optimization, why not gradient descent?

Tough constraints and a tough likelihood make it hard to calculate the gradient, required for gradient descent!

# “Expectation Maximization” Algorithm (EM) for optimization

1. Choose a random set of **parameter values** which satisfy our constraints:

$$\Theta = \{\alpha_1, \mu_1, \sigma_1, \dots, \alpha_k, \mu_k, \sigma_k\}$$

You can be more clever than ‘totally random’; for example, using a clustering technique!



# “Expectation Maximization” Algorithm (EM) for optimization

1. Choose a random set of **parameter values** ( $\Theta$ ) which satisfy our constraints
2. Expectation step: Compute the expected value of our log-likelihood. In words: *what is the most likely component a single datapoint belongs to?* A probability matrix which enumerates the probability of each data point (1-N) belonging to each component (1-K)

$$\begin{vmatrix} w_{1,1} & w_{1,2} & \dots & w_{1,K} \\ w_{2,1} & \dots & \dots & \dots \\ \dots & \dots & w_{i,k} & \dots \\ w_{N,1} & \dots & \dots & w_{N,K} \end{vmatrix}$$

$$w_{i,k} = \frac{\alpha_k p_k(x_i | \mu_k, \sigma_k)}{\sum_{m=1}^K \alpha_k p_m(x_i | \mu_m, \sigma_m)}$$

# “Expectation Maximization” Algorithm (EM) for optimization

1. Choose a random set of **parameter values** ( $\Theta$ ) which satisfy our constraints
2. Expectation step: Compute a probability matrix which enumerates the probability of each data point (1-N) belonging to each component (1-K)

$w_{1,1}$	$w_{1,2}$	...	$w_{1,K}$
$w_{2,1}$	...	...	...
...	...	$w_{i,k}$	...
$w_{N,1}$	...	...	$w_{N,K}$

*Rows sum to 1, or in words:  
there is a 100% chance a  
point has to belong to one  
of the components!*

# “Expectation Maximization” Algorithm (EM) for optimization

1. Choose a random set of **parameter values** ( $\Theta$ ) which satisfy our constraints
2. Expectation step: Compute a probability matrix which enumerates the probability of each data point (1-N) belonging to each component (1-K)
3. Maximization step:
  - a. We have new cluster params! Calculate the effective number of samples in each cluster

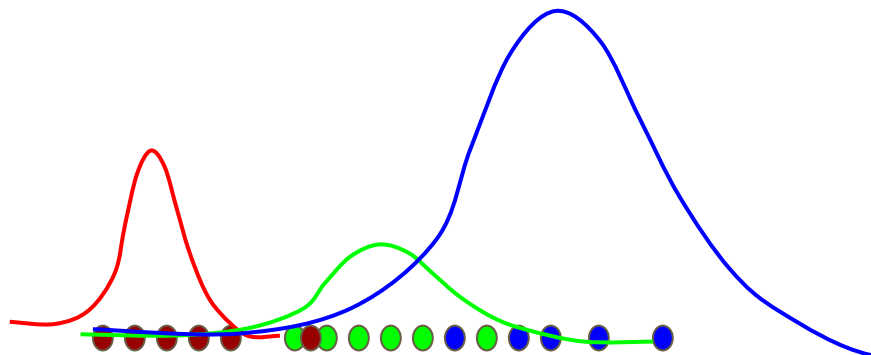
$$N_k \equiv \sum_{i=1}^N w_{i,k}$$

$w_{1,1}$	$w_{1,2}$	$\dots$	$w_{1,K}$
$w_{2,1}$	$\dots$	$\dots$	$\dots$
$\dots$	$\dots$	$w_{i,k}$	$\dots$
$w_{N,1}$	$\dots$	$\dots$	$w_{N,K}$

# “Expectation Maximization” Algorithm (EM) for optimization

1. Choose a random set of **parameter values** ( $\Theta$ ) which satisfy our constraints
2. Expectation step: Compute a probability matrix which enumerates the probability of each data point (1-N) belonging to each component (1-K)
3. Maximization step:
  - a. Calculate the effective number of samples in each new cluster
  - b. After doing ~math~, the most likely value of the new component weights is:

$$\alpha_k^{\text{new!}} = \frac{N_k}{N}$$



# “Expectation Maximization” Algorithm (EM) for optimization

1. Choose a random set of **parameter values** ( $\Theta$ ) which satisfy our constraints
2. Expectation step: Compute a probability matrix which enumerates the probability of each data point (1-N) belonging to each component (1-K)
3. Maximization step:
  - a. Calculate the effective number of samples in each new cluster
  - b. Calculate the new parameters, then the Gaussian parameters:

$$\mu_k^{\text{new!}} = \frac{1}{N_k} \sum_{i=1}^N w_{i,k} x_i$$

$$(\sigma_k^2)^{\text{new!}} = \frac{1}{N_k} \sum_{i=1}^N (x_i - \mu_k)^2$$

# “Expectation Maximization” Algorithm (EM) for optimization

1. Choose a random set of **parameter values** ( $\Theta$ ) which satisfy our constraints
2. Expectation step: Compute a probability matrix which enumerates the probability of each data point (1-N) belonging to each component (1-K)
3. Maximization step:
  - a. Calculate the effective number of samples in each new cluster
  - b. Calculate the new parameters, then the Gaussian parameters
4. Repeat steps 2/3, each time checking the likelihood. The algorithm has converged when the likelihood remains ~constant

# We now have a tool box of 3 clustering techniques:

Gaussian Mixture Models

K-Means

DBSCAN

# Parameters?

## Gaussian Mixture Models

Properties of each  
Gaussian component

Hyperparameter:  
Number of components

## K-Means

Centers of each cluster

Hyperparameter:  
Number of Clusters

## DBSCAN

Hyperparameter:  
Neighborhood Size

Hyperparameter:  
Minimum density

Note: Hyperparameter means that the algorithm by itself does not optimize this parameter



# Pros and Cons

## Gaussian Mixture Models

**Pro: Extremely interpretable**

**Pro: Density estimate available everywhere**

## K-Means

**Pro: Minimal parameters**

**Pro: Computationally scalable to large number of samples**

## DBSCAN

**Pro: Minimal parameters**

**Pro: Arbitrary cluster shapes**

# Pros and Cons

## Gaussian Mixture Models

**Pro: Extremely interpretable**

**Pro: Density estimate available everywhere**

**Con: Challenging to scale to high dimensions**

**Con: Strong assumption on cluster shape**

## K-Means

**Pro: Minimal parameters**

**Pro: Computationally scalable to large number of samples**

**Con: Can be non-trivial to pick the “correct” number of clusters**

## DBSCAN

**Pro: Minimal parameters**

**Pro: Arbitrary cluster shapes**

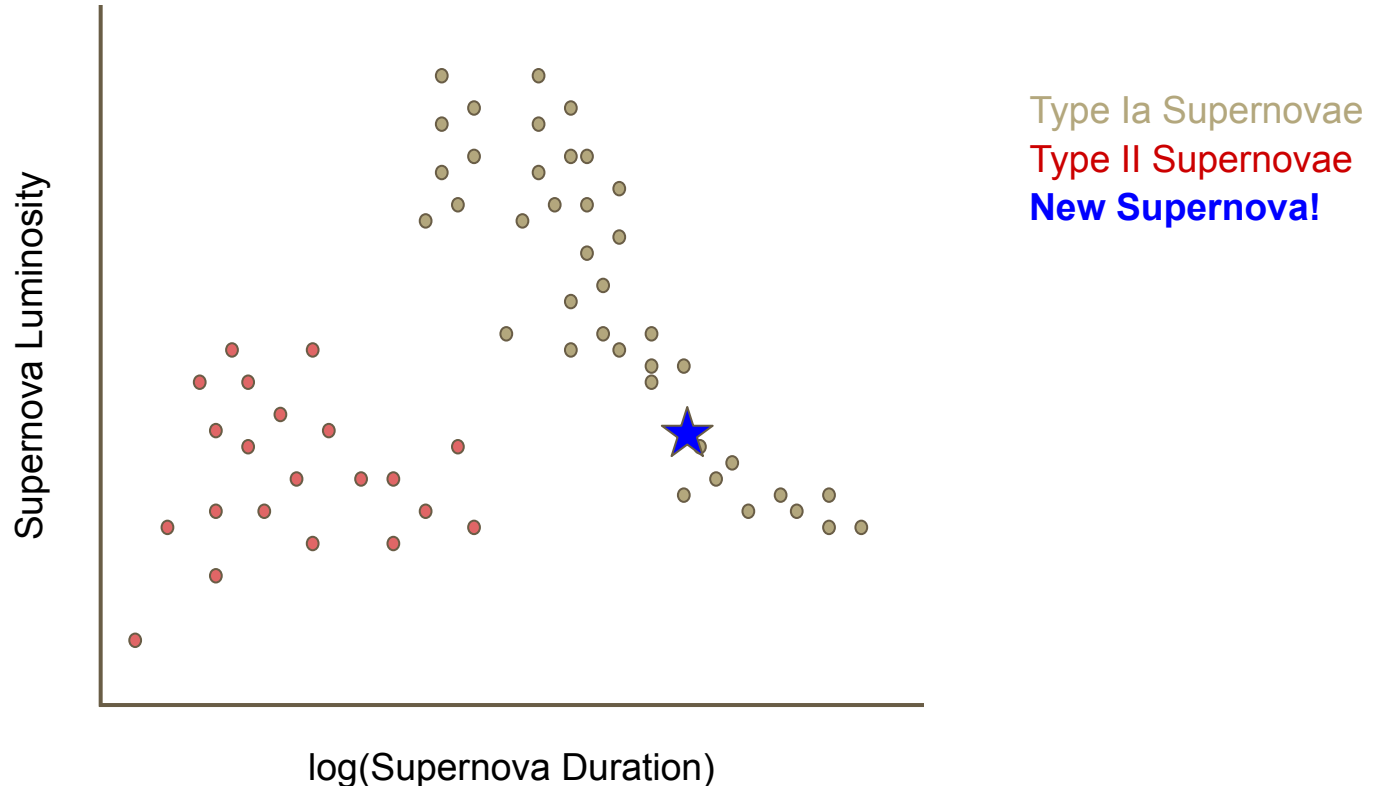
**Pro/Con: Not every point will end up in a cluster**

# Supervised Learning

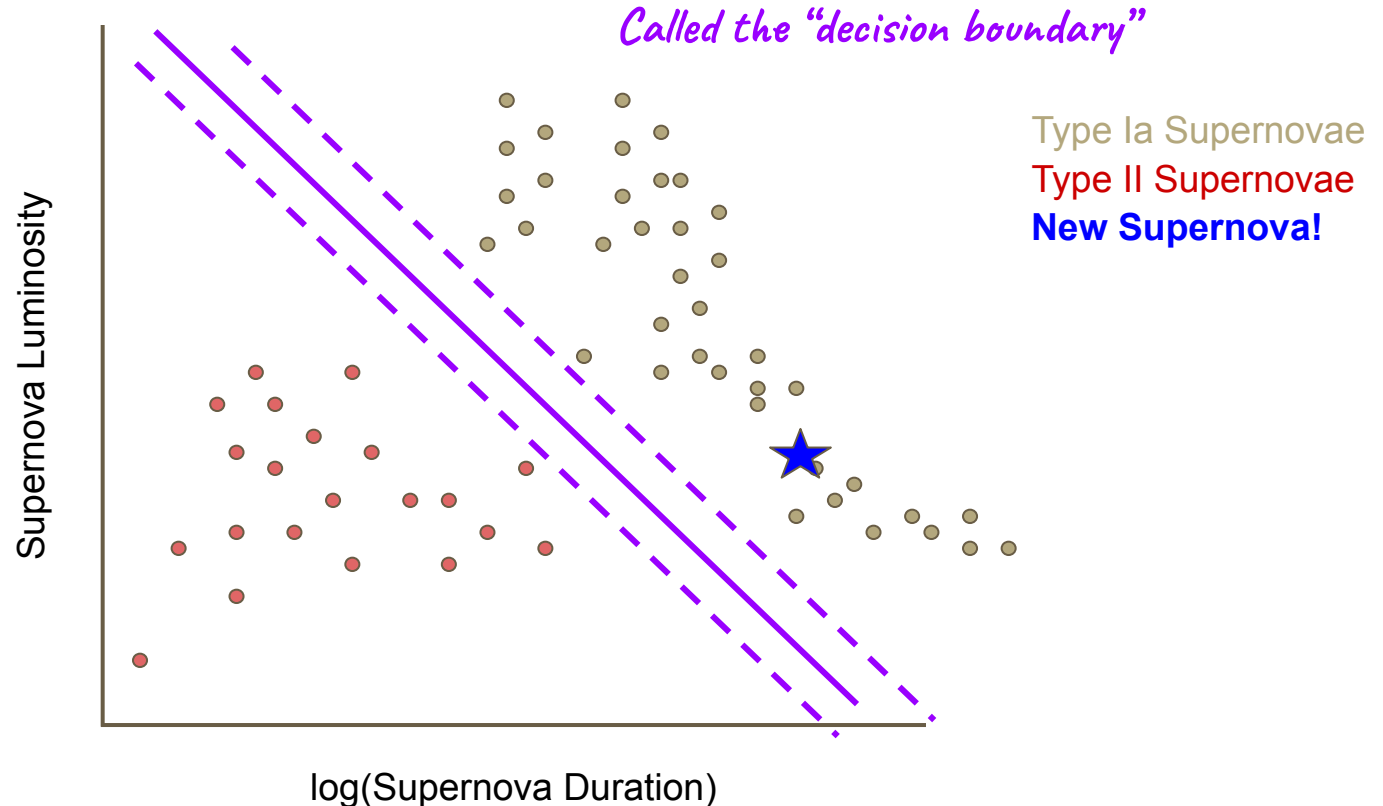
In supervised learning, we know the “answers” apriori for a training set, and we want to train an algorithm to report some quantity (a classification, a luminosity, etc) given a new observation.

Here we will explore just 2 algorithms: Support Vector Machines and Random Forests. In both cases, we'll explore **classification**

# Classification: Can I build a model to label a new supernova as a Type I vs Type II?

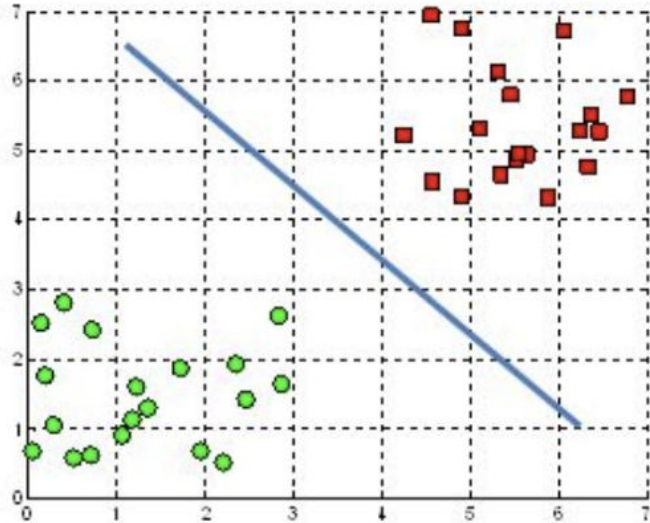


# Support Vector Machine: Find the best line to divide the classes

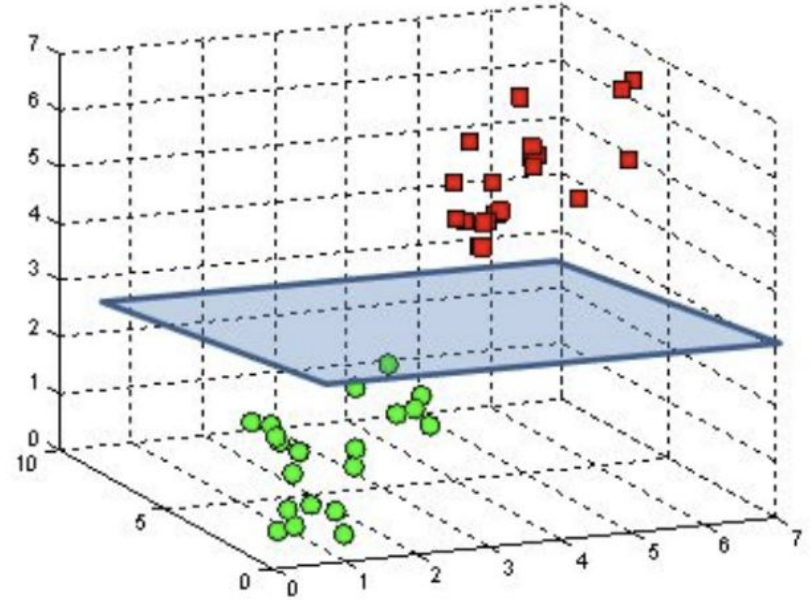


# More generally, we find the hyperplane (of $N-1$ dimensions) for $N$ -dimensional data

A hyperplane in  $\mathbb{R}^2$  is a line



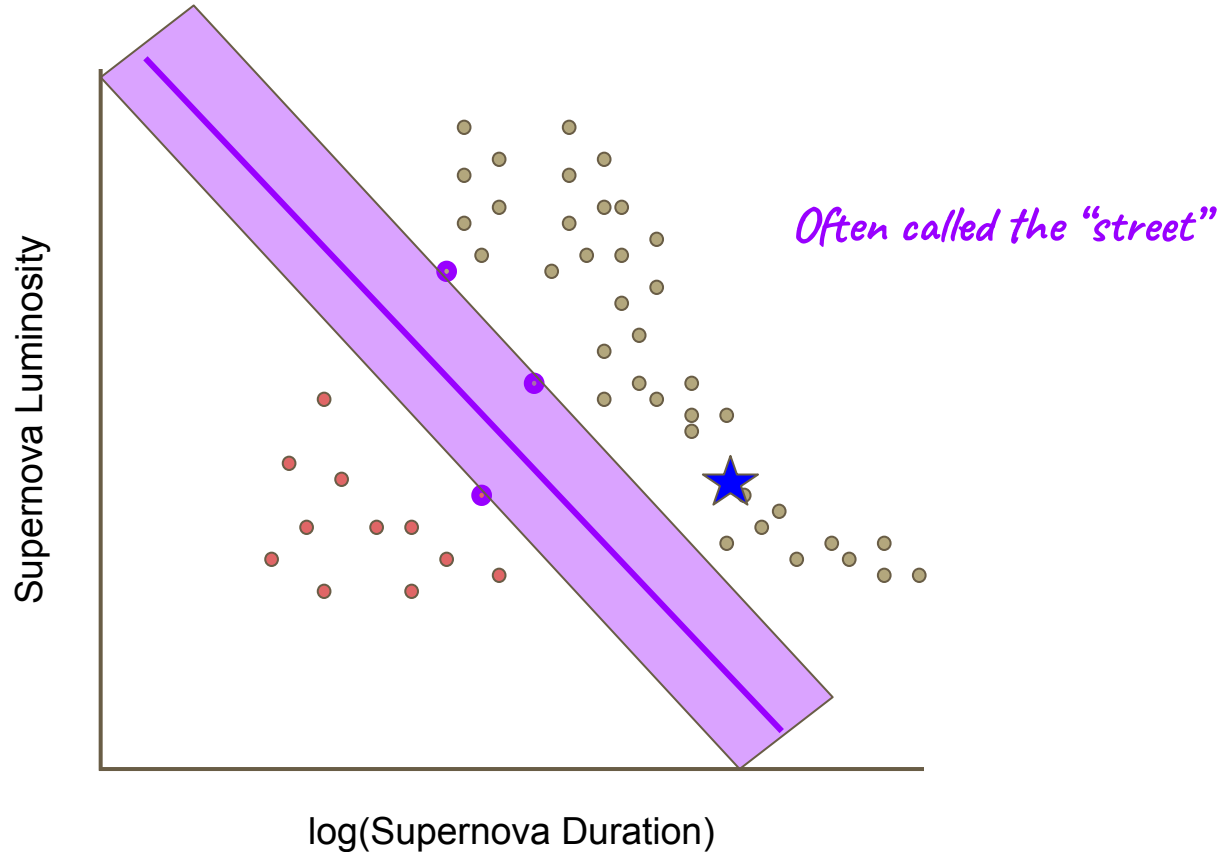
A hyperplane in  $\mathbb{R}^3$  is a plane



**Let's only think about the 2D case. Let's define our objective function:**

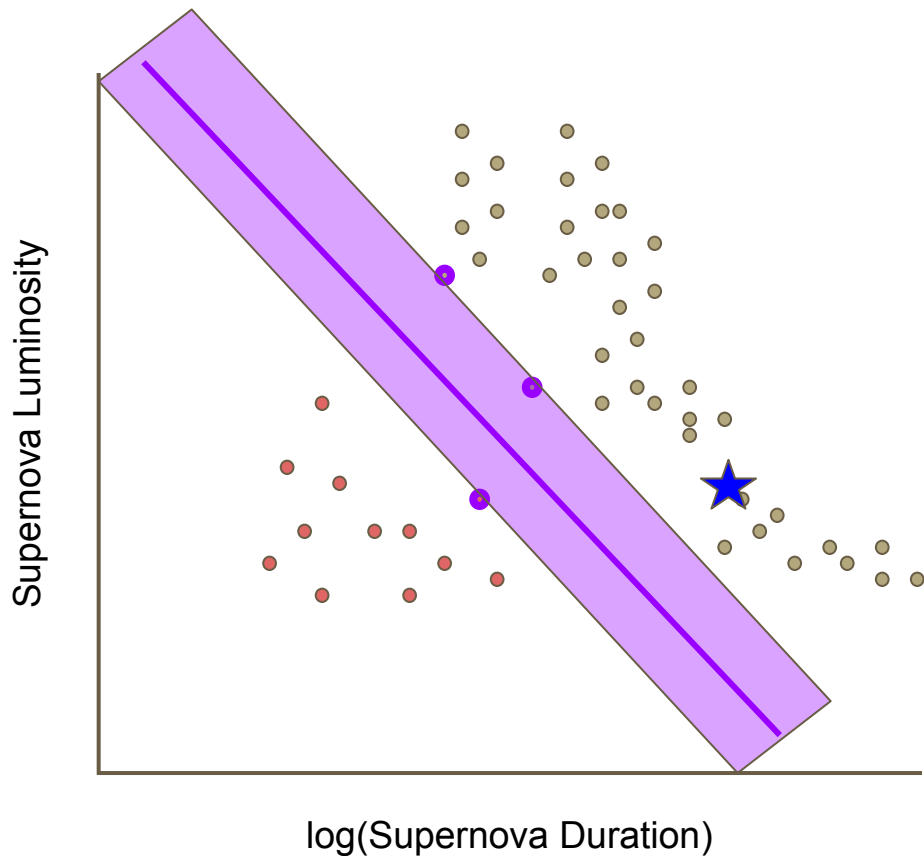
**How do we choose the “best” line to divide the classes?**

We want to draw our line such that we have the widest separation between our classes.

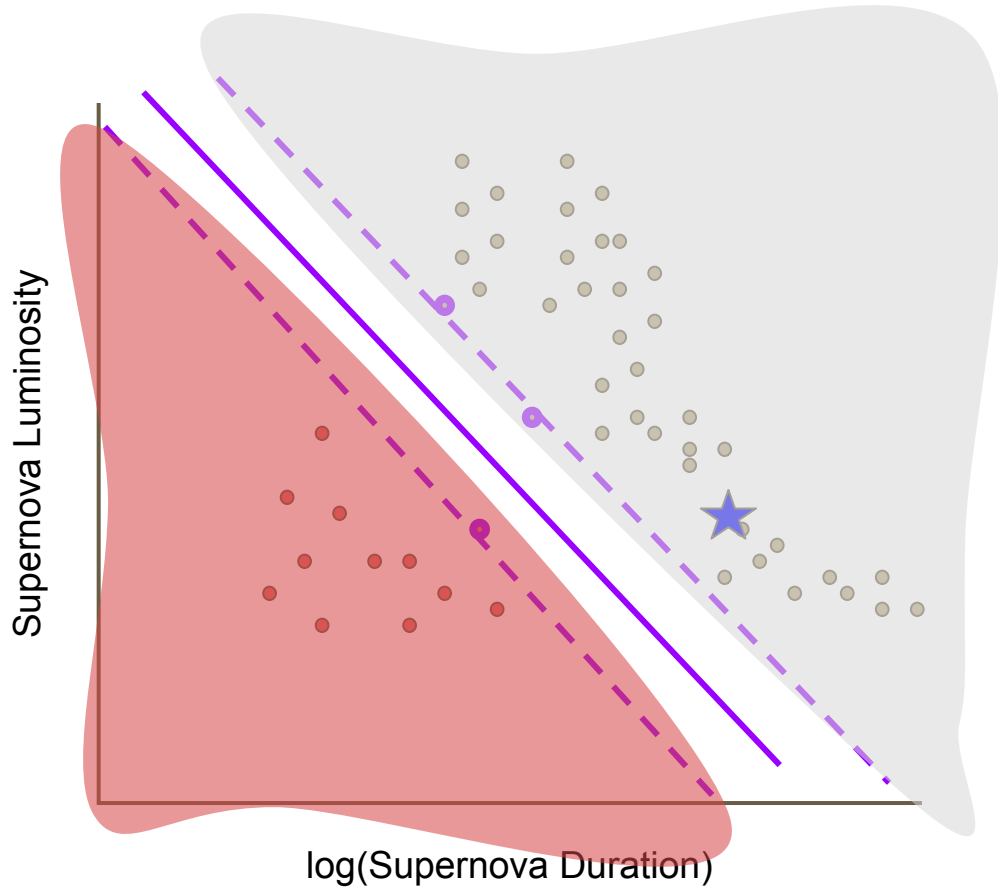


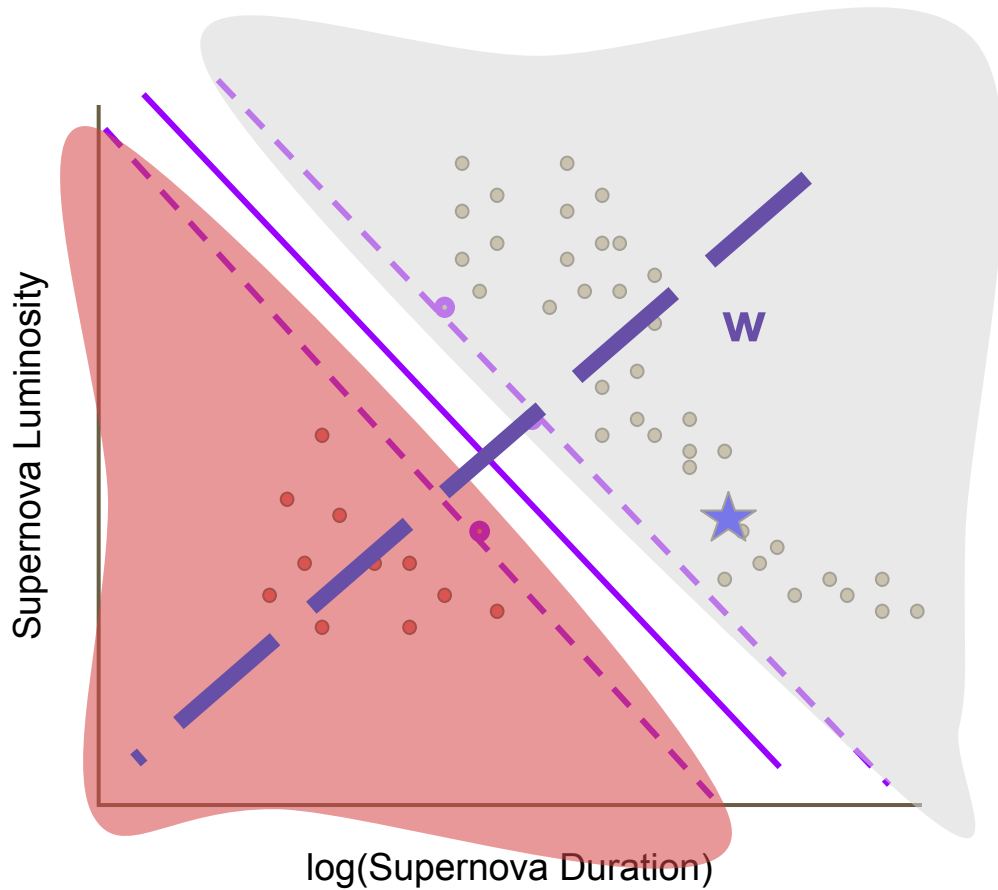


Three points are needed to define two parallel planes which separate the classes. These are called the **support vectors**



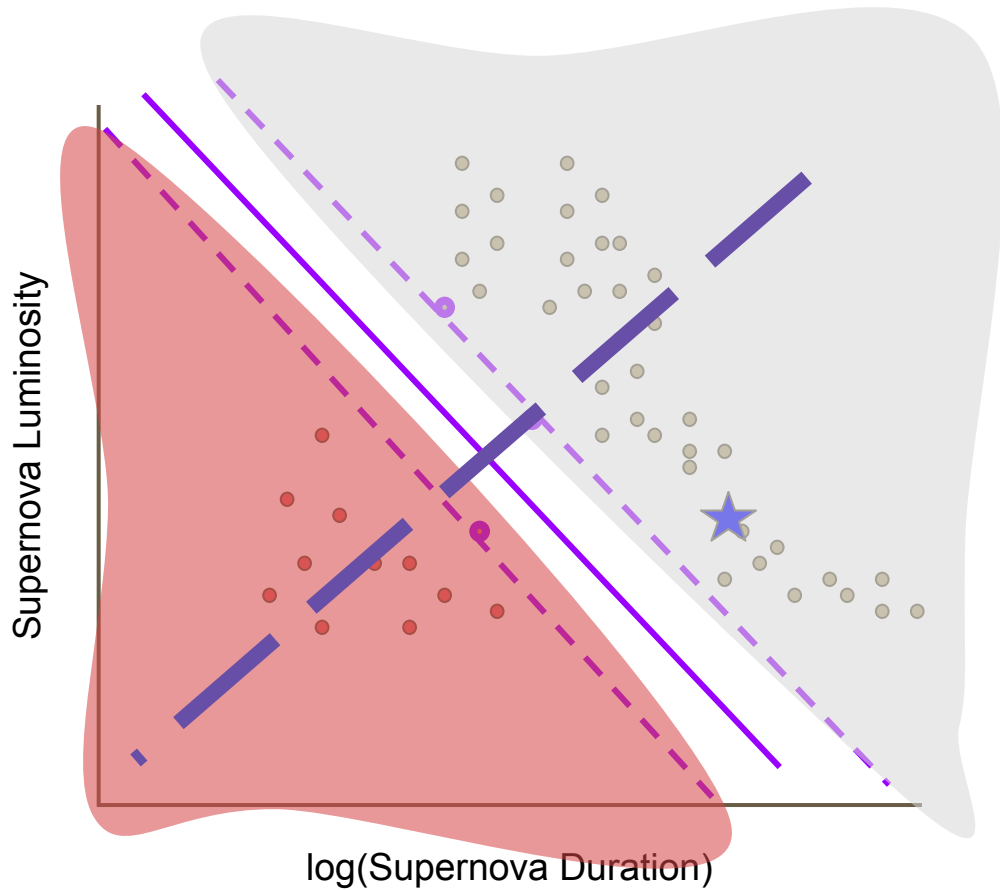
Our class will be determined by which side of the “street” we sit on...





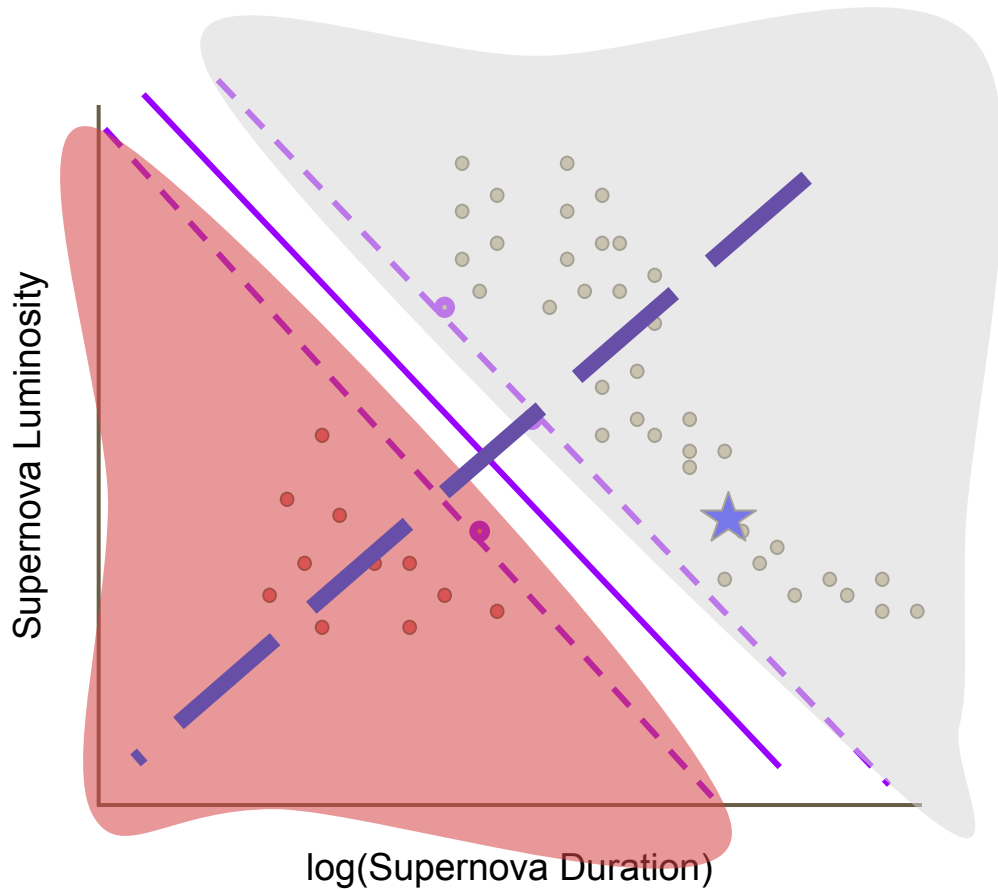
Our class will be determined by which side of the “street” we sit on...

Or mathematically, we can define the perpendicular plane to the street and determine the distance along this vector:



$$\vec{x}_i \cdot \vec{w} + b \geq +1 \quad \text{Type Ia}$$

$$\vec{x}_i \cdot \vec{w} + b \leq -1 \quad \text{Type II}$$



$$\vec{x}_i \cdot \vec{w} + b \geq +1$$

$$\vec{x}_i \cdot \vec{w} + b \leq -1$$

We want to maximize the width of the street, while subject to the two equality constraints listed above.

Defining our **objective function** will be the job of Lagrangian math

# From the detailed math\*, three important pieces of information on the objective function emerge:

1. The objective function only depends on the support vectors - i.e., the observational points which lie on the very edge of my street

\*See notes or reading for detailed math

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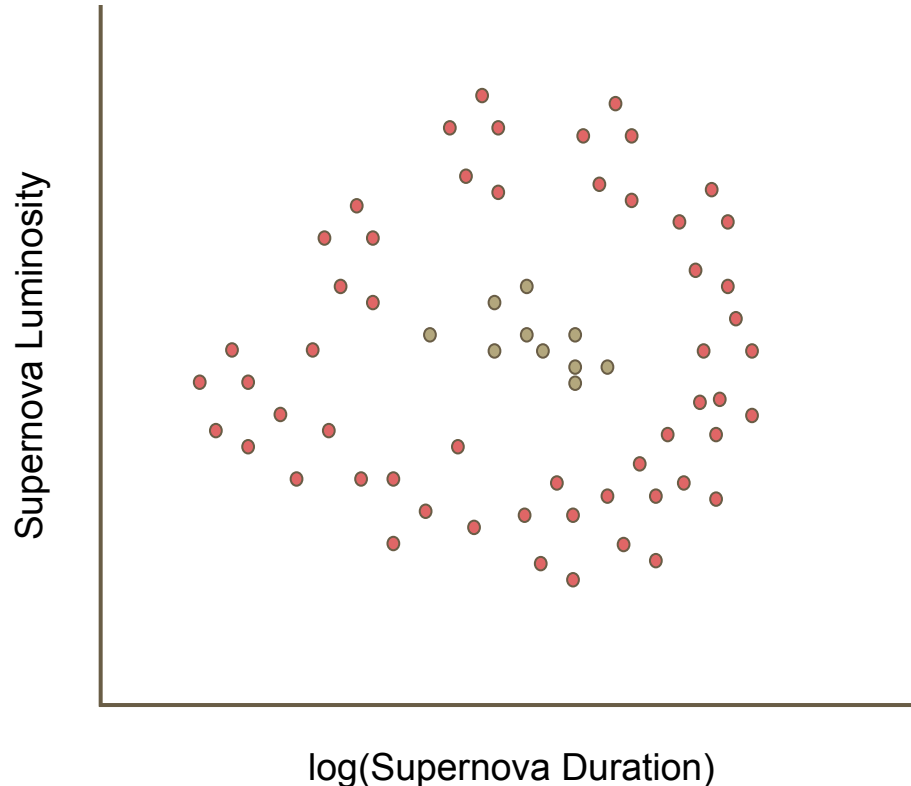
1. The objective function only depends on the support vectors - i.e., the observational points which lie on the very edge of my street
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# From the detailed math\*, three important pieces of information on the objective function emerge:

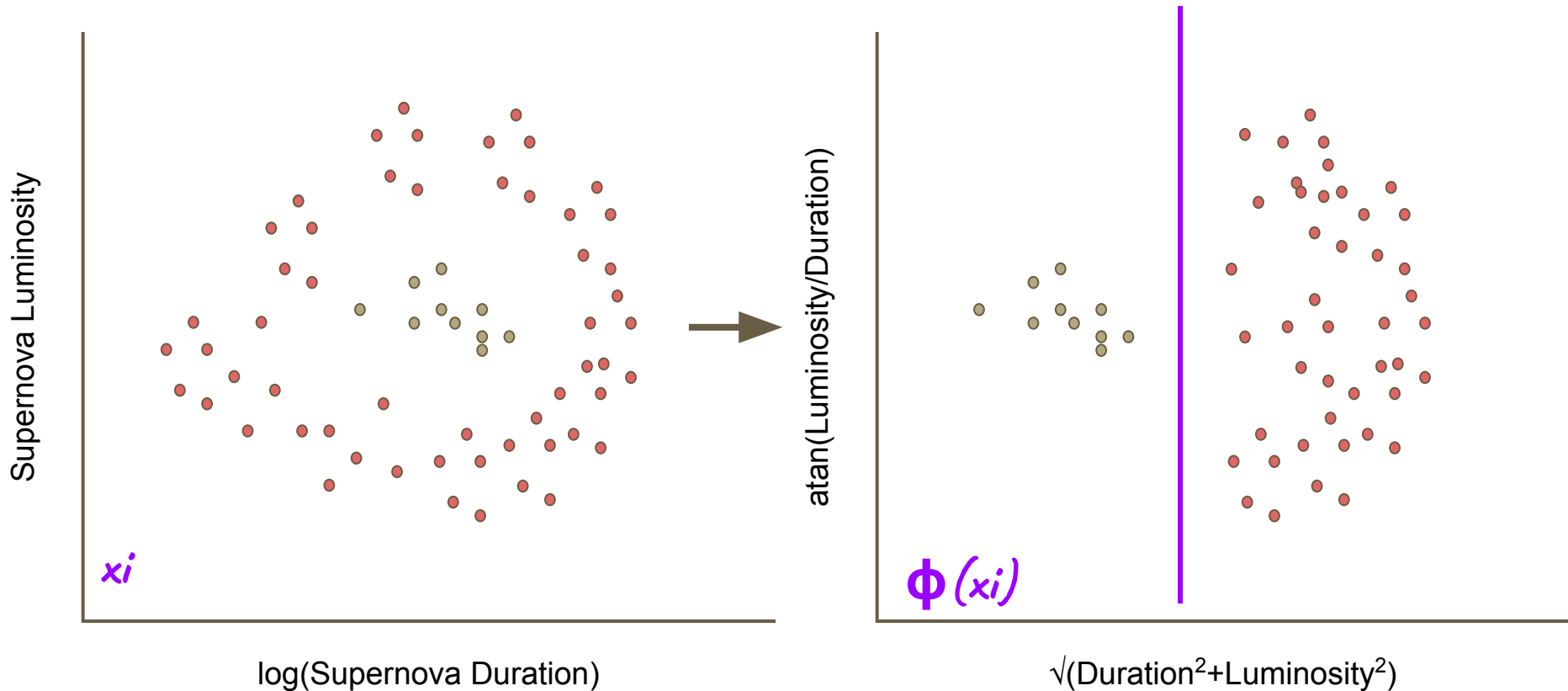
1. The objective function only depends on the support vectors - i.e., the observational points which lie on the very edge of my street
2. The objective function will be differentiable, so we can **optimize** via gradient descent
3. The objective function only depends on **the similarity (dot product) between pairs of support vectors,  $x_i \cdot x_j$**



# What if my data cannot be separated by a line (linearly separable)?



In previous classes, we learned about mapping one feature space into another latent space



**But, I don't actually need to know what  $\Phi(x)$  is, because my objective function only depends on  $\Phi(x_i) \cdot \Phi(x_j)$**

But, I don't actually need to know what  $\Phi(x)$  is, because my objective function only depends on  $\Phi(x_i) \cdot \Phi(x_j)$  ...

So let us define a function, which we'll call a Kernel, which defines dot products in this new space:

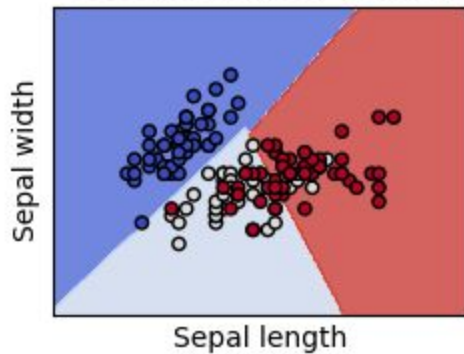
$$K(x_i, x_j) \equiv \phi(x_i) \cdot \phi(x_j)$$

*This is called the “kernel trick!”*

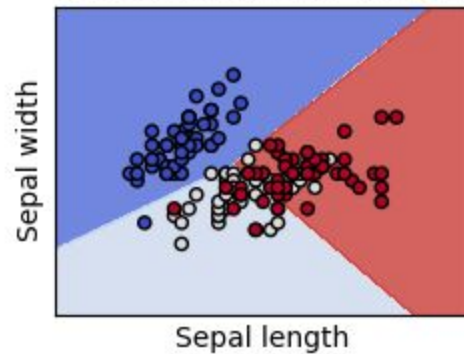
One popular example of a kernel function:

$$K(x_i, x_j) = \exp \left( - \frac{||x_i - x_j||^2}{2\sigma^2} \right)$$

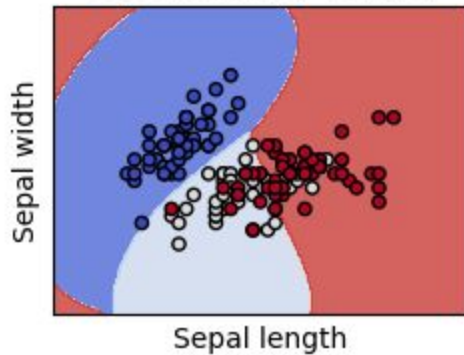
SVC with linear kernel



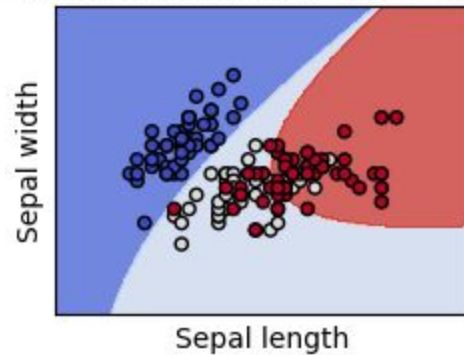
LinearSVC (linear kernel)



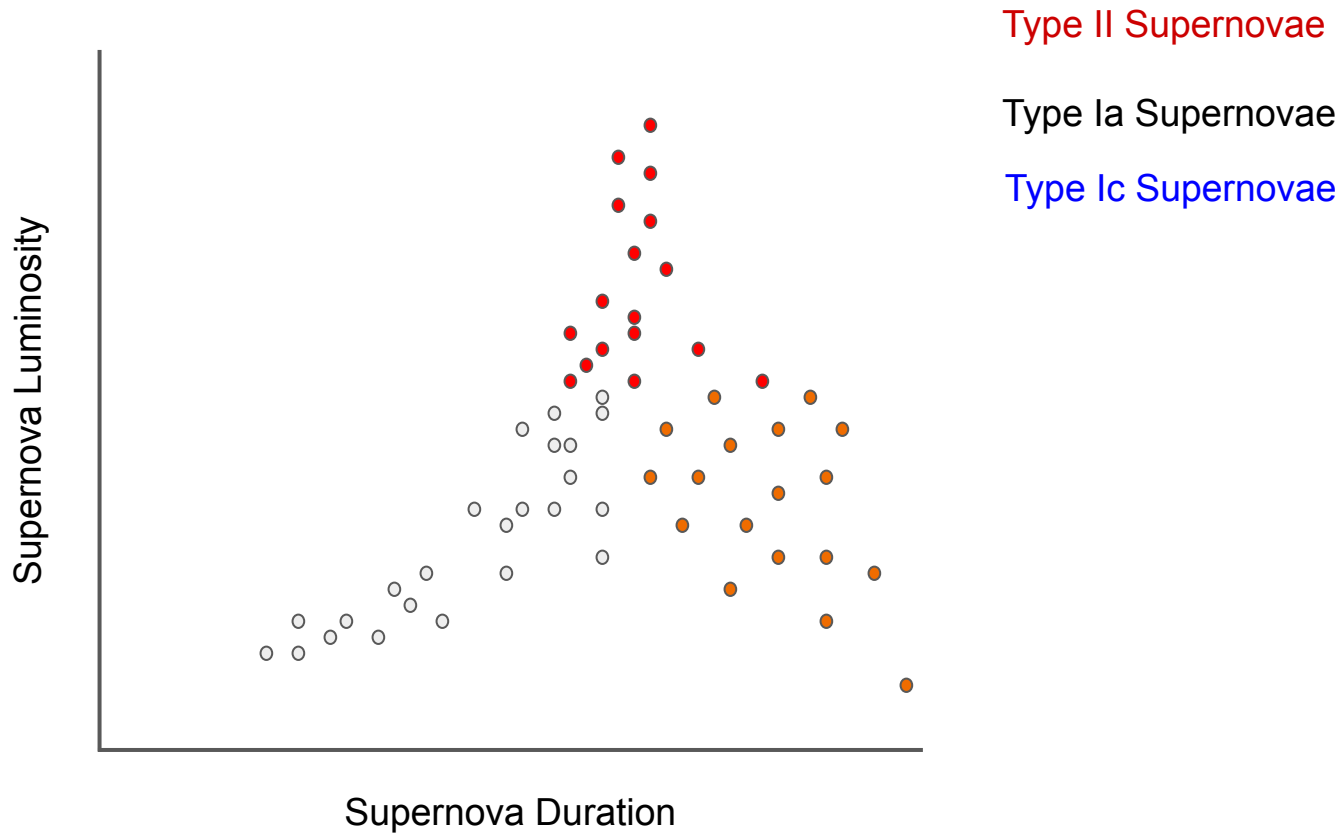
SVC with RBF kernel



SVC with polynomial (degree 3) kernel

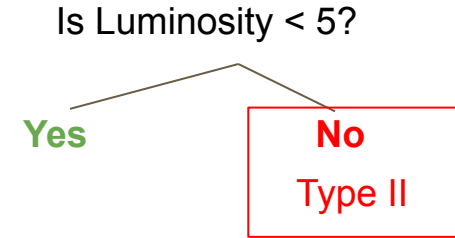
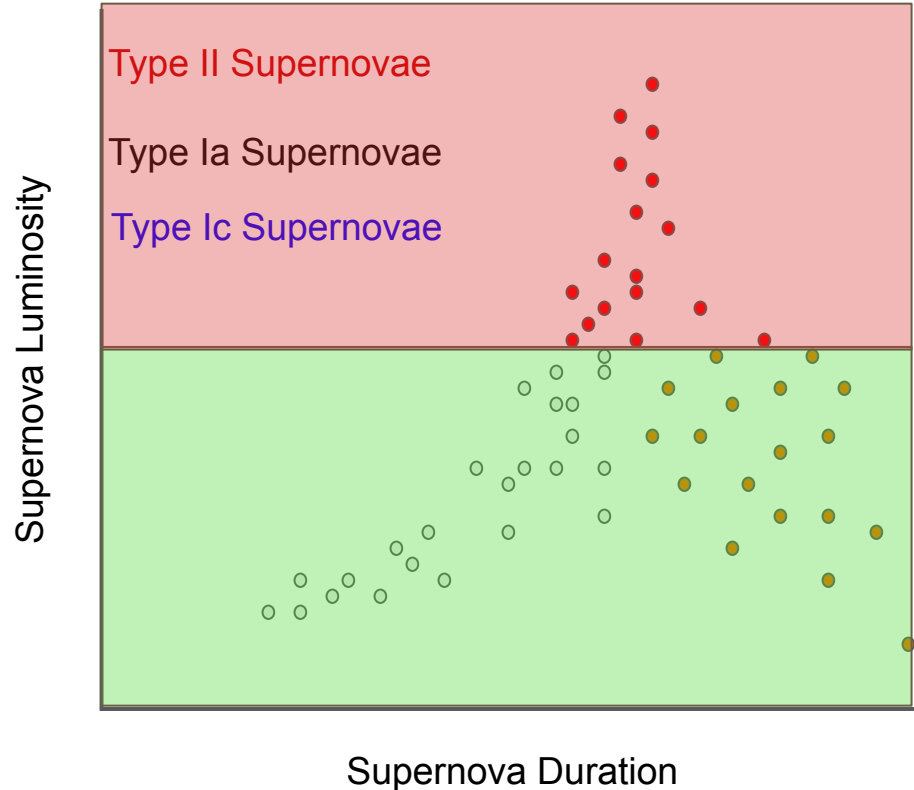


# **Decision Trees as a Supervised Classification Method**

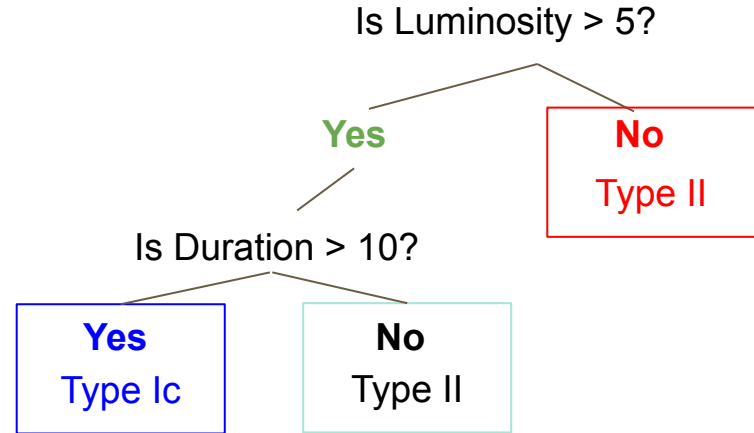
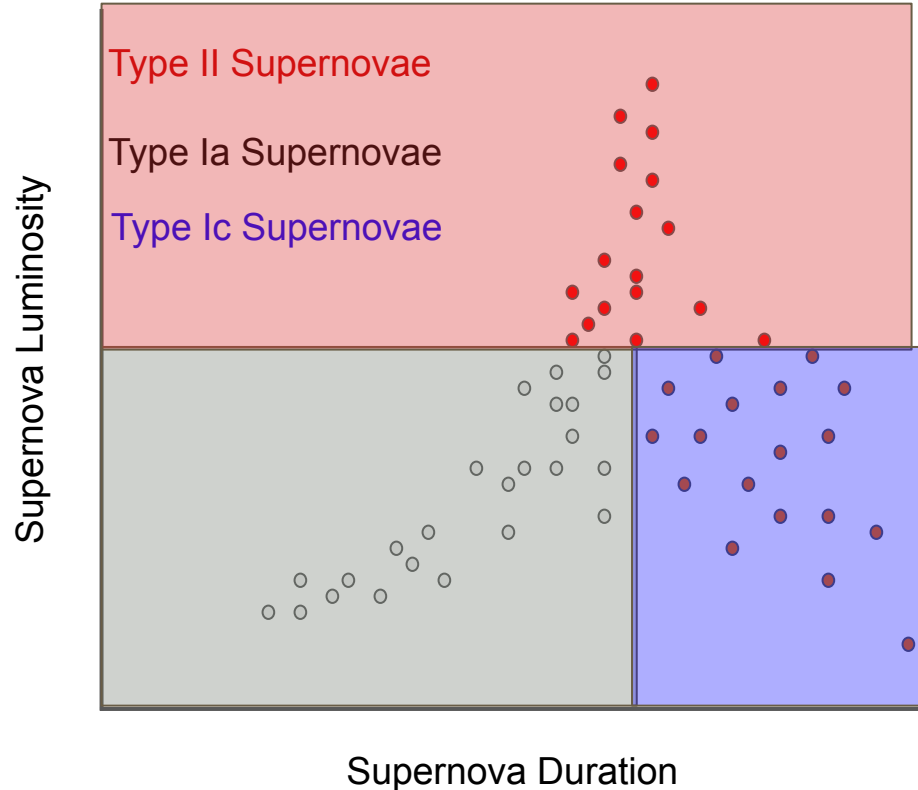




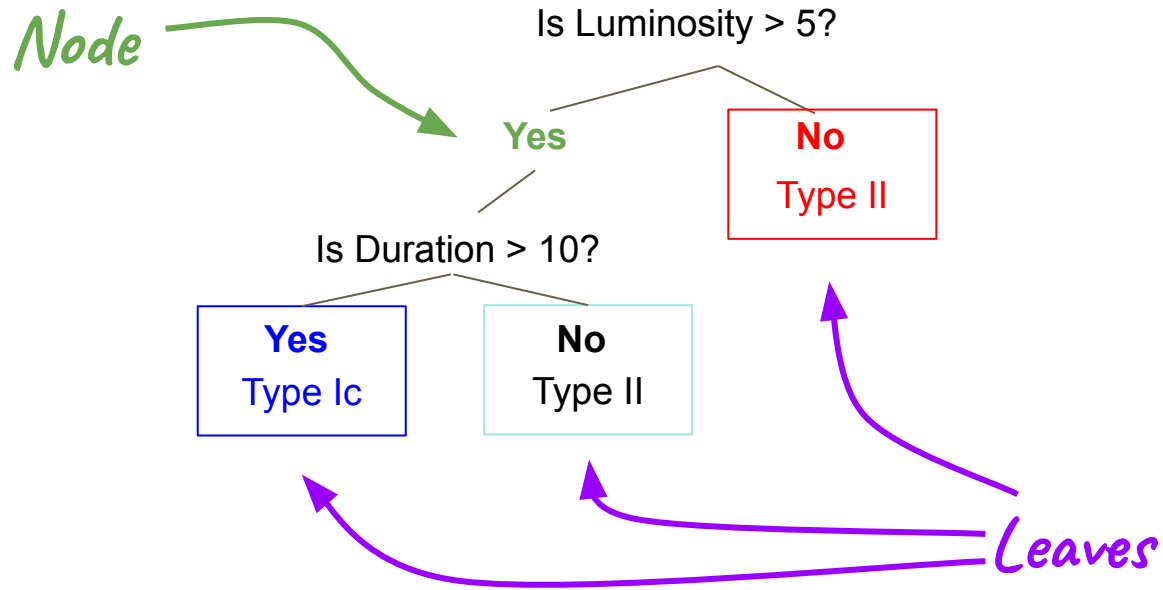
# A decision tree makes a series of binary cuts to sort data



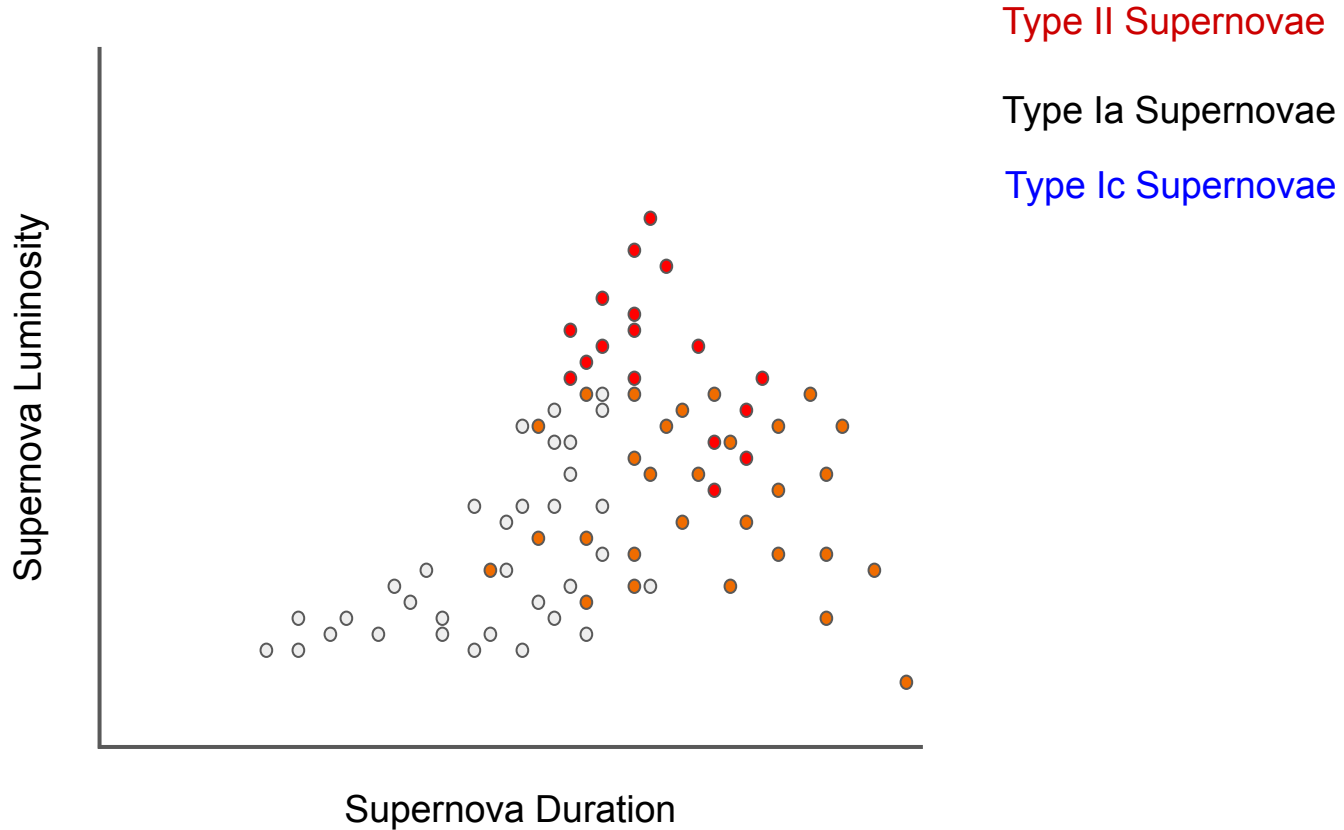
# A decision tree makes a series of binary cuts to sort data



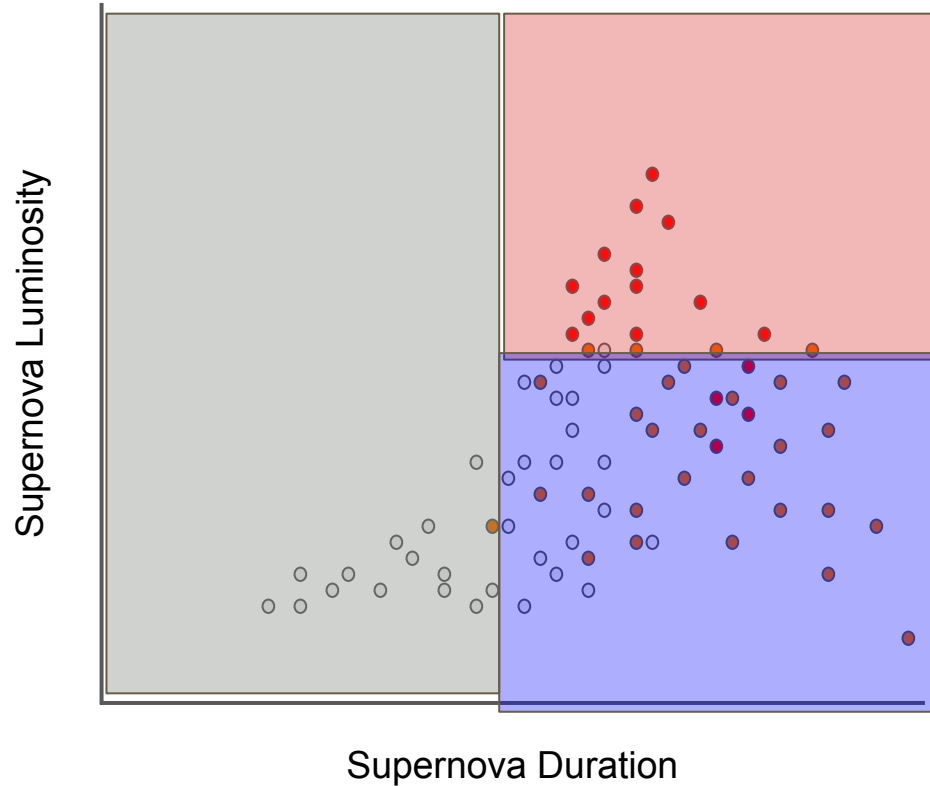
# Some terminology



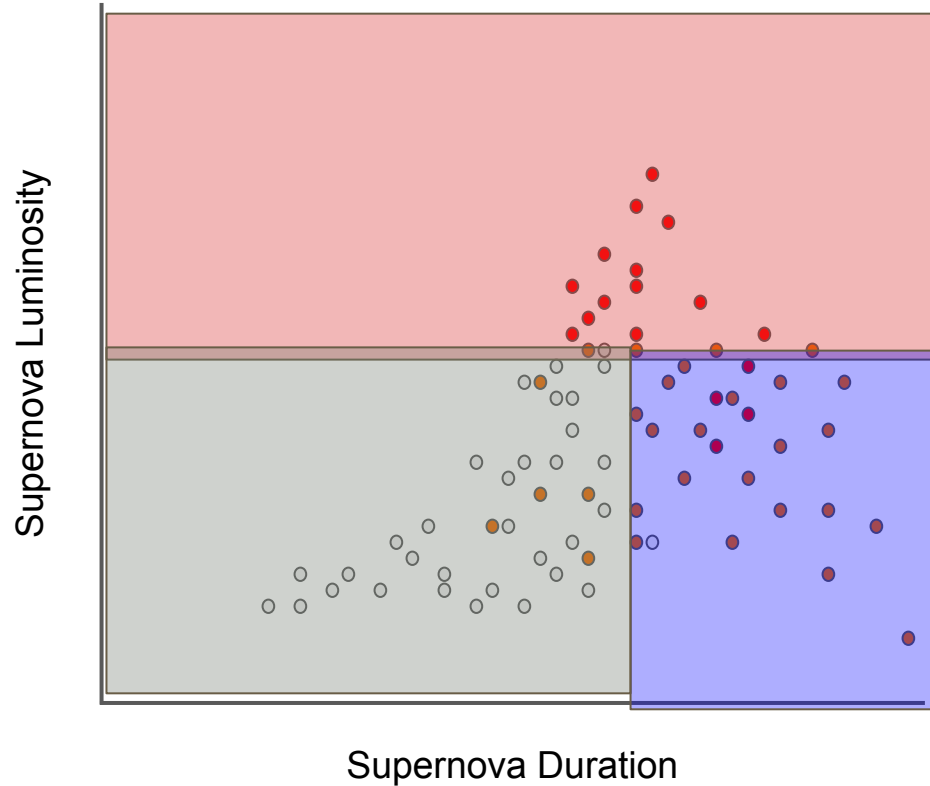
# That was pretty easy! What if our classes were more mixed?



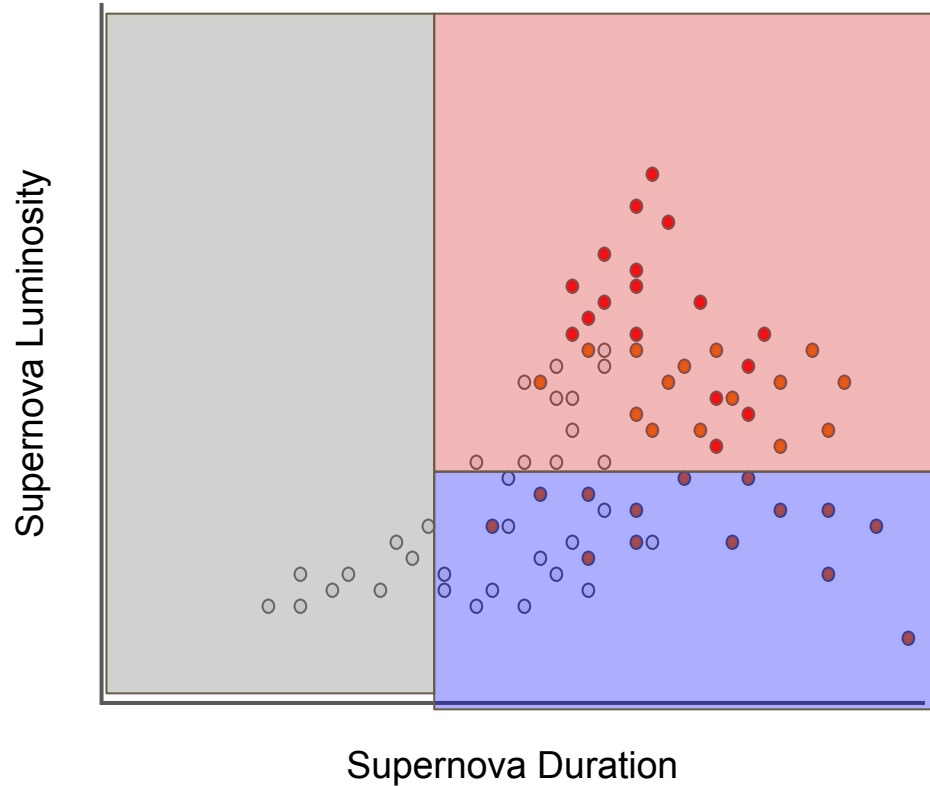
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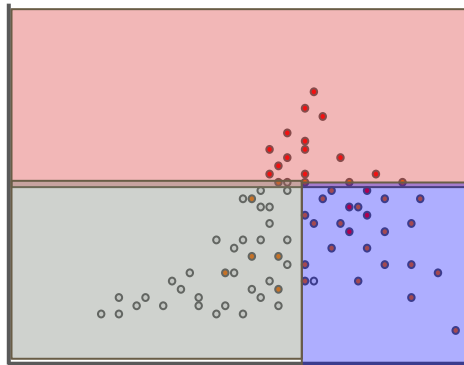
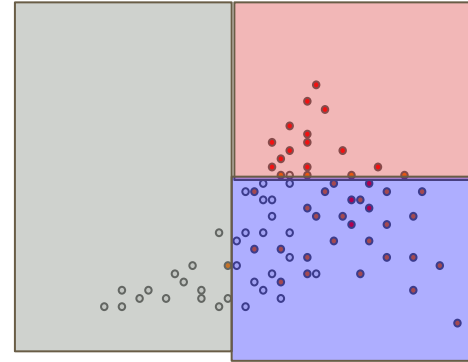
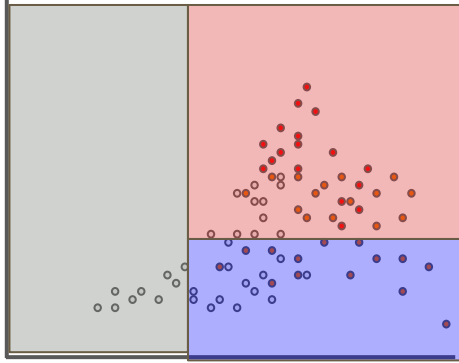
That was pretty easy! What if our classes were more mixed?



# That was pretty easy! What if our classes were more mixed?



# A random forest combines these decision trees to decide on a final classification





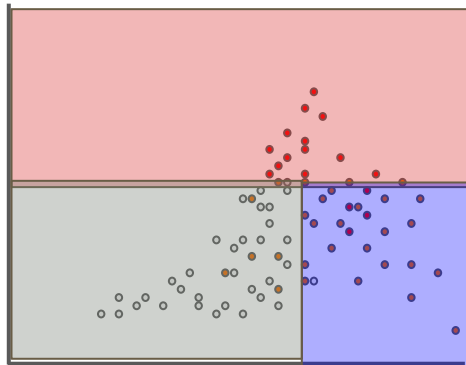
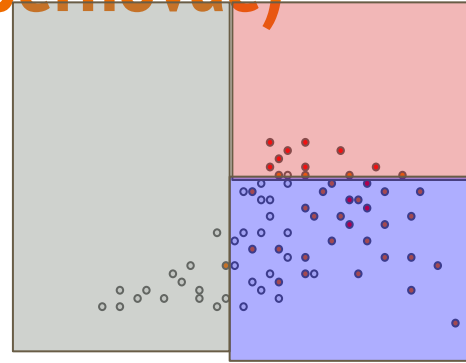
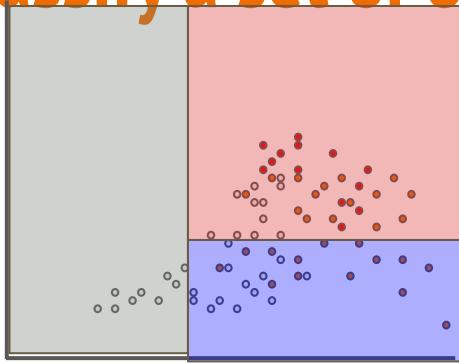
M(odel):

O(bjective function):

O(ptimization):



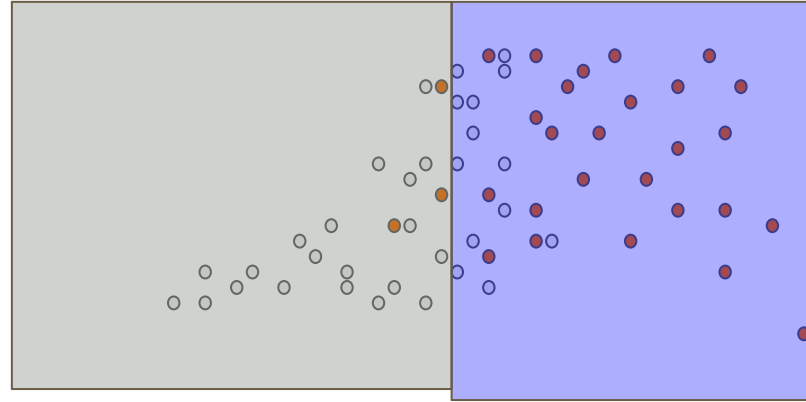
**M(odel): A series of set of decision trees which attempt to classify a set of objects (like supernovae)**



Let's zoom into one tree. How do we choose decision boundaries?

$$1 - \sum_k^K p_k^2$$

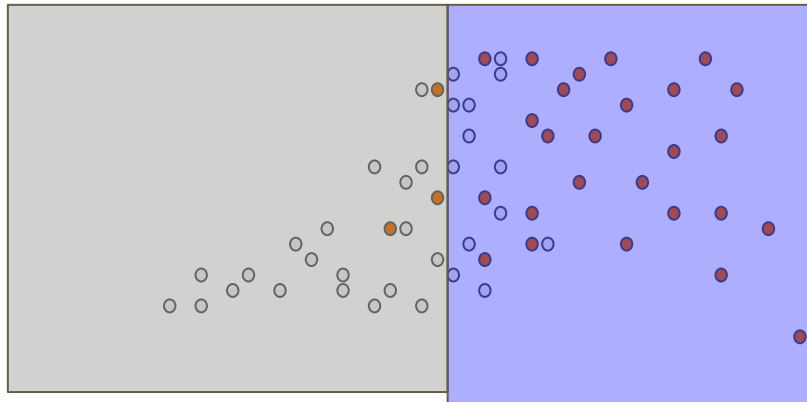
# Objective function): Gini Impurity



Total SNe\*: 23  
Total Type Ia: 20  
Total Type Ic: 3

Total SNe\*: 37  
Total Type Ia: 13  
Total Type Ic: 24

# Objective function): Gini Impurity



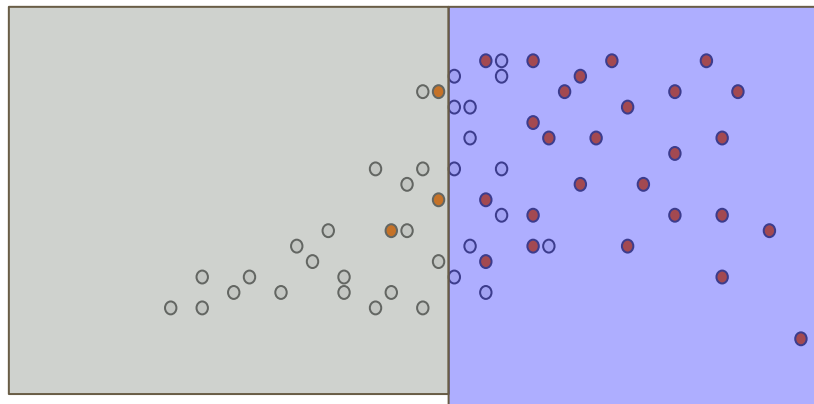
Total SNe\*: 23  
Total Type Ia: 20  
Total Type Ic: 3

$p(\text{Ia}) = 20/23 = 0.87$   
 $p(\text{Ic}) = 3/23 = 0.13$

Total SNe\*: 37  
Total Type Ia: 13  
Total Type Ic: 24

$p(\text{Ia}) = 13/37 = 0.35$   
 $p(\text{Ic}) = 24/37 = 0.65$

# Objective function: Gini Impurities (for each leaf)



Total SNe\*: 23  
Total Type Ia: 20  
Total Type Ic: 3

$p(\text{Ia}) = 20/23 = 0.87$   
 $p(\text{Ic}) = 3/23 = 0.13$

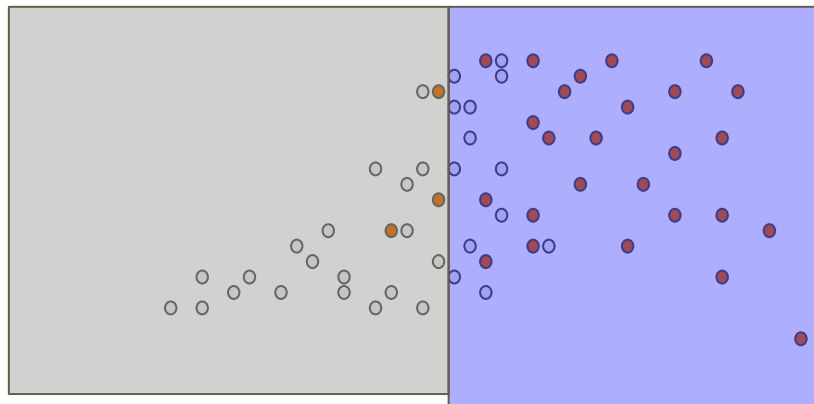
Total SNe\*: 37  
Total Type Ia: 13  
Total Type Ic: 24

$p(\text{Ia}) = 13/37 = 0.35$   
 $p(\text{Ic}) = 24/37 = 0.65$

$$1 - (0.87^2 + 0.13^2) = 0.23$$

$$1 - (0.35^2 + 0.65^2) = 0.46$$

# Objective function: Weighted Mean Gini Impurities



Total SNe\*: **23**  
Total Type Ia: 20  
Total Type Ic: 3

$p(\text{Ia}) = 20/23 = 0.87$   
 $p(\text{Ic}) = 3/23 = 0.13$

Total SNe\*: **37**  
Total Type Ia: 13  
Total Type Ic: 24

$p(\text{Ia}) = 13/37 = 0.35$   
 $p(\text{Ic}) = 24/37 = 0.65$

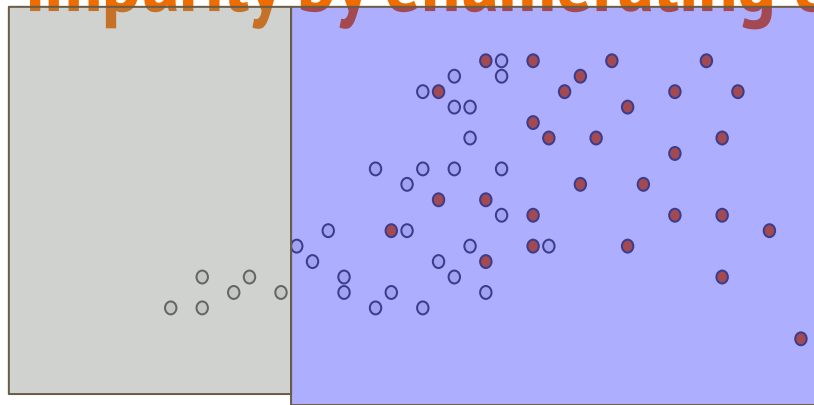
$$23/60 * 0.23$$

+

$$37/60 * 0.46$$

$$= 0.37!$$

# A random forest minimizes this weight mean Gini impurity by enumerating every option



$$6/60 * 0$$

+

$$54/60 * 0.75$$

Total SNe\*: **6**  
Total Type Ia: 6  
Total Type Ic: 0

$p(\text{Ia}) = 6/6 = 1$   
 $p(\text{Ic}) = 0/6 = 0$

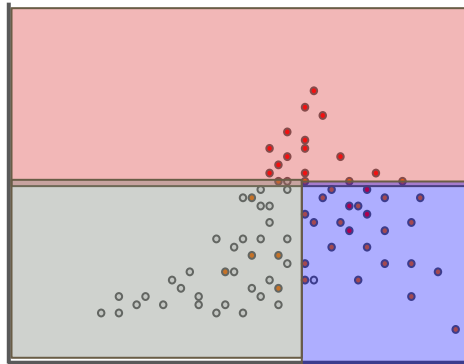
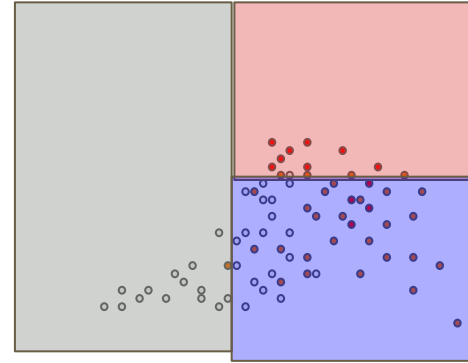
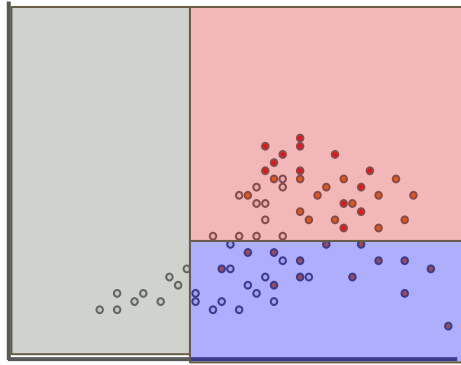
Total SNe\*: **54**  
Total Type Ia: 27  
Total Type Ic: 27

$p(\text{Ia}) = 13/37 = 0.5$   
 $p(\text{Ic}) = 24/24 = 0.5$

= 0.68!



# Each tree works on a random subset of the data



# Conclusions

Supervised/Unsupervised Learning are families of statistical problems which can aid in: understanding relationships between variables, dimensionality reduction, clustering, classification and regression.

Today we covered a wide variety of topics, from k-means to random forests.

Questions?