Recap day 4

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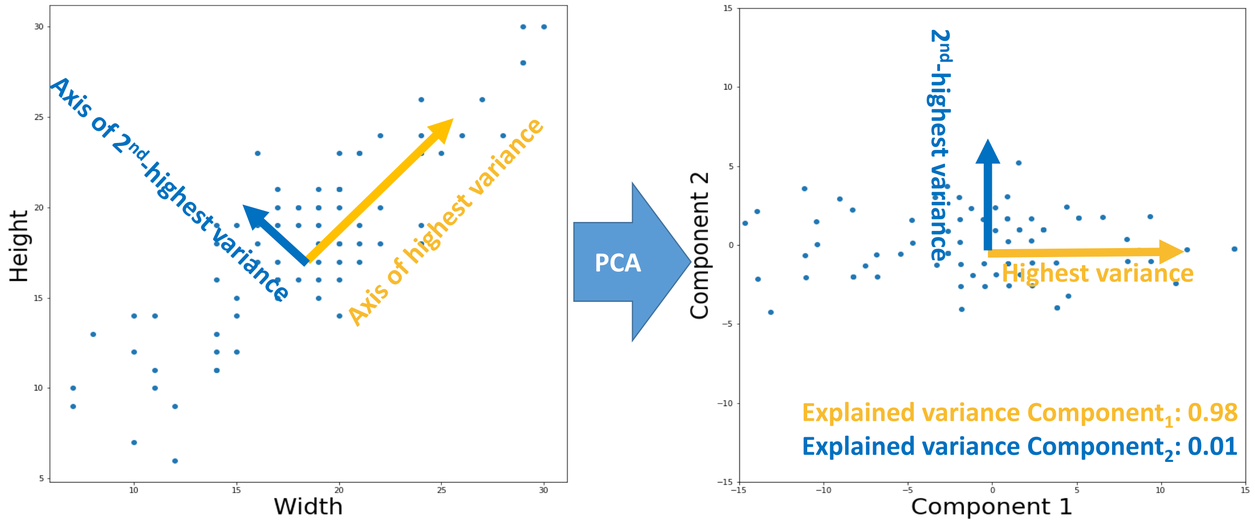
Dimensionality reduction and clustering



PCA: Linear transformation and identifies axes that explain most of the variance in the data

→ If the explained variances of component$_1$ and component$_2$ are [0.32, 0.2], we…

Need more components	Cry	Will find no groups in the data

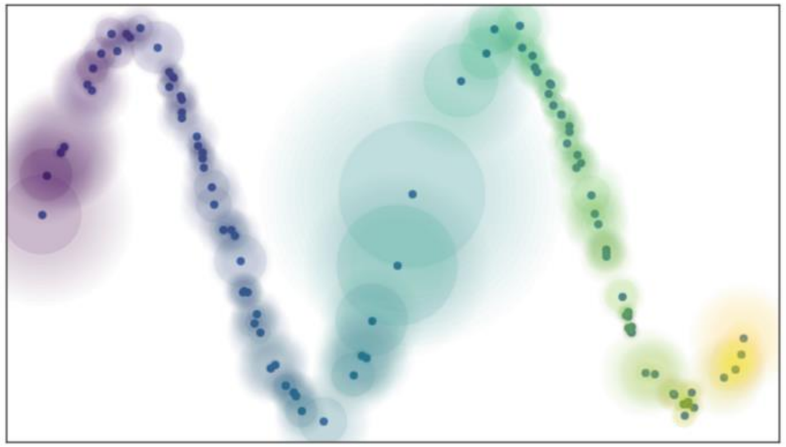
→ If we add more data to a PCA-transformed set of data, we …

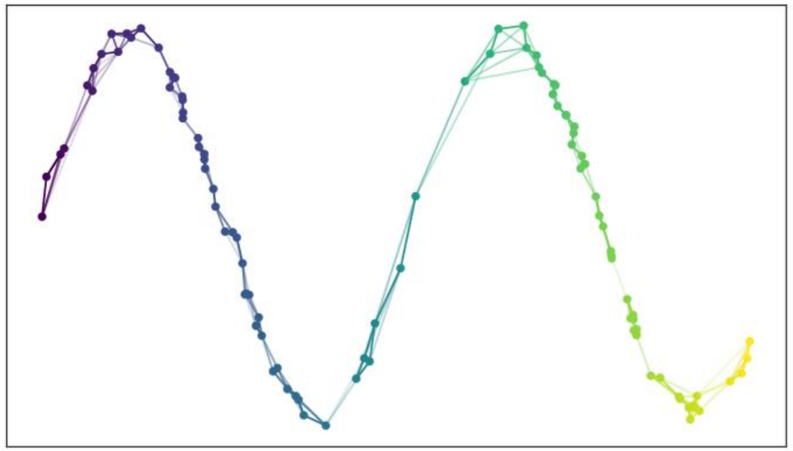
Need to re-run the PCA	Can use the same PCA components	Cannot use PCA at all

→ We can measure meaningful differences between data point in terms of component$_1$ and component$_2$

True	False

UMAP





UMAP:

→ Link neighboring points by introducing point-wise distance metrics

→ “Relax” neighborhood graph to be able to display it in fewer dimensions while preserving its topology

We can measure meaningful differences between data points in terms of $UMAP_0$ and $UMAP_1$

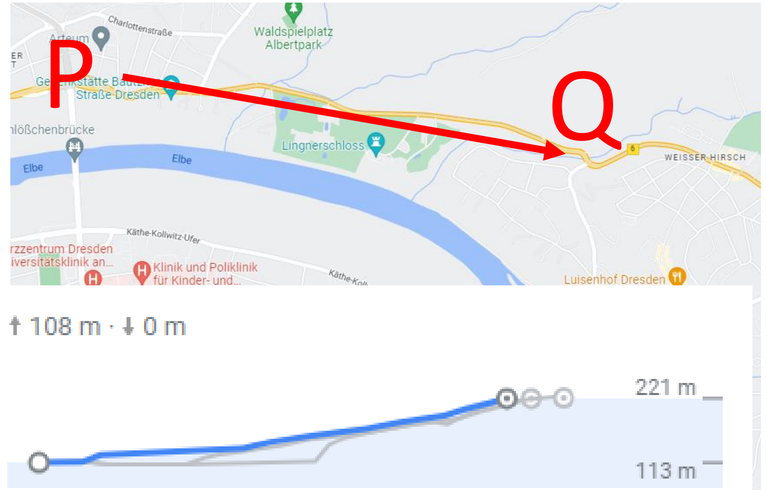
True | False

If we add new points to an existing UMAP projection, we can use the same projection

True | False

Running a UMAP twice will give the same result

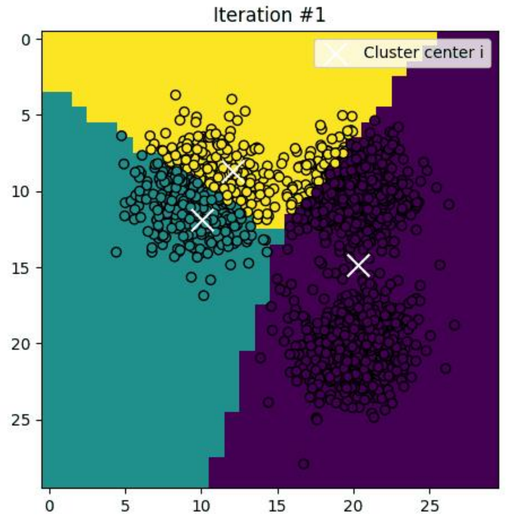
True | False



↑ 108 m · ↓ 0 m

Source: https://hdbscan.readthedocs.io/en/latest/how_hdbscan_works.html

Clustering



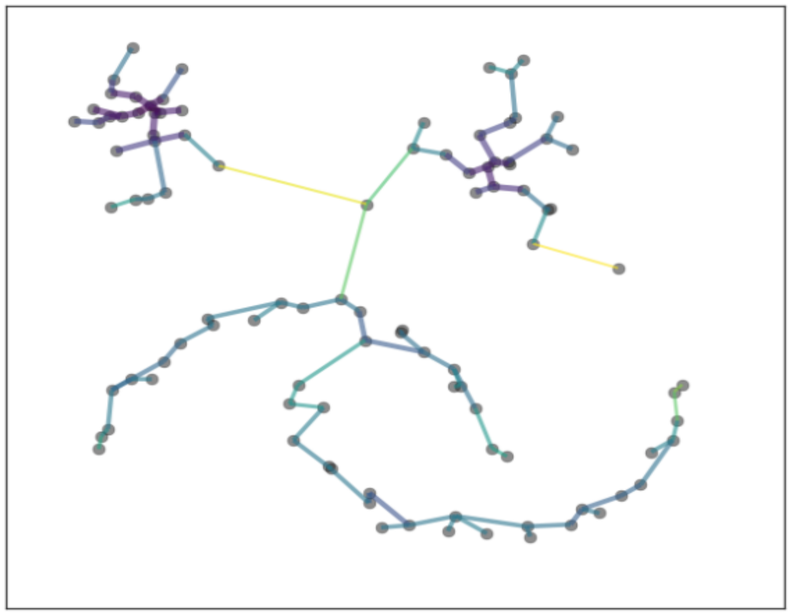
K-Means clustering:

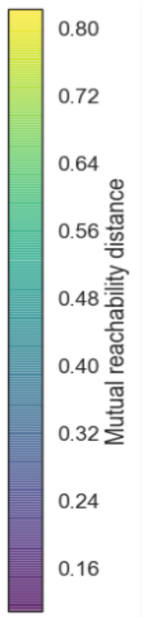
If we add more data to the pool, we can infer the cluster of a new point from the previously determined clusters

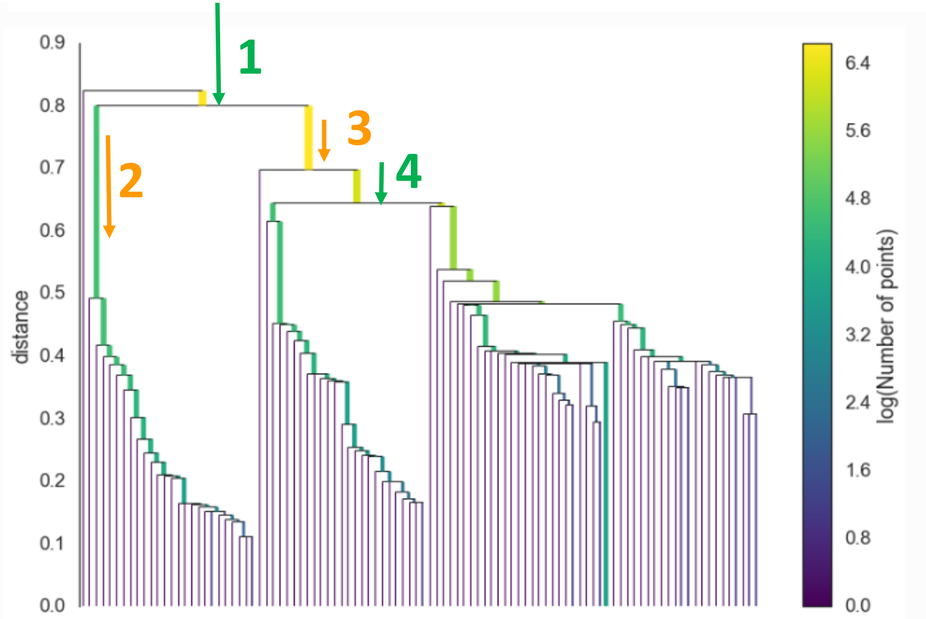
True

False

HDBSCAN: If we add more data to the pool, we can infer the cluster of a new point from the previously determined clusters







True

False

An important parameter is…

The point density

Data units

Minimal cluster size

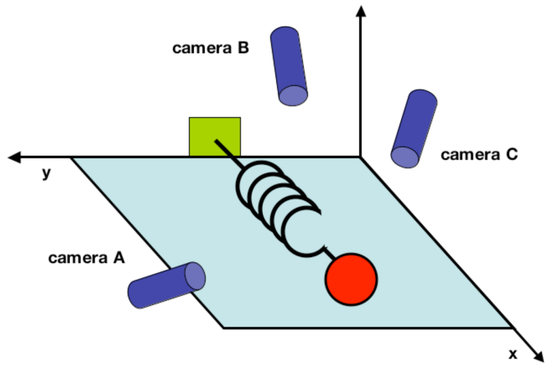
Source: https://hdbscan.readthedocs.io/en/latest/how_hdbscan_works.html

PCA

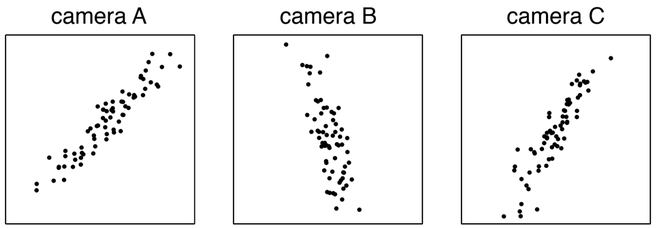
A Tutorial on Principal Component Analysis

[Jonathon Shlens](#)

https://arxiv.org/abs/1404.1100



$$\mathbf{X} = \begin{bmatrix} \mathbf{x_1} \\ \vdots \\ \mathbf{x_m} \end{bmatrix}$$



covariance matrix $\mathbf{C_X}$.

$$\mathbf{C_X} \equiv \frac{1}{n}\mathbf{X}\mathbf{X}^T.$$

Is there another basis, which is a linear combination of the original basis, that best re-expresses our data set?

$$\mathbf{PX} = \mathbf{Y}$$

SVD is a more general method for change of basis. $\mathbf{X} = \mathbf{U}\Sigma\mathbf{V}^T$

$\mathbf{C_X}$ captures the covariance between all possible pairs of measurements. The covariance values reflect the noise and redundancy in our measurements.

- In the diagonal terms, by assumption, large values correspond to interesting structure.
- In the off-diagonal terms large magnitudes correspond to high redundancy.

$$\begin{aligned} \mathbf{C_Y} &= \frac{1}{n}\mathbf{Y}\mathbf{Y}^T \\ &= \frac{1}{n}(\mathbf{PX})(\mathbf{PX})^T \\ &= \frac{1}{n}\mathbf{PXX}^T\mathbf{P}^T \\ &= \mathbf{P}(\frac{1}{n}\mathbf{X}\mathbf{X}^T)\mathbf{P}^T \\ \mathbf{C_Y} &= \mathbf{P}\mathbf{C_X}\mathbf{P}^T \end{aligned}$$

A symmetric matrix is diagonalized by a matrix of its orthonormal eigenvectors.

$$\mathbf{A} = \mathbf{E}\mathbf{D}\mathbf{E}^T$$

$$\begin{aligned} \mathbf{C_Y} &= \mathbf{P}\mathbf{C_X}\mathbf{P}^T \\ &= \mathbf{P}(\mathbf{E}^T\mathbf{D}\mathbf{E})\mathbf{P}^T \end{aligned}$$

If we select P as the eigenvectors of C_x: $\mathbf{P} \equiv \mathbf{E}^T$

$$\begin{aligned} &= \mathbf{P}(\mathbf{P}^T\mathbf{D}\mathbf{P})\mathbf{P}^T \\ &= (\mathbf{P}\mathbf{P}^T)\mathbf{D}(\mathbf{P}\mathbf{P}^T) \\ &= (\mathbf{P}\mathbf{P}^{-1})\mathbf{D}(\mathbf{P}\mathbf{P}^{-1}) \\ \mathbf{C_Y} &= \mathbf{D} \end{aligned}$$

Quiz

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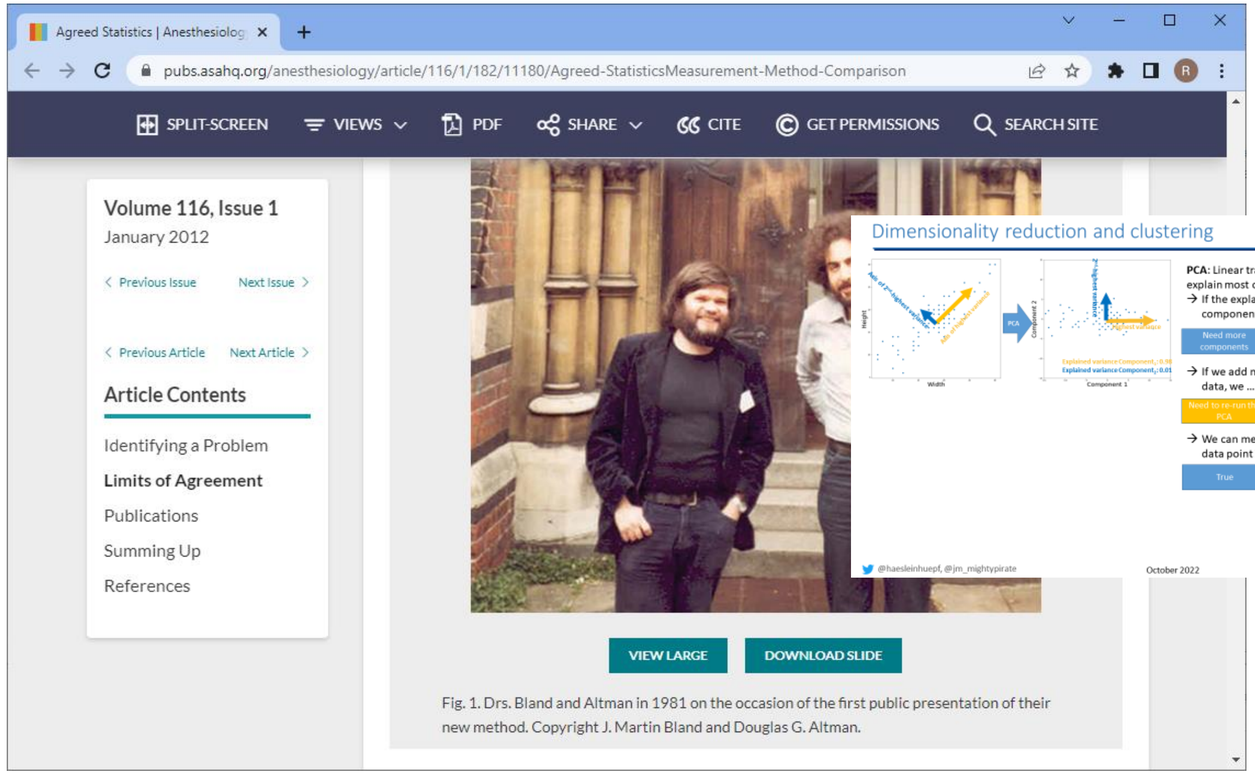

Yes

No

Source:
https://anesthesiology.pubs.asahq.org/article.aspx?articleid=1933992

Quiz

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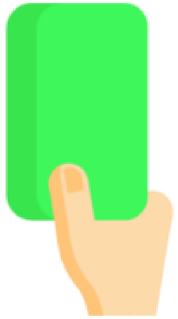

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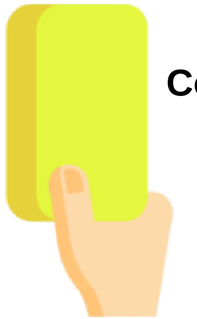

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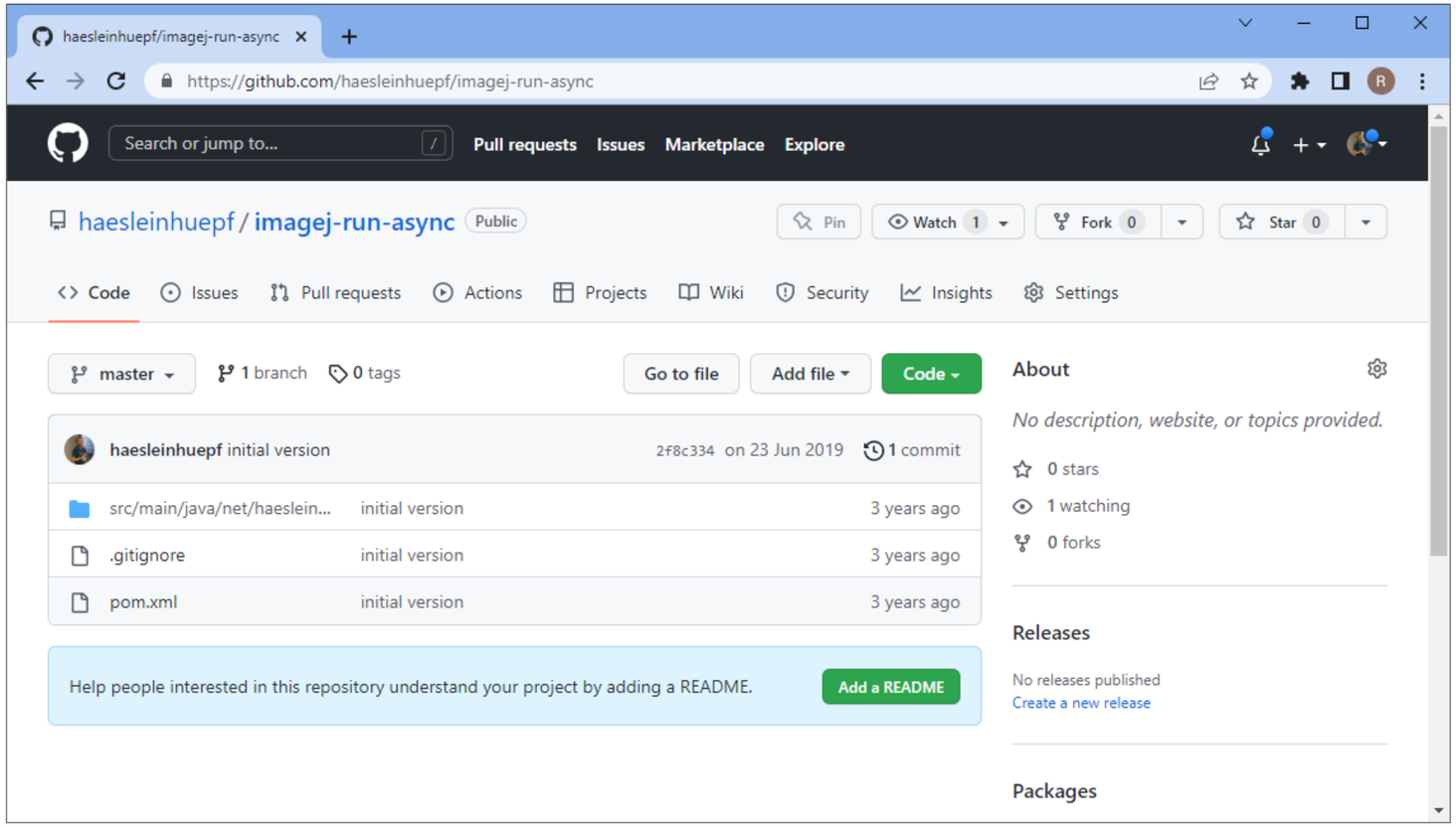

Quiz

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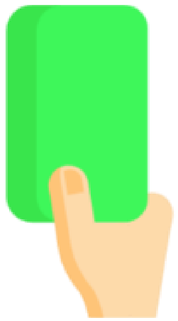

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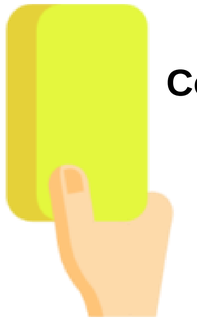

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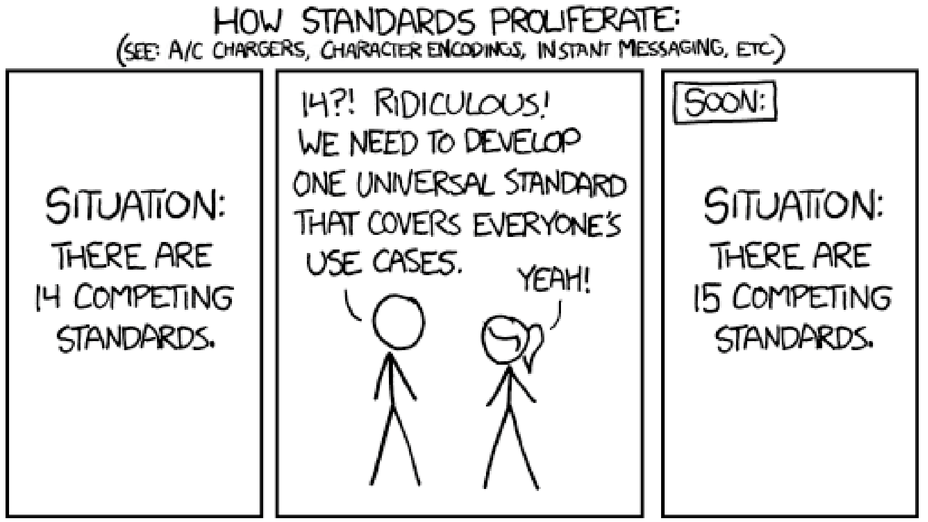

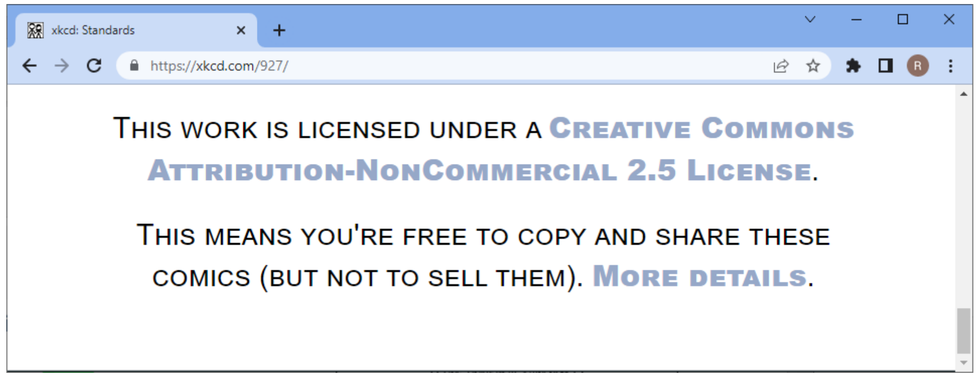

https://xkcd.com/927/