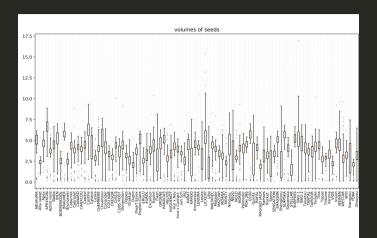
Looking at microCT data of Brassica pods

I am not a biologist, please stop me and correct me if I say silly things.

Pod Width

Sphericity

Volume



Surface Area

Correlation<u>s</u>

Filtering false seeds



- Image analysis produces many false seeds at the beak tip
- · Density and size is comparable to seed
- Hard to recognise by graphical methods alone
- · Recognise them by mathematical means instead

Spine fitting

- For every CT slice we have the centroid of the object
- Fit X and Y position as cubic functions of z

 Define 'real z' as the distance measured along the fitted curve from the beak to the z coordinate of the point



Distinguishing between beak tip and Real Seeds™

Failed approaches:

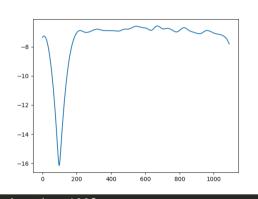
- Assert that seeds must not be implausible Removed insufficiently many seeds
 - Too close to the ends of the pod
 - Too large given pod dimensions
- 2. Real z position of seeds of a pod is a sample from some probability distribution, fit and paramterize the distribution to classify seeds.
 - Sum of two normal(-ish) distributions noise at beak might be normal, everything else definitely is not
 - More complicated distribution too complicated
- 3. K-Means clustering Silly for 1 dimensional data
- 4. Jenks Natural Breaks Optimisation Should work in theory, did not work well in practice

Break at Minimum Kernel Density Estimation (KDE)

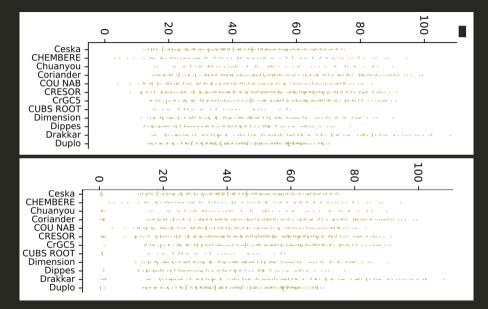
- Beak has no Real Seeds[™] and low density
- · Expect a gap in real z of detected seeds



Use KDE to find density of seeds as function of real z



- First seed has real z less than 100?
- Find the local minimum at lowest real z where log(KDE)<-10
- Keep seeds with greater real z
- Profit



Beak and Silique length

Use the seed with lowest real z to mark the boundary of beak and silique:

