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

Correlations

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

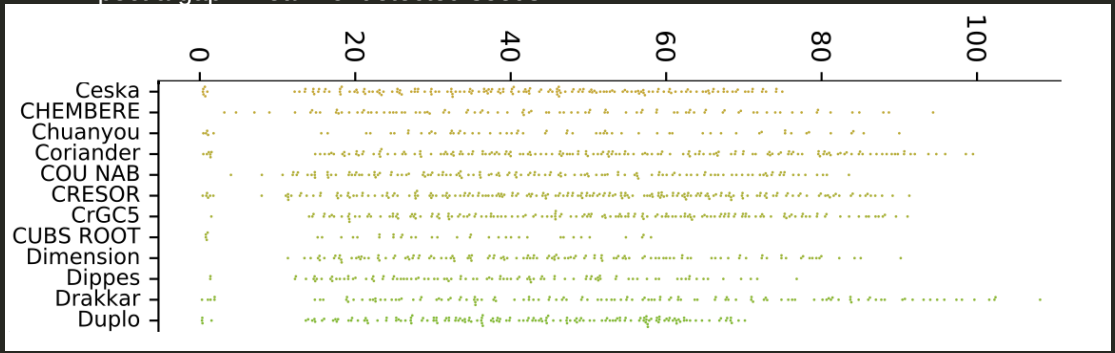
Distinguishing between beak tip and Real Seeds™

Failed approaches:

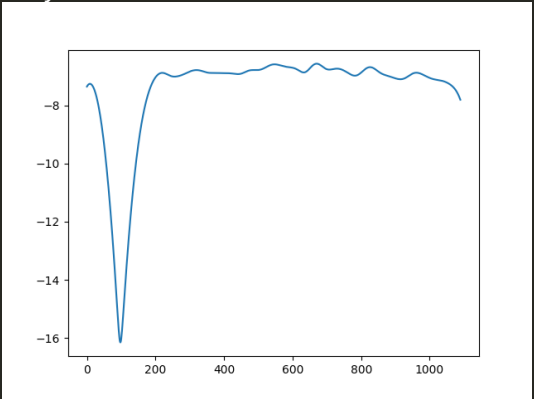
1. Assert that seeds must not be implausible - Removed insufficiently many seeds
    - Too close to the ends of the pod
    - Too large given pod dimensions
2. Real z position of seeds of a pod is a sample from some probability distribution, fit and paramterize the distribution to classify seeds.
    - 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)

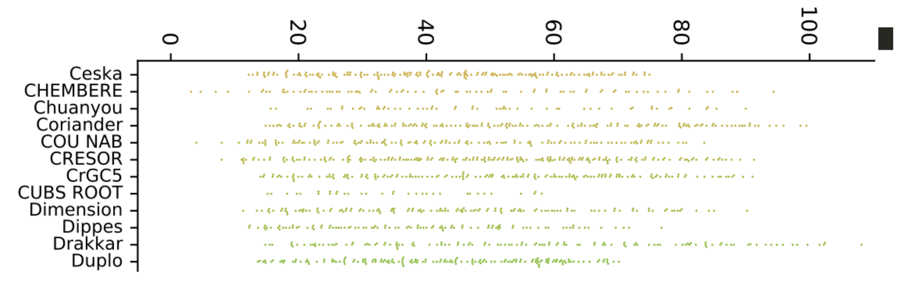
- Beak has no Real Seeds™ and low density
- Expect a gap in real z of detected seeds



- 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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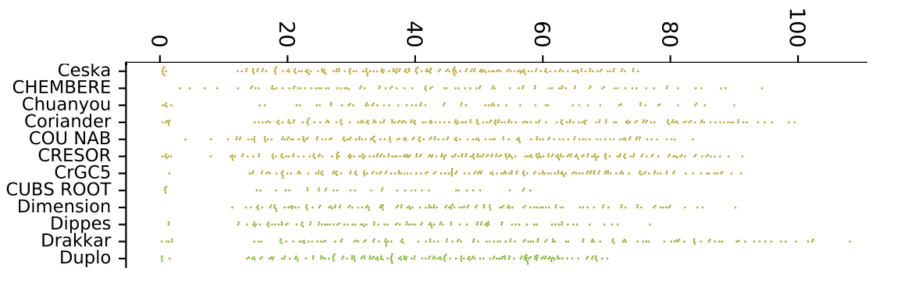
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Duplo

Beak and Silique length

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

TODO: insert silique length and beak length graphs