Canopy Height Models (CHMs) & Digital Surface Models (DSMs)SEFS 433/533 Lab 4

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Objectives:

- Create Canopy Height Models (CHMs) & Digital Surface Models (DSMs)
- Individual Tree Detection (ITD)

Data and Software:

- Las tiles downloaded previously for lab 3.
- Washington DNR Lidar Portal to download las tile and meta data for Arboretum
- RStudio
- ArcGIS Pro (Optional)

What you will turn in:

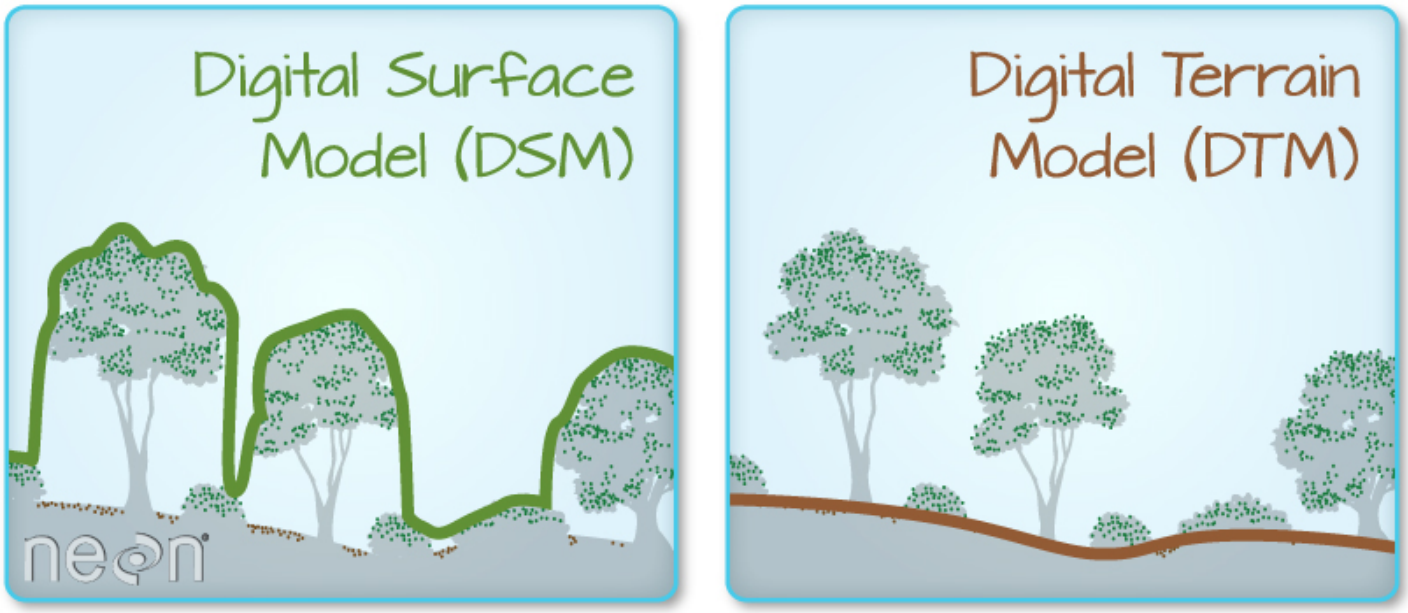
- Lab 4 Submission Quiz on Canvas

Welcome to Lab 4 for ESRM433/SEFS533!

In this lab you will create and assess canopy height models (CHMs), then use these models in an individual tree detection (ITD) routine. CHMs are a primary product of LiDAR for use in forest measurement. It is very important that you understand how they are made and how various parameters affect their characteristics. ITD is a more niche field of study; however, it is good to understand how it works and what its limitations are.

Some definitions (https://www.neonscience.org/chm-dsm-dtm-gridded-lidar-data (https://www.neonscience.org/chm-dsm-dtm-gridded-lidar-data))

- **Digital Terrain Model** - This product represents the elevation of the ground.
- **Digital Surface Model** - This represents the elevation of the tallest surfaces at that point. Imagine draping a sheet over the canopy of a forest, the DEM contours with the heights of the trees where there are trees but the elevation of the ground when there is a clearing in the forest.
- **Canopy Height Model** - This represents the difference between a Digital Terrain Model and a Digital Surface Model and gives you the height of the objects (in a forest, the trees) that are on the surface of the earth.



The difference between a DTM and a DSM

PART 1 Mapping tiles and clipping data

Hopefully, you still have the las tiles downloaded from lab 3. To continue, you will need to have the two tiles located in a folder `"LAB3/TILES"` . There is no need to move them to a new lab 4 folder.

Start RStudio. I recommend just loading the R script from lab 3 and then re-saving it as `"LAB4.R"` There are several lines of code that will be the same.

Set your working directory `setwd` and you will need to have the packages `lidR` , `rgl` , `sf` , & `mapview` downloaded using `install.packages` the load them into the R script and R Studio running `library` . You don't need the `gstat` , but I am keeping it in my list of packages at the top of my script just so I know that it is needed to run some line of script.

```
#install.packages("mapview")
setwd("/Users/Anthony/OneDrive - UW/University of Washington/Teaching/SEFS433_Lidar/Labs")
```

```
library(lidR)
library(rgl)
library(sf)
```

```
## Linking to GEOS 3.11.0, GDAL 3.5.3, PROJ 9.1.0; sf_use_s2() is TRUE
```

```
library(mapview)
library(gstat)
```

Assuming that you still have the las tiles `q47123g8201.laz` and `q47123g8206.laz` located in `"LAB3/TILES"` , run the the `readLAScatalog` command to find the files in the Lab 3 folder

```
ctg <- readLAScatalog("Lab 3/ONPlidar/datasetsA/hoh_2013/laz/")
```

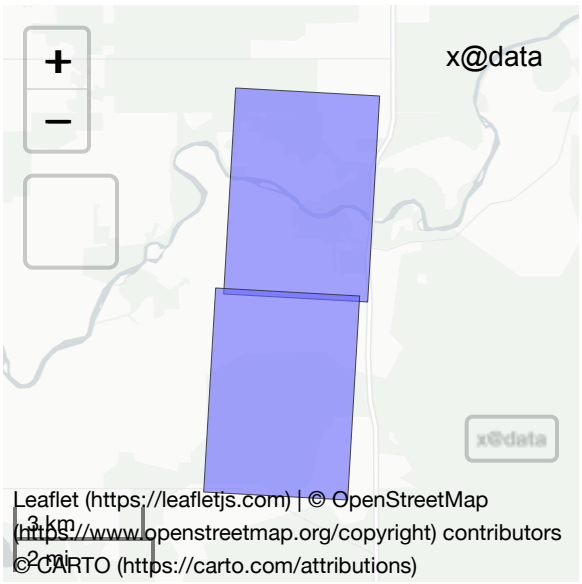
```
## Be careful, some tiles seem to overlap each other. lidR may return incorrect outputs with edge
artifacts when processing this catalog.
```

Remember, the ? pulls up documentation about the function and `help` can find package's documentation. These are the best places to look for the required syntax and the possible options for every R command.

Lets use mapview to plot where our tiles are in the world.

You can use the layers option to select what basemap you want to display.

```
#help(package = "mapview")
plot(ctg, mapview = T)
```



We know that our tiles should be on the Olympic peninsula, not way up in Canada. This is the effect of the units being displayed as meters when they should be feet.

You can query what Coordinate Reference System is being used for the catalog and you already know how to deal with CRS issues.

```
projection(ctg)
```

```
## [1] "+proj=lcc +lat_0=45.3333333333333 +lon_0=-120.5 +lat_1=47.3333333333333 +lat_2=45.8333333
333333 +x_0=500000 +y_0=0 +datum=NAD83 +units=m +no_defs"
```

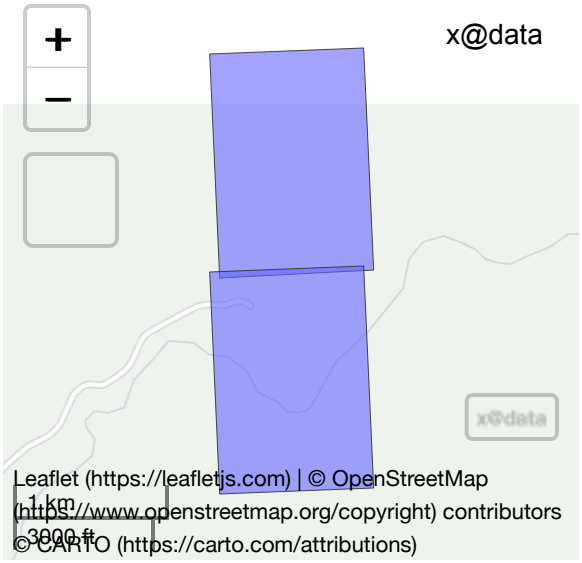
It has the known issue of meters being used instead of feet. Change the CRS to EPSG 2927

```
st_crs(ctg) <- 2927 # remember this is the epsg code
projection(ctg)
```

```
## [1] "+proj=lcc +lat_0=45.3333333333333 +lon_0=-120.5 +lat_1=47.3333333333333 +lat_2=45.8333333
333333 +x_0=500000.0001016 +y_0=0 +ellps=GRS80 +units=us-ft +no_defs"
```

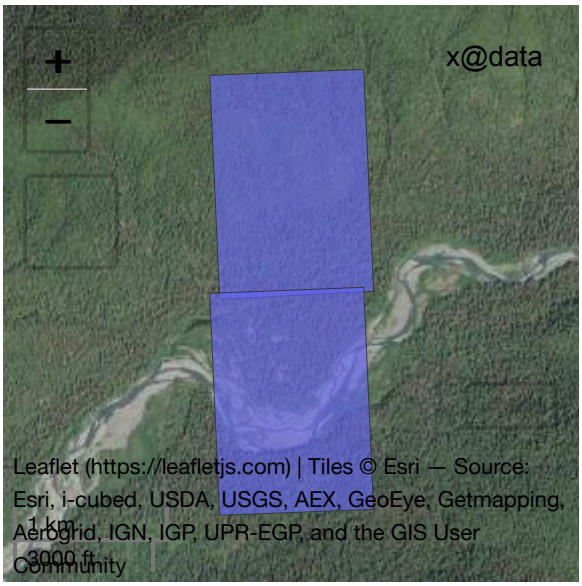
It looks good, so plot the tiles again using mapview:

```
plot(ctg, mapview = T)
```



Remember, you can use any base map you want. You can define what base map to use in the line of R code. For example, to display our tiles using Esri world imagery (the top map shown here). You would run:

```
plot(ctg, mapview = T, map.types = "Esri.WorldImagery")
```

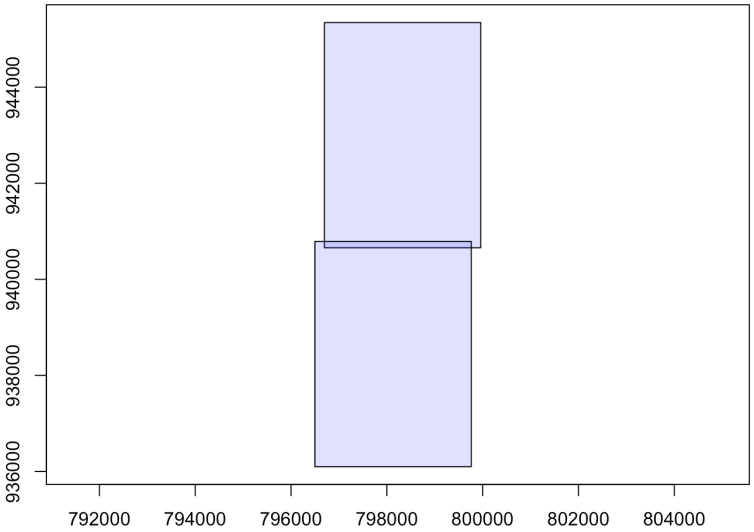


To see what base map options are available beyond the 5 default ones that are listed, you can use the `?mapview` help command, and then search "base maps" to find a web site that lists all of the options for base maps

QUESTION 1: Use `?mapview` command to track down the website that lists all of the base map options for mapview. Pick a base map that is not one of the 5 default (Carto.DB, OpenStreetMap, OpenTopoMap, or Esri.WorldImagery) and plot your tiles. Give the website address, the base map you used, and include a screen shot of your plot.

Now make a basic plot of your tiles with the x and y axis displayed using

```
plot(ctg)
```

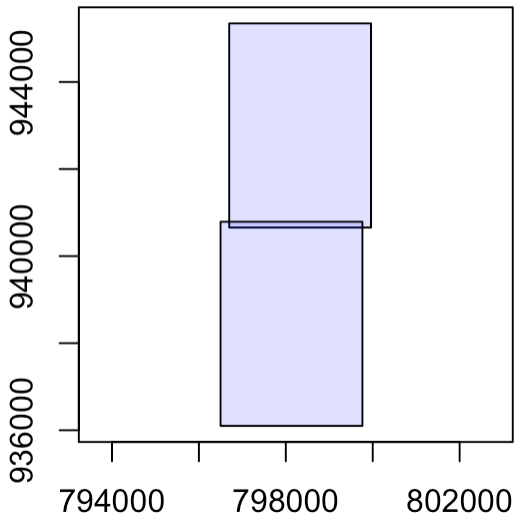


We want to make a clip of the forest on the hillside to use to practice making digital surface models (DSM). The project wide DSM is available for download, just like the DTM, but we are going to make our own.

The red x is a good location for us to practice with and it is approximately located at 798000, 944000. You could plot this point in a GIS program like ArcGIS or QGIS, with those numbers, as long as you specified it was EPSG: 2927.

Let us clip a 200 ft radius circle at that location. Run:

```
lasclip <- clip_circle(ctg, 798000, 944000, 200) # creates a circle of 200 units from the point c
louds projection
```

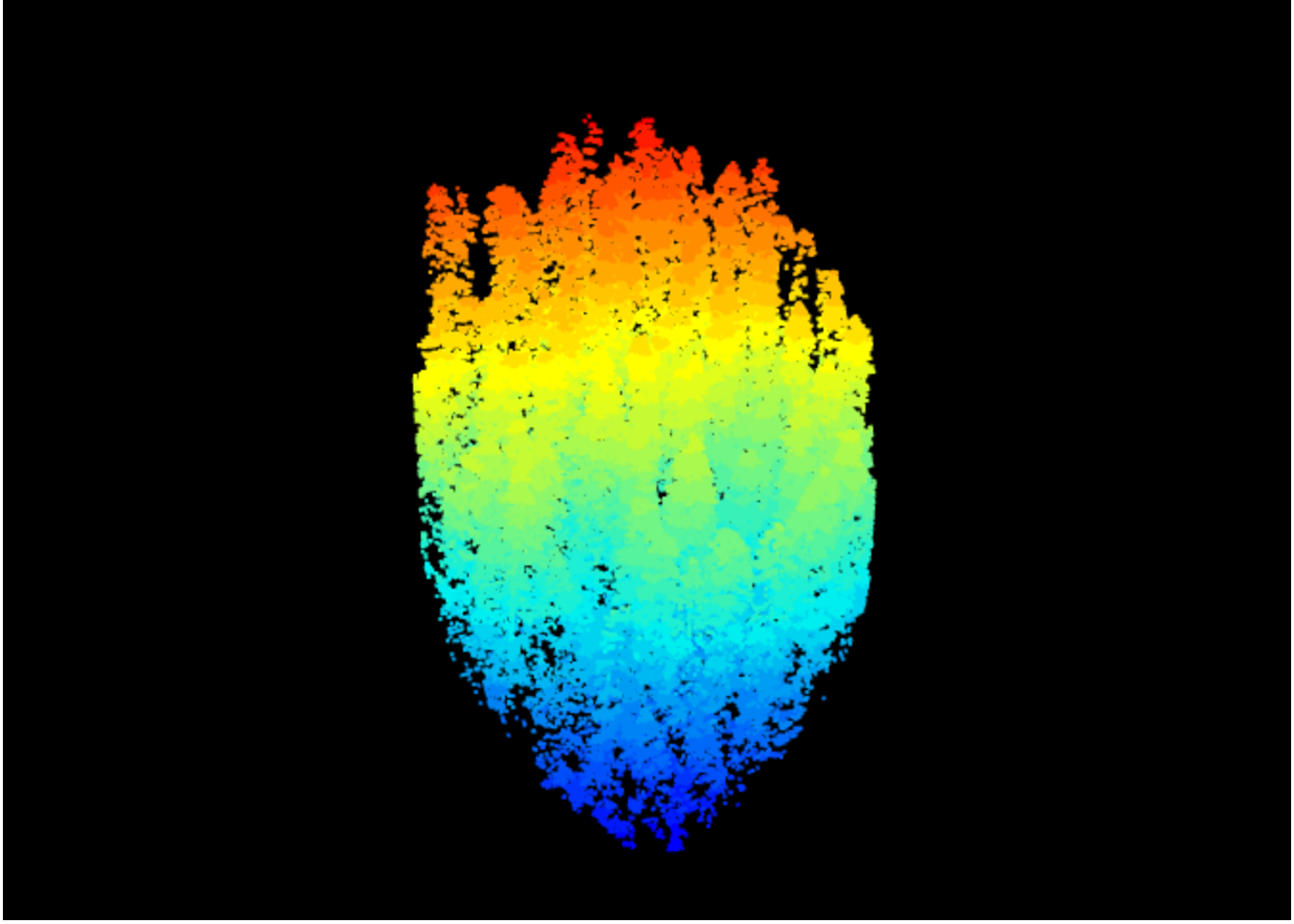



```
## Chunk 1 of 1 (100%): state ✓
```

A cool feature of processing within a las catalog in lidR, is that it gives you a graphic display about what it is processing, and how the processing is doing. In this case we see our clip, and that the processing was “OK”

Take a look at the point cloud within the clip:

```
plot(lasclip)
```



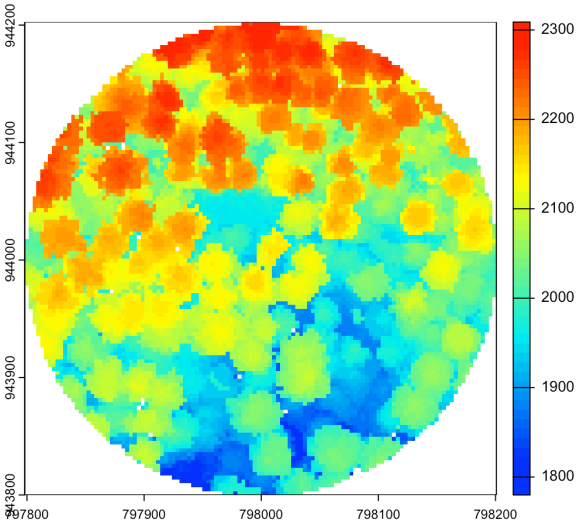
Part 2: Rasterizing Canopy Height Models

Part 2 of this lab was largely converted from the lidR wiki page found here: https://github.com/Jean-Romain/lidR/wiki/Rasterizing-perfect-canopy-height-models (https://github.com/Jean-Romain/lidR/wiki/Rasterizing-perfect-canopy-height-models)

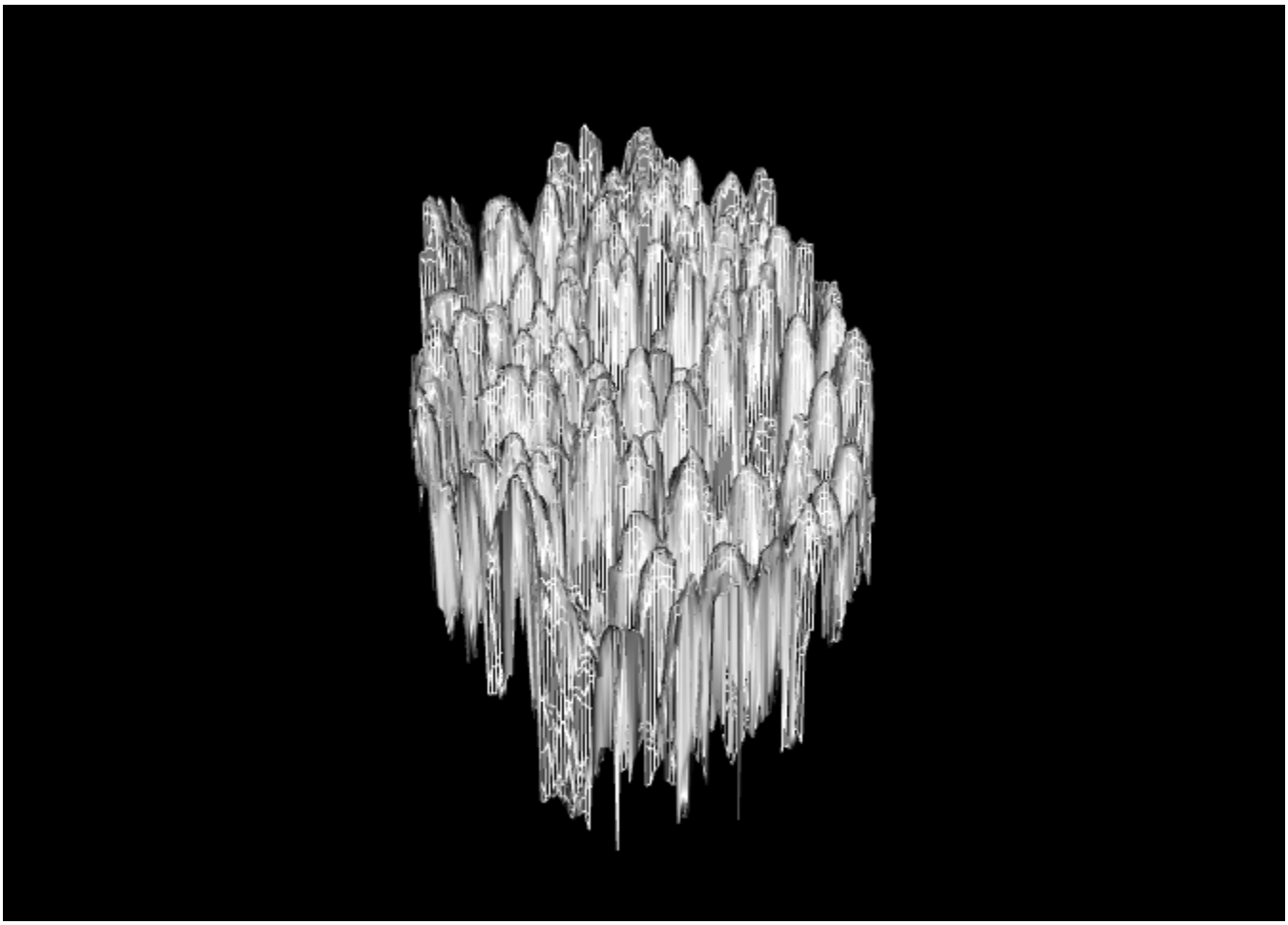
updated lidR book is here: https://r-lidar.github.io/lidRbook/ (https://r-lidar.github.io/lidRbook/)

We have our clip and it is on a significant slope… We are interested in the trees but any height information derived from the point cloud now, will also include height due to elevation. Lets take a look at a raster output of the point cloud using the maximum Z value for each pixel. This is essentially the same thing as outputting a raster in cloud compare. Run:

```
chmHILL <- rasterize_canopy(lasclip, 3.3, p2r())
plot(chmHILL, col = height.colors(50))
```



```
plot_dtm3d(chmHILL)
```



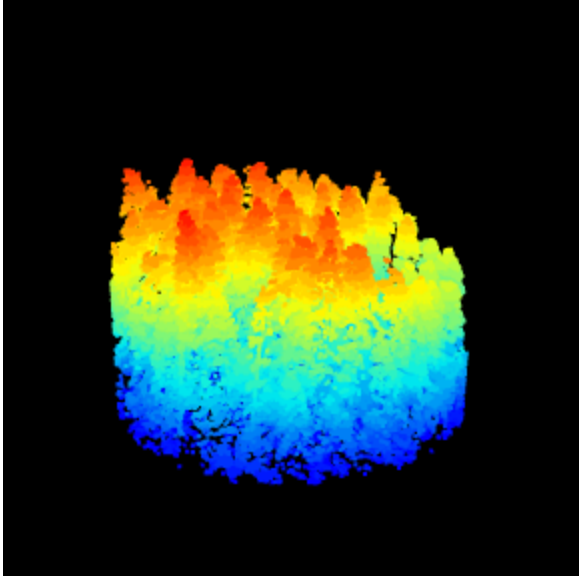
It certainly looks cool, we can absolutely see where there are trees, but we can't get tree height here because we don't know **exactly what the slope of the hill is**, and even if we knew the slope, there are variations in slope so a singular value won't give us a realistic model of the hill. We need to **"normalize"** the point cloud. You have seen this term previously when you have checked out point clouds in `lidR`. So far, all your point clouds have not been normalized. We are going to normalize this clip so we can get information about the trees with the slope values (Z values) "normalized".

We are going to use the function "normalize_height". Take a moment to read the description and scan the help documentation. Run:

```
?normalize_height
```

`normalize_height` uses ground classified points to create a DTM, and then subtracts that value for all points above. `normalize_height` is dependent on the las file having classified ground points, OR, you provide a DTM raster. For this step, we will only provide our clip of lidar data that does have ground points classified and let the function first create a DTM, and then subtract those values from all non-ground points. This is all done in one simple line of code:

```
NORMclip <- normalize_height(lasclip, tin())
plot(NORMclip)
```



Note that we defined 'tin'. normalize_height could also use knnidw or kriging.

QUESTION 2: Include a screenshot of your `plot(NORMclip)`

QUESTION 3: Run rasterize_canopy on your NORMclip. Use all the same values you did in the rasterize_canopy step above, but change lasclip to NORMclip, and change chmHILL to chmNORM. Include 2 screenshots. One of your plot(chmHILL), and one of your plot(chmNORM). You can use any colorramp you want (i.e. col=height.colors(50)). Comment on the similarities and the differences. What does the change in the numbers on the legend bar indicate?

Let us explore `rasterize_canopy` more. Make sure you check out the documentation in `?rasterize_canopy`

```
chmNORM <- rasterize_canopy(NORMclip, 3.3, p2r())
```

Code	Description
`chmNORM`	The name of the output object we are creating
`rasterize_canopy`	The function that we are using that looks at the points with the highest Z value within a defined range.
`NORMclip`	The las data that will be used
`3.28 ,`	The resolution of the output. In this case, 3.23 ft or 1 m
`p2r()`	The algorithm used. This can be p2r, dsmtin, or pitfree

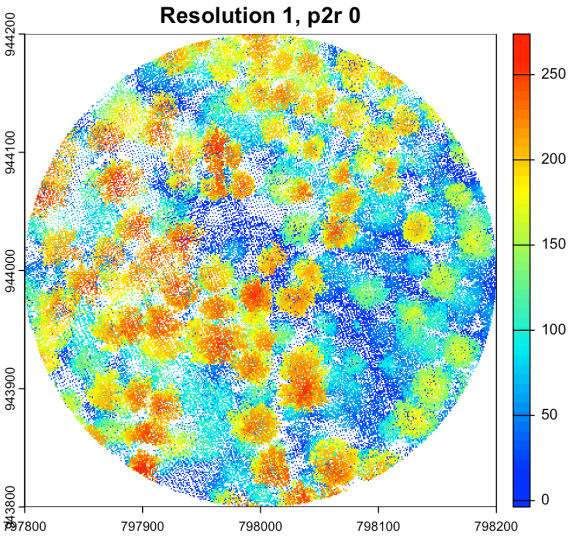
QUESTION 4: Using the ?rasterize_canopy help documentation, what are the descriptions for p2r, dsmtin, and pitfree?

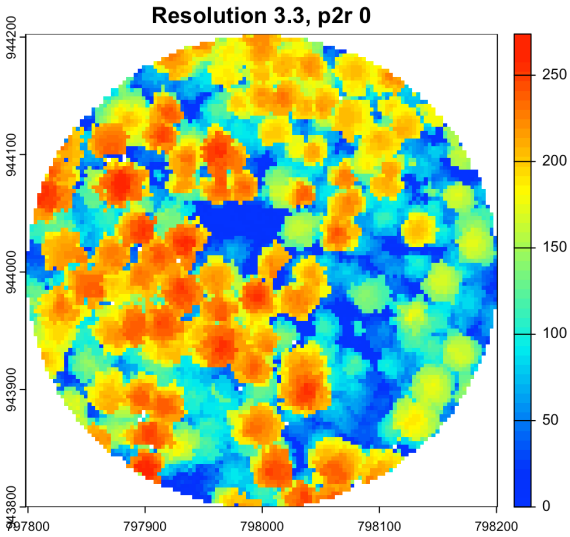
When you create a DEM, cells with no value (empty cells) can cause major issues. There are a few methods that can be used to try and fill those voids.

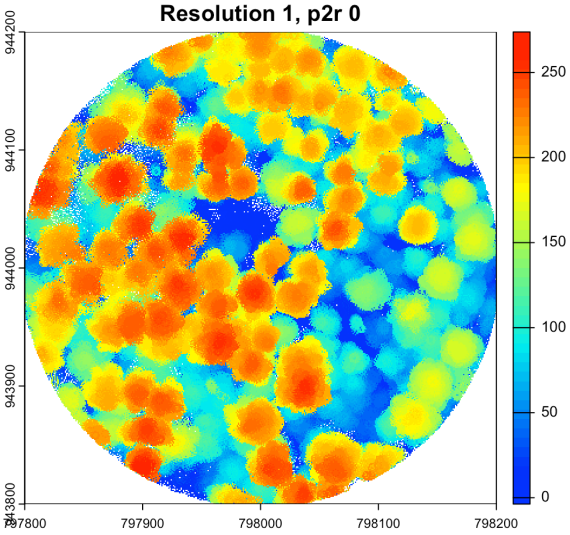
- You can decrease the resolution of the output, but this effectively erases a lot of data that we likely want to retain.
- You can use different algorithms to fill the voids, but the more sophisticated the algorithm, the more computationally intensive it is to run.

Let us start by looking at the output DSM created by decreasing the spatial resolution, and by applying the p2r algorithm. Run:

```
chm1 <- rasterize_canopy(NORMclip, 1, p2r())
plot(chm1, col = height.colors(50), main = "Resolution 1, p2r 0")
#plot_dtm3d(chm1)
chm2 <- rasterize_canopy(NORMclip, 3.3, p2r())
plot(chm2, col = height.colors(50), main = "Resolution 3.3, p2r 0")
#plot_dtm3d(chm2)
chm3 <- rasterize_canopy(NORMclip, 1, p2r(3))
plot(chm3, col = height.colors(50), main = "Resolution 1, p2r 0")
#plot_dtm3d(chm3)
```





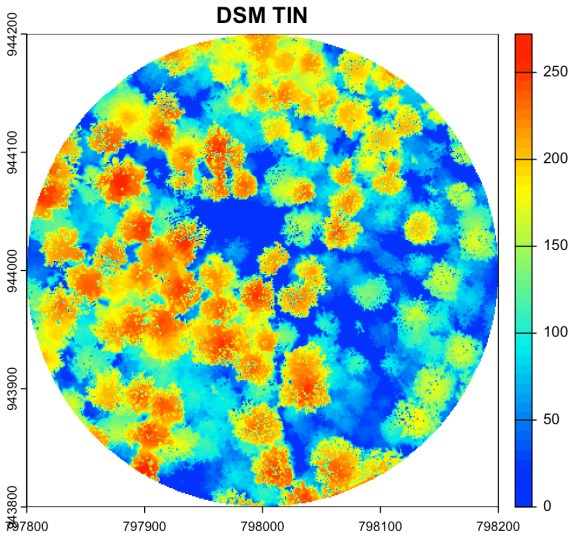


Take a moment to compare the outputs and especially the dtm3d outputs which I have commented out.

QUESTION 5: Include screenshots of the 2D plot outputs of "Res3.28, p2r0" and "Res1,p2r3". How are they similar and how are they different? What is p2r3 doing to fill the holes?

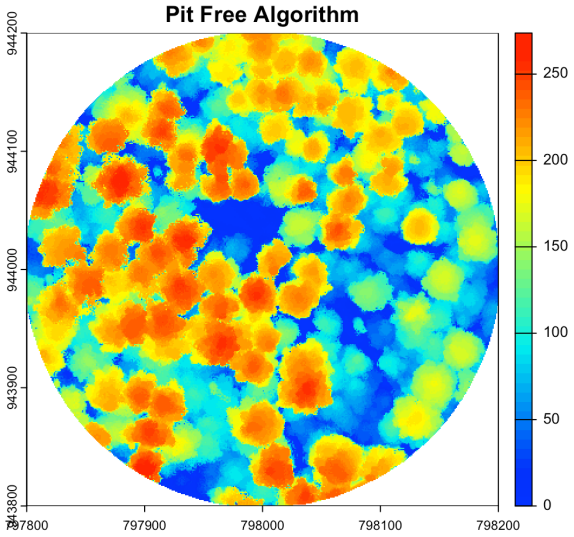
Let us check out the outputs from using `dsmtin` and `pitfree` Run:

```
chm4 <- rasterize_canopy(NORMclip, 1, dsmtin())
plot(chm4, col = height.colors(50), main = "DSM TIN")
```




```
#plot_dtm3d(chm4)

chm5<- rasterize_canopy(NORMclip, 1, pitfree(subcircle = 2))
plot(chm5, col = height.colors(50), main = "Pit Free Algorithm")
```




```
#plot_dtm3d(chm5)
```

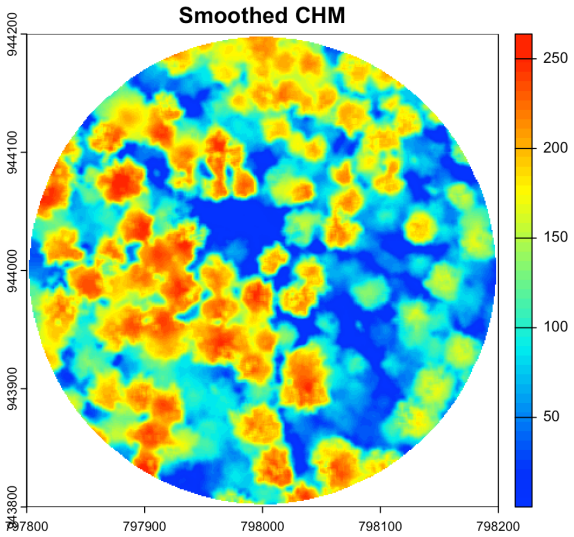
QUESTION 6: Include screenshots of the 3D plot_dtm3d outputs of "dsmtin" and "pitfree". How are they similar and how are they different? They both use Delaunay triangulation to create the DSM, what is pitfree doing to eliminate the spikey "pits" that are present in dsmtin?

The pitfree algorithm will likely generate a consistently better DSM from point cloud data, but the processing power required to run it across an entire acquisition is potentially prohibitively large. It is possible to smooth the spikes from a "spikey" DSM using the focal function from the terra package. Check out: `?terra::focal`

The smoothing happens by running an image kernel across the image. Think of a small moving window with varying sizes, but typically a 3x3pixel window or 5x5pixel window. This is the same thing that filters in image processing programs do. Have your "sharpened" an image you took on your phone? It was likely done using an image kernel. It is beyond the scope of this lab to go in depth on image kernels but more information can be found here: https://setosa.io/ev/image-kernels/ (https://setosa.io/ev/image-kernels/)

Run:

```
chmSmooth <- terra::focal(chm4, w = 5, fun = mean)
plot(chmSmooth, col = height.colors(50), main = "Smoothed CHM")
```



`chm4` should be your DSM produced from `dsmtin`. Make sure to read the ?focal documentation. The matrix values are the size and values for the smoothing window, and `fun` is the function used (i.e. mean, median, min, max). Run a few combinations of matrix sizes and different functions until you find a combination that produces a relatively smooth DSM that captures the locations and shapes of the trees reasonably well, without "pits".

QUESTION 7: Include a screen shot of your output from plot and plot_dtm3d of your chmSmooth. What values did you use for the smoothing? Why?

PART 3 Tree Detection and Segmentation

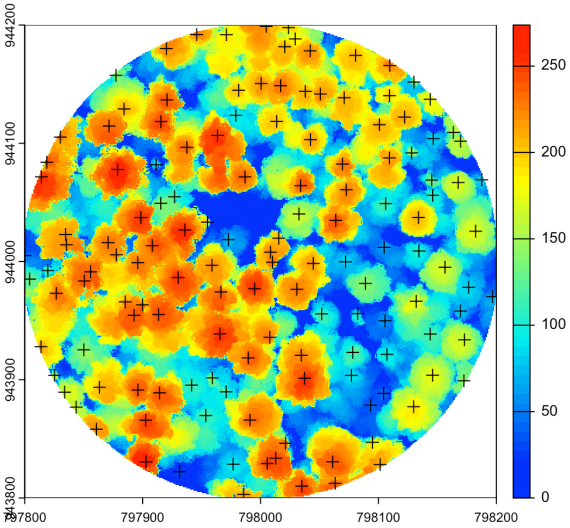
Part 3 of this lab was largely converted from the lidR online book. Refer to the book for a more extensive exploration of the tools.

We will first be detecting individual trees within our point cloud. We will be using locate_trees. Take a moment to read the documentation for the tool `?locate_trees`

Familiarize yourself with the arguments and also the paper that the algorithm `lmf` was derived from. The most important argument in `lmf` is the window size `(ws)`. Create an object `ttops` for the tree tops detected in our original `lasclip`.

```
ttops <- locate_trees(lasclip, lmf(ws = 15))

plot(chm5, col = height.colors(50))
plot(sf::st_geometry(ttops), add = TRUE, pch = 3)
```



The line of code `sf::st_geometery` is just calling the sf package to overly the `ttops` location information on our `chm5` canopy height model. `pch=3` is just defining the symbol used.

You can also display the `ttops` in 3D on the original lidar clip.

```
Tops <- plot(lasclip, bg = "white", size = 2)
add_treetops3d(Tops, ttops)
```

As you can imagine, the window size `ws` can impact the results dramatically. Play around with a few different `ws` values and remember that our point cloud units are feet.

QUESTION 8: Include a screen shot of the 2D output (like the upper left image) using a different chm and/or different ws value for locate trees. Find a combination that you feel is the best and report the values you used.

That is all we are going to cover for individual tree detection. Tree segmentation is a bit different.

Will be using the segment_trees and crown_metrics. As always, check out the documentation for both tools - `?segment_trees - ?crown_metrics`

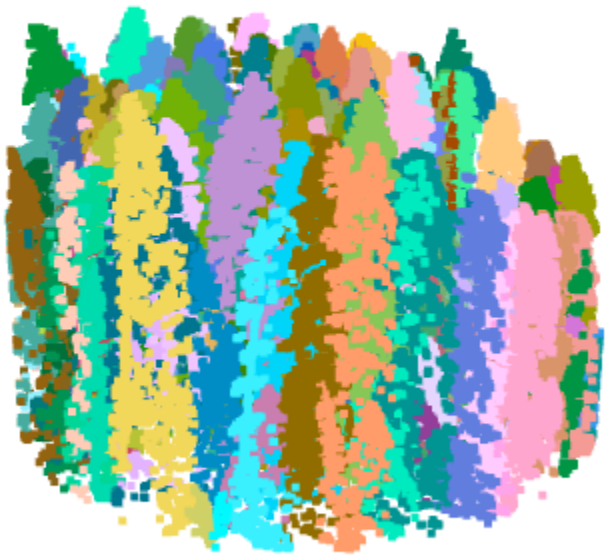
When looking through the ?segment_trees documentation, note that there are many algorithms that can be used for tree segmentation.

QUESTION 9: Read the descriptions for all the algorithm options in ?segment_trees. 4 of the options are named after an author and year. What are those papers? Copying and pasting the citation from RStudio is acceptable.

Feel free to try out all of the different segmentation algorithms. We will mostly be focused on `li2012` and `dalponte2016` but there isn't a single best algorithm to use. Each forest and tree type will likely preform differently with different segmentations. Let's perform a segmentation on our `NORMclip`.

Also check out the documentation for the `filter_poi` tool. This is super helpful for filtering points in the dataset - `?filter_poi`

```
lasT <- segment_trees(NORMclip, li2012(R = 15, hmin = 6, speed_up = 30))
lasT <- filter_poi(lasT, !is.na(treeID))
plot(lasT, bg = "white", size = 4, color = "treeID")
```



Make sure you understand what the inputs for the `li2012` algorithm are. Also remember that the units for the examples in the documentation are assuming that your units for the point cloud are meters. Our units are feet so multiplying any value given that refers to a unit of measurement you should triple.

The `filter_poi` line is filtering points and removing all points that don't have a `treeID` number associated with them.

QUESTION 10: Experiment with the inputs for li2012. You can add additional values beyond just R and speed_up. You should be able to improve the segmentation beyond the values given. Take a screen shot of the segmentation you prefer and report that values you used.

There is now a list of trees in your point cloud. You can plot individual trees from your point cloud:

```
tree24 <- filter_poi(lasT, treeID == 24)
plot(tree24, size = 5, bg="white")
```

QUESTION 11: Try several tree numbers until you find a good one. Include a screenshot of your individual tree. You can color it however you like.

Now that you have done all this processing on a las file, you will likely want to save the file so you can open it in a better visualizing program such as CloudCompare. You write your outputs like this:

```
writeLAS(lasT, file = "Lab 4/trees.las")
```

Check your Lab4 folder and you should now have a new las file in there. With points that have a treeID as an additional scalar field. Take it into CloudCompare to check it out.

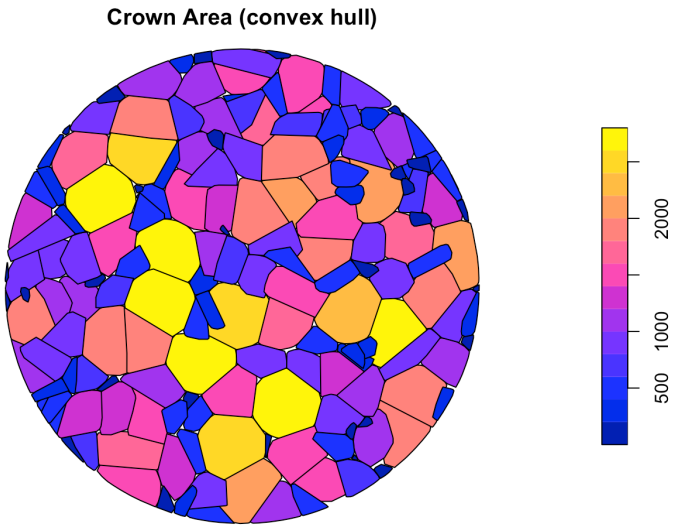
There is so much we could do with segment_trees and I encourage you to continue playing around with the inputs and reference the lidR book. (https://r-lidar.github.io/lidRbook/index.html)

We can also create 2D maps of the crowns using `crown_metrics.` Using your `lasT` lidar data that you have spent some time on refining the tree segmentation, you can find statistics about your trees such as height (Z) and crown area:

```
crowns <- crown_metrics(lasT, func = .stdtreemetrics, geom = "convex")
summary(crowns)
```

```
##      treeID             Z             npoints       convhull_area
##  Min.   :  1.00   Min.   :  8.87   Min.   :  16.0   Min.   :  12.64
##  1st Qu.: 42.75   1st Qu.:130.50   1st Qu.: 318.5   1st Qu.: 319.95
##  Median : 84.50   Median :201.63   Median : 748.0   Median : 814.56
##  Mean   : 84.50   Mean   :178.72   Mean   :1182.3   Mean   : 916.70
##  3rd Qu.:126.25   3rd Qu.:228.75   3rd Qu.:1689.2   3rd Qu.:1370.36
##  Max.   :168.00   Max.   :273.86   Max.   :6972.0   Max.   :2778.27
##           geometry
##  POLYGON      :168
##  epsg:2927    :  0
##  +proj=lcc ...:  0
##
##
##
```

```
plot(crowns["convhull_area"], main = "Crown Area (convex hull)")
```



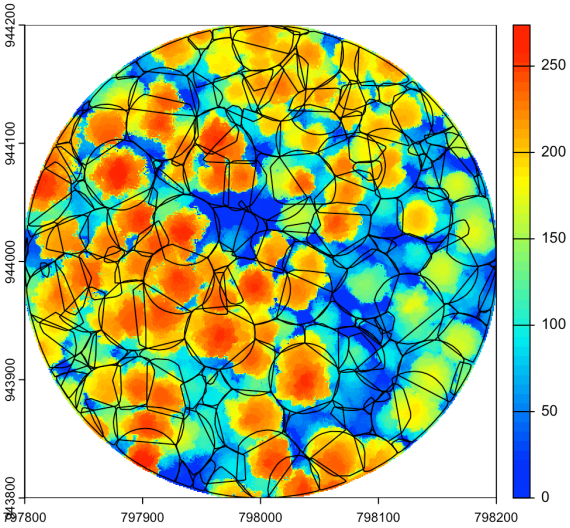
QUESTION 12: Include a screenshot of your Crown area and stats. They can be similar to mine, but they should be different.

QUESTION 13: Errors in tree identification can be classified as errors of omission (trees that exist but were not identified) and errors of commission (trees that were "made up," usually because one tree is split into several portions. Do you think your models are more likely to have errors of omission or commission? Do you think smoothing of the canopy height models effects these errors?

Ultimately, there is not one correct way to perform a tree segmentation. Tree density, height, and uniformity may all require a different approach to accurately estimate number of trees. The method used to produce the `DSM` also has a massive impact on how well trees are detected.

You can plot the hulls of your crowns with your chm:

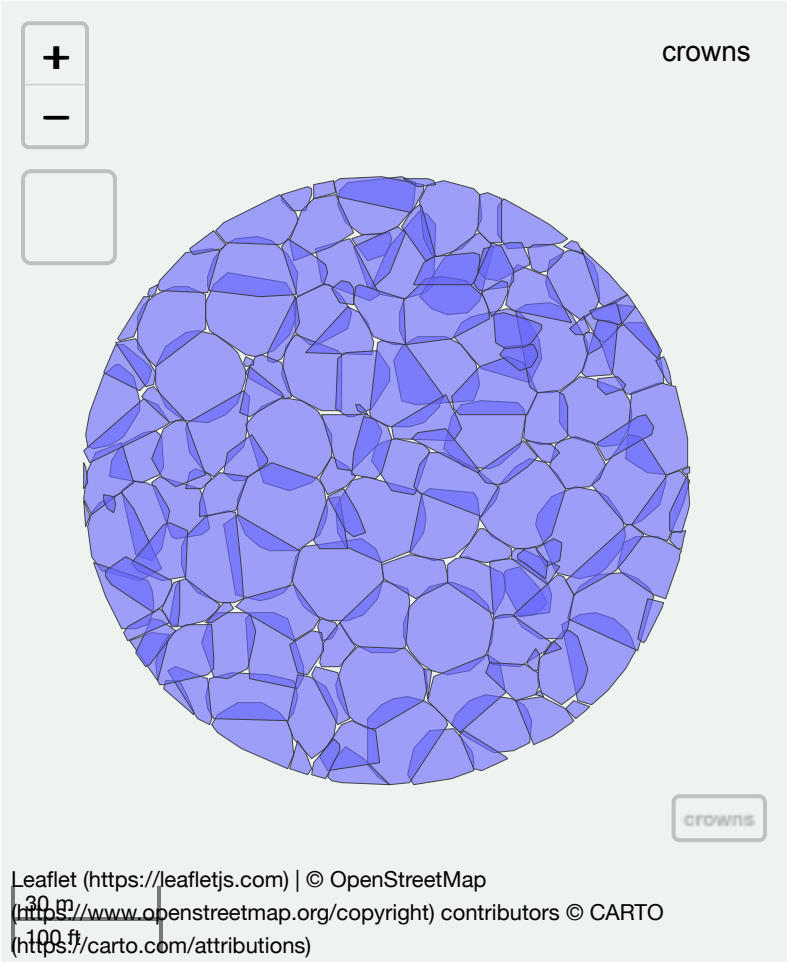
```
plot(chm5, col = height.colors(50))
plot(sf::st_geometry(crowns), add = TRUE)
```



You can also plot your hulls on the map!

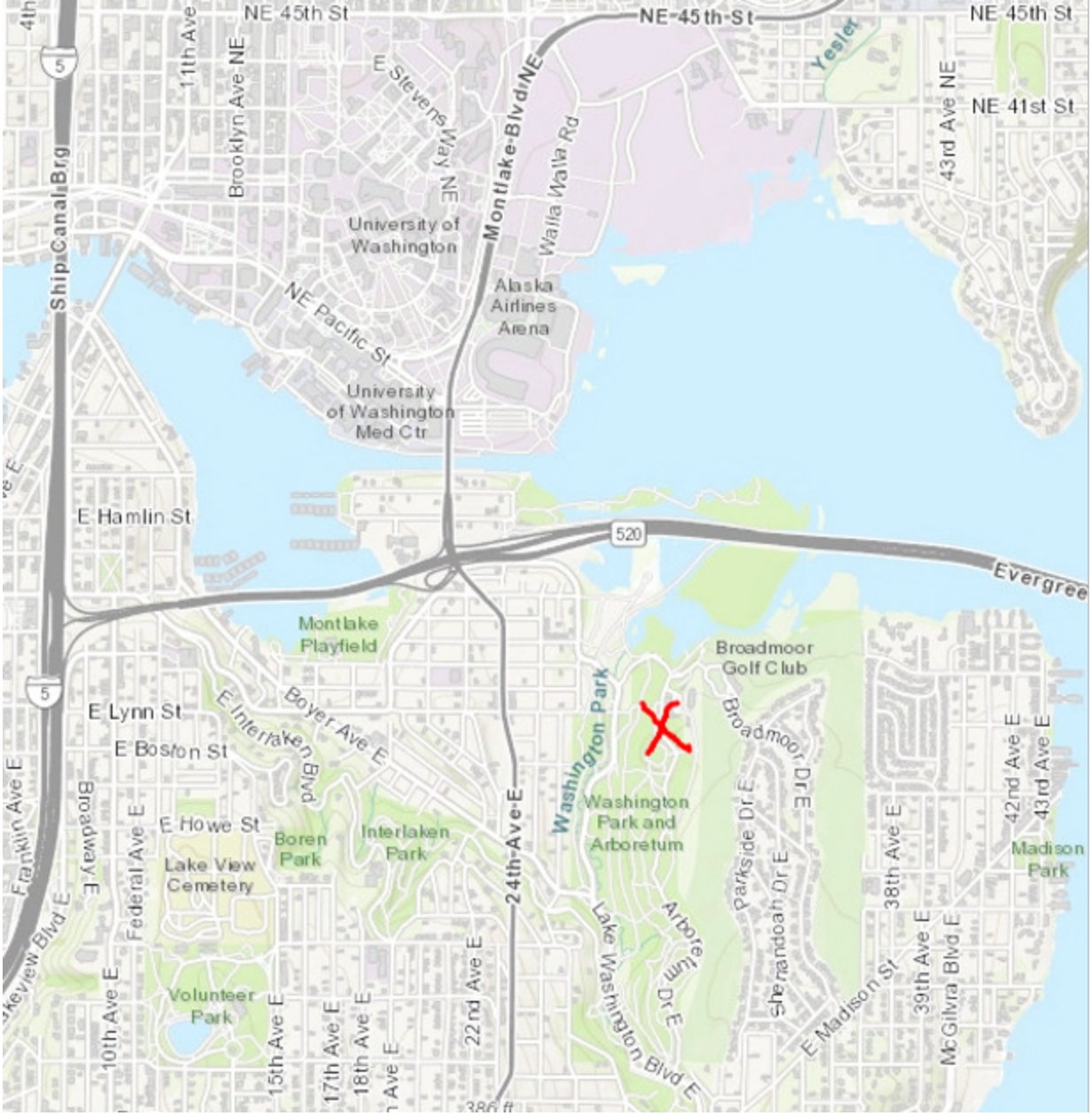
A lot of refinement needs to happen for the results to be reliable, but this lab is intended to point you in the right direction to apply individual tree detection across an area.

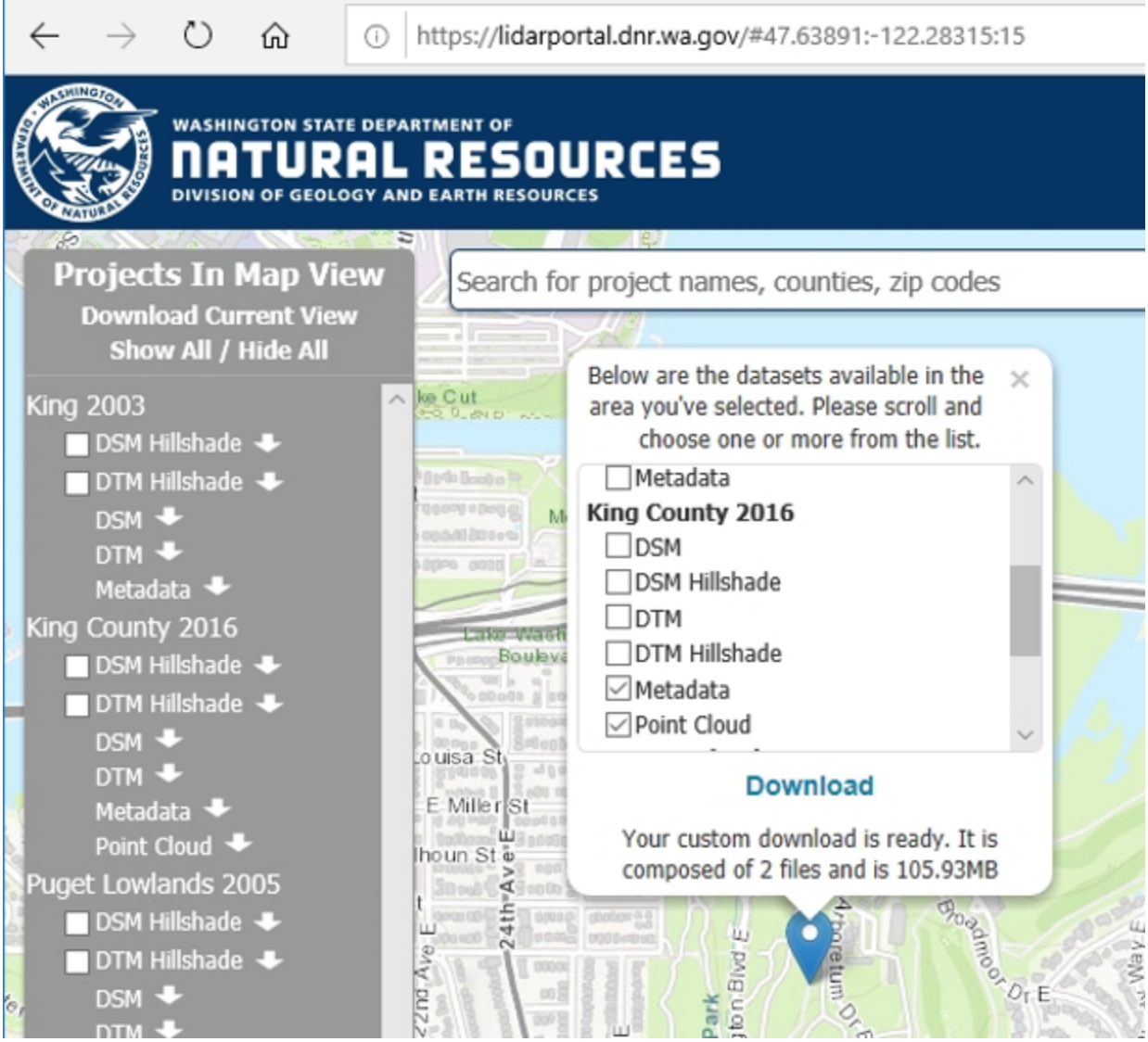
```
mapview(crowns)
```



PART 4 Tree map of the Arboretum

Go to the Washington DNR lidar portal and download the King County 2016 laz tile for the northern portion of the Arboretum. You should download the Metadata to get information about the dataset.


NE 45th St
NE 45th St
NE 45th St
NE 41st St
11th Ave
Brooklyn Ave NE
E Stevens Way NE
Montlake Blvd NE
Walla Walla Rd
Yesler
43rd Ave NE
Ship Canal Brg
University of Washington
Alaska Airlines Arena
NE Pacific St
University of Washington Med Ctr
E Hamlin St
520
Evergree
Montlake Playfield
Broadmoor Golf Club
E Lynn St
E Boston St
E Interlaken Blvd
Boyer Ave E
Washington Park
Broadmoor Dr E
Washington Park and Arboretum
E Howe St
Boren Park
Interlaken Park
Lake View Cemetery
24th Ave E
Parkside Dr E
Arboretum Dr E
Lake Washington Blvd E
Sheridan Dr E
E Madison St
38th Ave E
39th Ave E
42nd Ave E
43rd Ave E
Madison Park
McGilvra Blvd E
Broadway E
Federal Ave E
Franklin Ave E
Volunteer Park
10th Ave E
15th Ave E
17th Ave E
18th Ave E
22nd Ave E
380 ft



The tile you have should be named “q47122f3417_rp.laz”

You are going to run the following code. For each line of code you run, you are going to write a short description of what that line does in a `#comment` .

A single sentence will be enough, but make sure to say what the input values indicate. Using the code we have already run, here is an example:

```
Arborlas <- readLAS("Lab 4/king_county_2016/laz/q47122f3417_rp.laz") # This read in the q47122f34
17_rp.laz file using the readLAS function from lidR
```

For **QUESTION 14: Comment each line of code down below**

```
ArborClip <- clip_rectangle(Arborlas, 1197000, 845300, 1198200, 846700)
ArborNORM <- normalize_height(ArborClip, tin())
st_crs(ArborNORM) <- 2927
ArborCHM <- rasterize_canopy(ArborNORM, 1, p2r(3))
ArborT <- segment_trees(ArborNORM, li2012(R = 15, hmin = 6, speed_up = 30))
ArborT <- filter_poi(ArborT, !is.na("treeID"))
Arborcrowns <- crown_metrics(Arbor, .stdtreemetrics, geom = "convex")
mapview(Arborcrowns)
plot(ArborCHM, col = height.colors(50))
plot(sf::st_geometry(Arborcrowns), add = T)
writeLAS(ArborT, file = "Lab 4/ArborCrowns.las")
```

For **QUESTION 15: Include screenshots of your outputs from (3 screenshots total)**

You just created a tree map of a portion of the arboretum! You could use both tiles that cover the arboretum to make a complete tree map.

You will likely notice that not all trees have a polygon, and not all polygons are trees. What the algorithm is actually doing is just identifying “tall” objects. We could put some effort into removing buildings in the point cloud if that is deemed necessary.

Graduate Students

You cited several papers in question 9. Write a short paper summary on one of them. One or two paragraphs will suffice.