

## Objective:

When the trees are too close to each other, it makes it difficult for the larger trees to survive since it has to share its resources to nearby trees,

So we need to cut the trees for other trees long growth. We use the data to print out the data on a map and then after clustering we identify trees which can be cut down. This is an example of unsupervised learning. The process of cutting down less significant trees is called **Thinning**

## Thinning criteria:

Unless you need to edit, it's safer to stay in Protected View. Enable Editing

### Implementation Guide (in order of priority)

#### Leave Tree Mark (ponderosa pine $\geq 6"$ dbh)

**General:**

- Retain all yellow pine, Gambel oak, and juniper, regardless of form, health, or vigor. This supersedes all other specifications.
- Retain ponderosa  $>18"$  dbh with existing cavities, dead tops and lightning scars as wildlife trees
- Retain inaccessible trees and trees that cannot be cut without causing significant damage to residual trees (bole damage to trees  $>6"$  dbh/drc or top breakage to trees  $>9"$  dbh/drc).
- Tree groups should be created across 50% of the stand area. Interspaces and regeneration openings should be created across the remaining 50% of the stand area.
- Retain a variable BA that averages  $\sim 50 \text{ ft}^2/\text{ac}$  at the stand-level (almost all ponderosa), including any deferrals.

**Special Considerations:**

- Use directional mark within 100' of FR 231 and 536.

#### Regeneration Openings (including VSS 1-2 groups):

- Create irregularly shaped regeneration openings across 10% of the unit.
- Openings shall be placed in areas containing no infected yellow pines that will be surrounded by little to no mistletoe infection after opening is created. Openings may contain Gambel oak/juniper. Priority for opening placement shall be as follows:
  1. In areas with moderate to abundant ( $>10 \text{ TPA}$ ) desirable young ponderosa  $<6"$  dbh.
  2. In areas overstocked with ponderosa from the most prevalent size classes (9-14" dbh).
  3. In small pockets of mistletoe infection ( $<1 \text{ acre}$ ) where all visibly infected trees plus a 30-40 foot buffer (to capture latent infection) can be removed.
- Opening size shall generally range from 0.3 to 1.0 acre, but may be as large as 2 acres. The maximum width for openings is 200 feet.
- Cut all ponderosa  $>6"$  dbh (except yellow pine) within regeneration openings with the following exceptions:
  1. Retain desirable young ponderosa 6-9" dbh.
  2. In openings  $>1 \text{ acre}$  not containing an abundance of desirable young ponderosa  $<9"$  dbh ( $>50 \text{ TPA}$ ), retain 3-5 reserve trees (largest, most desirable trees including yellow pine).

#### Tree Groups / Interspaces (in surrounding matrix):

- Thin ponderosa  $>6"$  dbh (except yellow pine), leaving trees in irregularly shaped groups.
- Concentrate groups in areas with (a) an abundance of desirable and acceptable trees, (b) an abundance of trees  $>18"$  dbh, (c) a prevalence of deep crowns and high vertical structural diversity, and (d) large logs  $>18"$  diameter. Pre-settlement evidences may be used to help guide group placement/size.
- Vary group size from 0.01 ( $\sim 2$  trees) to 1 acre, with approximately the following distribution:  
(a) 10% 0.01 to 0.1 acre (b) 30% 0.1-0.25 acre (c) 30% 0.25-0.5 acre (d) 30% 0.5-1.0 acre
- Within groups, thin to the average densities shown in Table 4, generally retaining desirable and acceptable trees (Table 5) from across the range of available size classes. Additional non-desirable trees may be left if needed to meet density targets. Strive for irregular spacing within groups, including clumps of trees with interlocking crowns separated by small canopy gaps up to the average width of the adjacent tree crowns.
- Leave  $\sim 10\%$  of groups unthinned, focusing in areas with deep crowns and high vertical structural diversity.
- Distance between groups, measured dripline to dripline, shall average 60-100 feet, but may be as small as 40 feet between smaller groups and up to 120 feet between larger groups. The distance between groups infected

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### Dataset details:

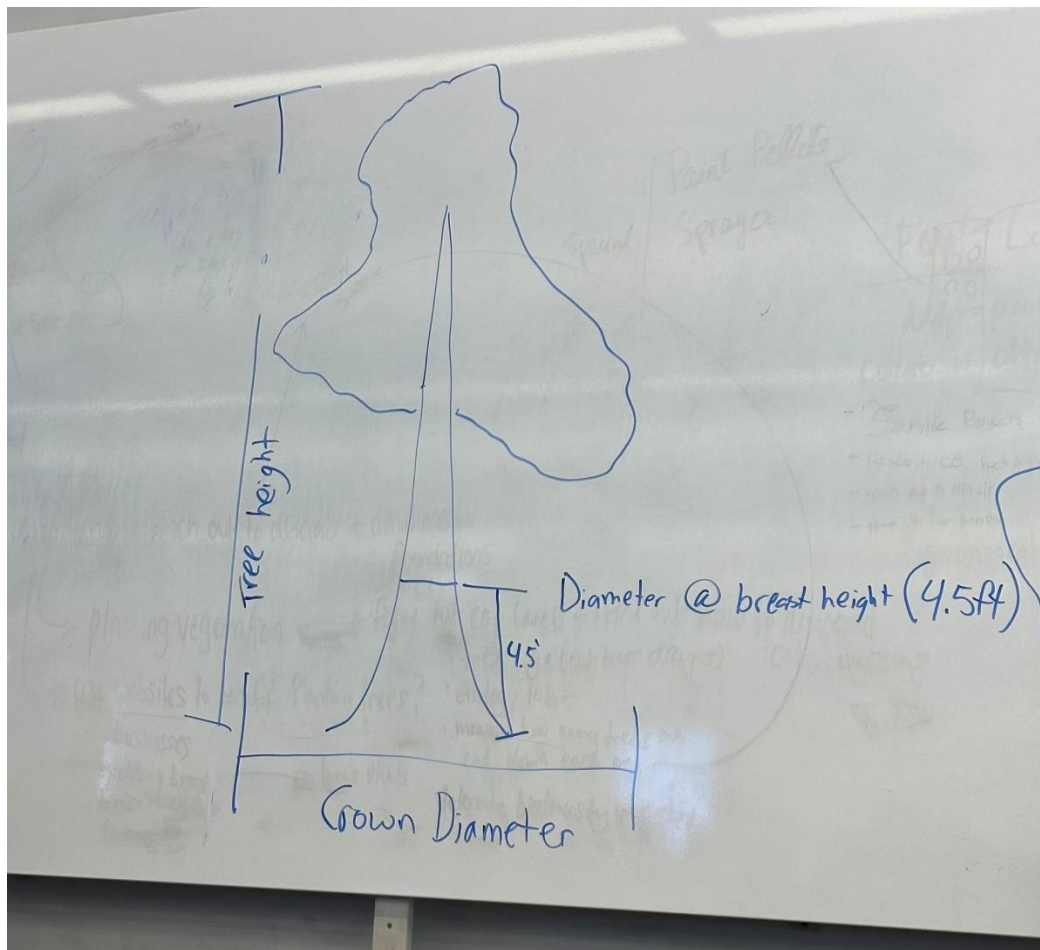
TreePosX, Y, Z ( gives the position of the trees)

DBH(tree height in metre-diameter breast height)

CrownDia(how wide is the tree essentially(like the spread of the tree)) this is measured between South to north and east to west.

CrownVol (from top of the tree to bottom of the tree )

Treeld(to identify each tree)



## Clustering algorithms used:

### K-means

*Here it sorts the trees within each cluster based on a combination of factors specified by the features\_for\_removal variable. Then, it selects a percentage of trees from the beginning of the sorted list for removal.*

