MUCP Algorithms

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Algorithm break down:

1. Compartment prioritization
2. Density calculation
3. Person days
4. Treatment costs
5. Flow calculation

Major differences between previous tool and opensource tool algorithms:

* Prioritization, density and flow should be the same as previous tool.
* Person days calculation has changed. Previously there was no slope dependence, now there is. Previous tool calculated something different than the person days Excel spreadsheet provided with the person days calculation.
* Costing algorithm uses the prioritization, density and person days in the base costing calculation. Due to the person days calculation correction, the costing (budgeting) will differ from the previous tool. Depending on the parameters for each compartment, the cost may be higher or lower than the outputs of the previous tool.
* User can now add their own user defined prioritization categories and not limited to the tools built in categories.
* User can calculate budgets for more than the 20 year limit.
* Herbicides and cost recovery not implemented yet (same as previous tool)
* A few column names, units and terms in the previous tool were corrected and implemented in the opensource tool.
* Opensource tool has opensource code and written in Python. There is a code base for the algorithms (mostly using Pandas package) and another code base for the viewer (Django package + other auxiliary packages).
* Opensource tool is in beta, there may be some bugs yet to fix, determined as users use the tool.

Pre-processing of gis mapping shapefile:

1. If nbal, miu and compartment column have same id’s, then coalesce into one entry by summing areas.
2. Note that if there is nbal, then you always have an miu, otherwise give warning to user.
3. Note that if there is nbal, but no miu in compartment, give warning to user

Take care of the treatment frequency, it is used in the density, person days, flow and costing algorithms.

# Compartment prioritization

Notes:

* Weights in prioritization table does not need to sum to 1. Can be more or less than 1, but better to have more than 1, maybe a user warning if less than 1.

Steps:

* Loop through column id in the compartment prioritization csv file. Eg. You have compartment id H\_123
* For each column heading do the following. E.g. headers in prioritization file are elevation and aggression.
* Match the column header to the reference table in the support priority fields table. Get the representation of the variable name within the tool. Eg. Elevation is elevation and aggression is aggressive in the table.
* Match the prioritization variable name to the support prioritization model values the user selected in gui inputs file. You now have the user weighting priority values [they should always be 0 and 1 for each field]. Eg. The user set aggressive to 0.2 and elevation to 0.9.
* Get the category for the prioritization variable and then determine the prioritization value by looking through the table values and seeing which range the value for the prioritization column header value lies in. eg. User has 50 for Aggression and 3 for Elevation in prioritization file. And category ranges below for elevation and Aggressive:

|  |  |  |  |
| --- | --- | --- | --- |
| elevation | | Aggressive | |
| Range | priority | range | priority |
| 0-4 | 1 | 0-30 | 1 |
| 5-10 | 2 | 31-60 | 2 |

Then priorities are 1 for elevation and 2 for Aggressive.

* Multiply the priority with the weighting. Eg. Elevation is 1\*0.9 = 0.9, Aggressive is 2\*0.2 = 0.4
* Sum up the resulting answers above. This gives you the prioritization for the compartment. Eg 0.9 + 0.4 = 1.3 🡨 final prioritization for compartment.

# Density

The following variables are used in the density calculation:

* Treatment frequency
* Idenscode column in nbal linked species excel file
* Age column in nbal linked species excel file
* Idenscode column in miu linked species excel file
* Age column in miu linked species excel file
* Initial reduction density in species tab
* Follow up reduction density in species tab
* Budget year

Algorithm, see the table on next page.

1. Loop through the miu linked species file
2. Group by miu compartment id

For example:

|  |  |  |  |
| --- | --- | --- | --- |
| M\_H60B400169 | Pinus pinaster | 30.000000 | Adult |
| M\_H60B400169 | Hakea sericea | 20.000000 | Young |
| M\_H60B400169 | Acacia longifolia | 5.000000 | Young |

|  |  |  |  |
| --- | --- | --- | --- |
| M\_H60B400176 | Pinus pinaster | 35.000000 | Young |
| M\_H60B400176 | Hakea sericea | 35.000000 | Young |
| M\_H60B400176 | Acacia longifolia | 20.000000 | Young |

1. For each entry in each group do the following:
   1. Through the gis mapping file, Check if the id matches an nbal id
      1. Check if the nbal id are the same and if the other information (idens code, species, age) entries are in the nbal linked species file
      2. If the entries are exactly the same do the following: (NOTE: for nbal, we do not use the initial density reduction, only the follow up density reduction factor). If it is year 1, use the idenscode in the nbal linked species file, if it is year 2 and beyond, use the previous calculated density values as reduction is applied on previous density in the nbal.
         1. For each entry get its current density fraction i.e. (100 – follow-up density reduction factor)/100
         2. Take the individual entry idenscode (if year 1, otherwise use the previously calculated density for year 2, 3, 4… etc) and multiply it with the density fraction calculated above
         3. This gives you the individual contribution for density for that compartment. Sum the individual contributions to get the density for that compartment
      3. If the idenscodes are different do the following:
         1. For each entry get its current density fraction and divide it by 2 i.e. (100 – follow-up density reduction factor)/100/2
         2. Take the individual entry idenscode in the miu linked species file (not the nbal linked species file!) (if year 1, otherwise use the previously calculated density for year 2, 3, 4… etc) and multiply it with the modified density fraction calculated above
         3. This gives you the individual contribution for density for that compartment. Sum the individual contributions to get the density for that compartment
      4. If the ages are different do the following (e.g. entry in miu is Adult while in nbal it is Young)
         1. For each entry get its current density fraction and multiply it by 2 i.e. (100 – follow-up density reduction factor)/100\*2
         2. Take the individual entry idenscode (if year 1, otherwise use the previously calculated density for year 2, 3, 4… etc) and multiply it with the density fraction calculated above
         3. This gives you the individual contribution for density for that compartment. Sum the individual contributions to get the density for that compartment
      5. If idenscodes and ages are different do the following:
         1. For each entry get its current density fraction and multiply it by 2 i.e. (100 – follow-up density reduction factor)/100\*2
         2. Take the individual entry idenscodes for the miu and nbal files and add them together to get a total idenscode, then using this summed idenscode (if year 1, otherwise use the previously calculated density for year 2, 3, 4… etc), multiply it with the density fraction calculated above
         3. This gives you the individual contribution for density for that compartment. Sum the individual contributions to get the density for that compartment
   2. If doesn’t match an nbal id and it is only miu do the following:
      1. If it is year 1 do the following:
         1. For each entry get its current density fraction i.e. (100 – initial density reduction factor)/100
         2. Take the individual entry idenscode (only for year 1) and multiply it with the density fraction calculated above
         3. This gives you the individual contribution for density for that compartment. Sum the individual contributions to get the density for that compartment
      2. For year 2, 3, 4… etc
         1. For each entry get its current density fraction i.e. (100 – follow-up density reduction factor)/100
         2. Take the previous year calculated density and multiply it with the density fraction calculated above
         3. This gives you the individual contribution for density for that compartment. Sum the individual contributions to get the density for that compartment
   3. If it is compartment only in gis file, assign a 0 density
2. To incorporate the treatment frequency, take 12 and divide it by the treatment frequency to get the number of times of treatment in a year: for example a treat frequency of 3 and 24 months respectively gives 12/3= 4 and 12/24 = 0.5. Then do the following:
   1. If the number of times of treatment in year is bigger than 0:
      1. Repeat the density reduction algorithm above the same number of times + 1. This value for density is now the density for the next year 2, 3, 4, 5 … etc, e.g. repeat algorithm 4+1 = 5th time, take the density as the density reduction for year 1, repeat for 5 (according to how you count, it might be 4 times not 5) times again to get the density for year 2 etc….
   2. If the number of times of treatment in year is less than 0:
      1. Invert the number of treatments in a year , i.e. 1/number of treatments = 1/0.5 = 2 i.e. every two years (You can round the value for the number of years if there is a decimal)
      2. Do the density reduction algorithm above once and apply the same value for inverted number of treatments i.e. 2 years. i.e. year 1 will have the same value as year 2, density reduction is done again and year 3 and year 4 have the same value, etc…
3. Repeat the above until 20 year budget is done

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | Initial reduction factor | Follow up reduction factor | treaT FREQ | |  |  |  |  |  |  |  |  |
| M\_H60B400169 | Pinus pinaster | 30.000000 | Adult | 50 | 10 | 12 | 15.000000 | 27.500000 | 13.5 | 26 | 12.15 | 24.65 |  |  |  |
| M\_H60B400169 | Hakea sericea | 20.000000 | Young | 50 | 0 | 1 | 10.000000 |  | 10 |  | 10 |  |  |  |  |
| M\_H60B400169 | Acacia longifolia | 5.000000 | Young | 50 | 0 |  | 2.500000 |  | 2.5 |  | 2.5 |  |  |  |  |
| M\_H60B400170 | Pinus pinaster | 25.000000 | Adult | 50 | 10 |  | 12.500000 | 20.000000 | 11.25 | 18.75 | 10.125 | 17.625 |  |  |  |
| M\_H60B400170 | Acacia longifolia | 5.000000 | Young | 50 | 0 |  | 2.500000 |  | 2.5 |  | 2.5 |  |  |  |  |
| M\_H60B400170 | Hakea sericea | 10.000000 | Young | 50 | 0 |  | 5.000000 |  | 5 |  | 5 |  |  |  |  |
| M\_H60B400176 | Pinus pinaster | 35.000000 | Young | 50 | 10 |  | 17.500000 | 45.000000 | 15.75 | 43.25 | 14.175 | 41.675 |  |  |  |
| M\_H60B400176 | Hakea sericea | 35.000000 | Young | 50 | 0 |  | 17.500000 |  | 17.5 |  | 17.5 |  |  |  |  |
| M\_H60B400176 | Acacia longifolia | 20.000000 | Young | 50 | 0 |  | 10.000000 |  | 10 |  | 10 |  |  |  |  |
| M\_H60B400177 | Pinus pinaster | 10.000000 | Young | 50 | 10 |  | 9.000000 | 19.000000 | 8.1 | 18.1 | 7.29 | 17.29 | 6.561 | 16.561 |  |
| M\_H60B400177 | Acacia longifolia | 5.000000 | Young | 50 | 0 |  | 5.000000 |  | 5 |  | 5 |  | 5 |  |  |
| M\_H60B400177 | Hakea sericea | 5.000000 | Young | 50 | 0 |  | 5.000000 |  | 5 |  | 5 |  | 5 |  |  |
| M\_H60B400178 | Pinus pinaster | 50.000000 | Young | 50 | 10 |  | 25.000000 | 42.500000 | 22.5 | 40 | 20.25 | 37.75 |  |  |  |
| M\_H60B400178 | Acacia longifolia | 15.000000 | Young | 50 | 0 |  | 7.500000 |  | 7.5 |  | 7.5 |  |  |  |  |
| M\_H60B400178 | Hakea sericea | 20.000000 | Young | 50 | 0 |  | 10.000000 |  | 10 |  | 10 |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  | 18 | 28 | 16.2 | 26.2 |  |  |  |  |  |  |  |  |
|  |  |  |  | 5.000000 |  | 5.000000 |  |  |  |  |  |  |  |  |  |
|  |  |  |  | 5.000000 |  | 5.000000 |  |  |  |  |  |  |  |  |  |

If nbal age and miu age differs then double that density

*Loop through the compartments ids in gis file*

For each compartment determine the following

Cases:

1. Compartment only

Unknown

1. Miu (no nbal)

If there is a compartment id and a miu id (no nbal id) then do the following.

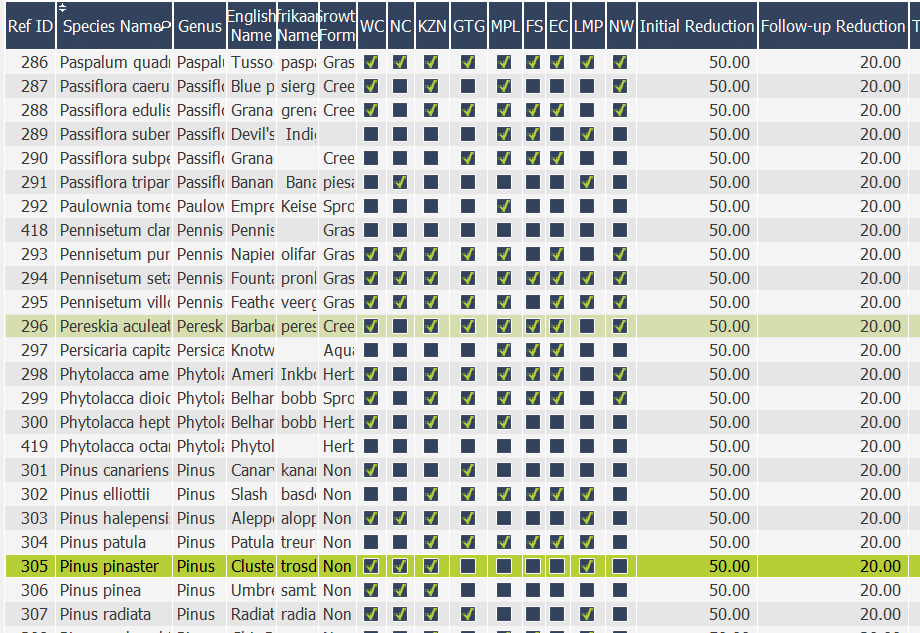
e.g. C\_H60B400180, M\_H60B400180

Go to the miu linked species file and filter on the miu id

e. g list as in fig here 

Get the list of invasive species with its associated idenscode

Go to the support species and filter on each invasive species and obtain the initial reduction and follow-up reduction values

e.g 50 and 20 as in fig below

Do the following calculation to get the density

For each species take the idenscode and divide by 100 to get the percentage fraction

e.g.

|  |  |  |
| --- | --- | --- |
| 50 /100 | X 50 | = 25 |
| 15 /100 | X 50 | = 7.5 |
| 20 /100 | X 50 | = 10 |

Multiply the percentage fraction with the initial reduction value to get the individual densities

Sum up the individual densities to obtain the final density

e.g 25+ 7.5+ 10 = 42.5

1. Nbal

If you have a compartment, miu and nbal id then.

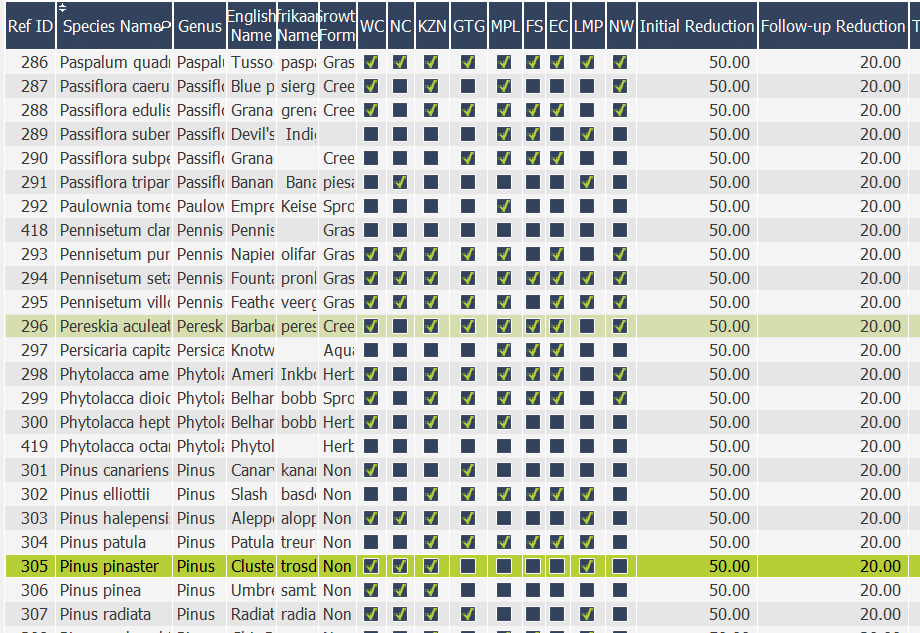
Do the same as the above calculation but multiply the density by the mysterious factor of 1.6

1. To propagate the density through the 20 year budget multiply the previous year by a density reduction factor which is derived as follows.
2. For the list of species find the initial reduction and follow up reduction i.e.

Graphical user interface, text, application

Description automatically generated

If you have the above species, then from the species table get the initial and follow up reduction:



|  |  |  |
| --- | --- | --- |
| species | Initial reduction | Followup reduction |
| Pinus pinaster | 50 | 20 |
| Acacia longifolia | 50 | 20 |
| Hakea sericea | 50 | 20 |

1. Sum the initial and follow up columns i.e. Sum\_initial = 50+50+50 = 150 and sum\_followuup = 20+20+20 = 60.
2. Divide the initial sum into the followup sum i.e. 60/150 = 0.4
3. Multiply the result by 2 i.e. density reduction factor = 0.4\*2 = 0.8
4. Propagate through the yearly budget. E.g. if you have a density of 100 in year 1, then year 2 is 100\*0.8 = 80. Year 3 density = 80\*0.8 = 64. Year 4 density = 64\*0.8 = 51.2, etc.

Note: include densification factor

Def densify(density, densification\_factor):

Return density\*(100+densification\_factor)/100

Def reducedensity(density, density\_reduction\_factor):

Return density\*(100+density\_reduction\_factor)/100

# Person days

Internal fixed variables:

1. Working day is 8 hours out of 24 (used)
2. 220 days per year working days out of 365 (not used)

Notes:

1. Vehicle cost/day includes all vehicle costs including its own fuel – unsure
2. You might want to consider making the above into an object functional form, i.e. something you can call like a function but its an object, reason being that when doing the costing, the person day needs to be calculated on the fly. A functional form where you pass the inputs can be very handy in this case.
3. Consider if you can modify the 8-hour working day used in the above calculations to a different number of working day by generalizing all the above formulae to:

, where WD is the new working day hours. If WD is > 12 or WD < 4, then cap at 12 or 4 respectively. If you cannot do this slight modification, then ignore.

1. Note that the current tool has a slope dependence only on slope == 10, at moment if it is slope ==10 then adjust normal or base person days by multiply by 1.4, **do not implement** this version in the code, rather use the algorithm for slope dependence below

Step 1: Start iterating over the gis mapping file:

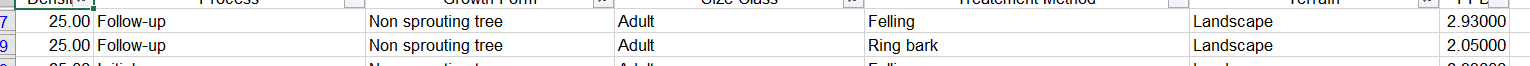
1. For each entry check if:
2. If there is a compartment only (no nbal and miu), then use no person days, no mapping person day – unsure (Inspection cost model used for obtaining costs)
3. If there is an miu and/or nbal present, filter the miu linked species file and find all entries for the current compartment id.
4. Follow the following algorithm below once the miu linked species entries for the compartment id has been found

There are two subroutines before the actual algorithm below:

Step 2: Code up subroutine 1

**Subroutine for choosing the treatment method**

Note that there is more than one treatment plan associated with the ppd in most cases i.e.



The above has ring bark and felling as both options for the same density, growth form, age and riparian. This is a special case as other norms may not have many options available. We should make this a special case in the code and not hard code this in.

1. If there is only one treatment method then choose that method
2. Else if there are **more than one treatment method**, choose according to the following ordered list with respect to priority:

* For “Adult” age category, choose treatment method “**Ring bark” (for landscape) and “Fell” (for riparian)**, if available
* Else if “Adult” age category, choose treatment method “**Bark Strip**”, if available
* Otherwise go for **Lopping/Pruning** if available

Step 3: Code up subroutine 2

**Subroutine for filtering for PPD**:

For each entry in the miu linked species file found, do the following on the support clearing norms data found in the mucp\_input file under the clearing\_norm spreadsheet:

1. Filter data according to Idenscode (excel miu linked species) [if year 1] or previously calculated density [if year 2 onwards] in column Density (clearing norm)
2. Filter remaining clearing norm data according to Age (excel) in column size class (clearing norm)
3. Match the miu id to the MIU shapefile to determine the riparian (“l” for land and “r” for reparian)
4. Filter the remaining clearing norm data according to riparian/terrain (change terrain [column header] to riparian, it was a concept mistake)
5. Use species (excel) to look up the entry in support\_species spreadsheet in the mucp\_input excel file. Obtain the growth form for the species. This will be Herbaceous, Sprouting, Non-sprouting, Grass etc.
6. Look in support\_growth\_form spreasheet, if the acquired growth form is in this table then continue, otherwise flag the entry and throw warning message.
7. Filter the remaining clearing norm data in clearing norm according to the growth form.
8. From gis mapping shapefile, if the compartment has only an miu attached, then filter the process column for “initial”. If there is an nbal attached and if the process in the nbal shapefile indicates an “Initial treatment”, then filter the process clumn for “initial” entries. Else if nbal attached and the process found in the nbal shapefile is follow up, then filter the process column in the clearning norms for “Follow-up”.
9. Use subroutine 1 to determine the treatment method. Filter on the treatment method. At this point there should only be one entry in the clearing norm left.
10. Obtain the PPD (person days per hectare).

End subroutines

Step 4: Obtain Person days:

1. Iterate over the years 1 until end of all years, for each year:
2. Iterate through the miu linked species entries, from the gis mapping shapefile, determine if the current miu has an nbal attached.
3. Obtain the following data regarding the current compartment/miu:
   1. area for the MIU compartment intersection, from gis file itself
   2. The drive and walk time form compartment shapefile, by matching the compartment id
   3. Match the miu id in the miu shapefile to determine the riparian (l or r)
4. If miu only (initial treatment, no follow up) or miu with nbal, but the nbal in the nbal shapefile has “Initial treatment” under its treatment, then
   1. If Year 1:
      1. Use subroutine 2 with the idenscode in miu file for the density, the riparian (l or r), growth form, process = initial, use age in miu file for that specific species and using subroutine 1 for selection of treatment method
      2. This will filter the clearing norms table to get the PPD,.
      3. Get the normal or base person days by multiplying the PPD and area i.e.
      4. Modify the normal or base person days to get the adjusted person day using the following formula:
   2. For year 2 and beyond:
      1. We have already obtained growth form, use process = follow-up, use already obtained riparian (r or l), use already obtained Miu age for specific species, use already obtained treatment method obtained from subroutine 1
      2. Obtain the density for the current year by looking at the previous year i.e. current year - 1 calculated density. Round off the density to the nearest integer except for the following ranges. Round off values below 5 to the nearest number presented in the table below:

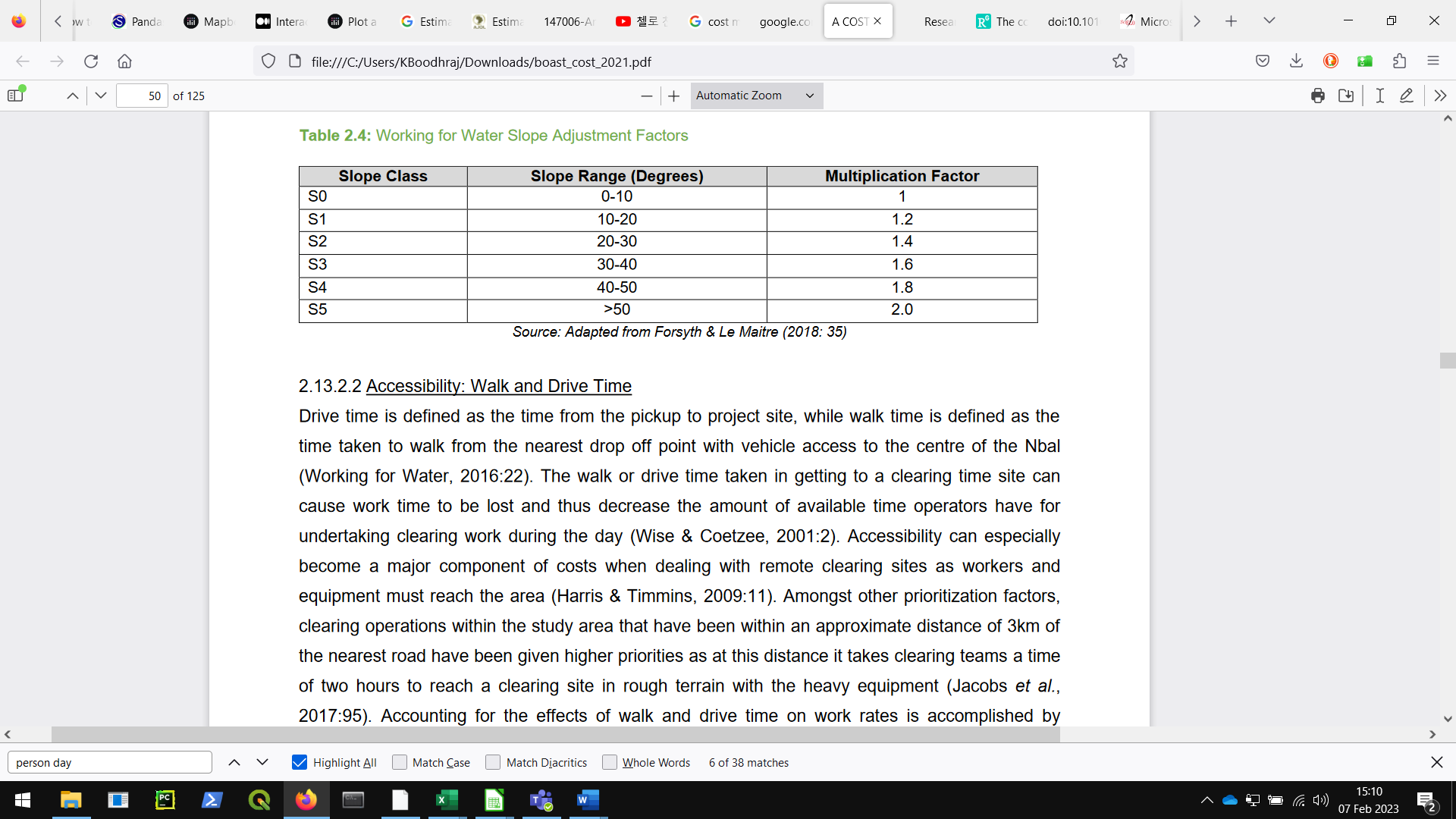
|  |  |
| --- | --- |
| **Density central points** | |
| 0.01 | 0.2 |
| 0.02 | 0.3 |
| 0.03 | 0.4 |
| 0.04 | 0.5 |
| 0.05 | 0.6 |
| 0.06 | 0.7 |
| 0.07 | 0.8 |
| 0.08 | 0.9 |
| 0.09 | 1.0 |
| 0.10 | 1.5 |
| 2.0 | 4.0 |
| 2.5 | 4.5 |
| 3.0 | 5.0 |
| 3.5 | 6.0 |

* + 1. Use subroutine 2 above to filter and get the new PPD for each in the clearing norms table, using the variables in the last two points
    2. Get the normal or base person days by multiplying the PPD and area i.e.
    3. Modify the normal or base person days using the following formula:

1. If nbal attached to miu (follow up treatment) and the nbal shapefile shows “follow up” treatment then:
   1. If year 1:
      1. Obtain the density by using the idenscode in miu file for the density
   2. Else if year 2 onwards:
      1. Obtain the density by looking at the previous year density calculation
   3. Round off the density obtained to the nearest integer except for the following ranges. Round off values below 5 to the nearest number presented in the table below:

|  |  |
| --- | --- |
| **Density central points** | |
| 0.01 | 0.2 |
| 0.02 | 0.3 |
| 0.03 | 0.4 |
| 0.04 | 0.5 |
| 0.05 | 0.6 |
| 0.06 | 0.7 |
| 0.07 | 0.8 |
| 0.08 | 0.9 |
| 0.09 | 1.0 |
| 0.10 | 1.5 |
| 2.0 | 4.0 |
| 2.5 | 4.5 |
| 3.0 | 5.0 |
| 3.5 | 6.0 |

* 1. We currently have the rounded density from the above, the riparian (l or r), growth form, process = follow-up, use age in miu file for that specific species and using subroutine 1 for selection of treatment method
  2. Use subroutine 2 above to filter and get the new PPD for each in the clearing norms table, using the variables in the last point
     1. Get the normal or base person days by multiplying the PPD and area i.e.
     2. Modify the normal or base person days using the following formula:



1. Slope adjustment is applied to the adjusted person days as follows:
   1. Using the compartment id, determine the slope from the compartment shapefile
   2. Find the multiplication factor in the table above by searching through the slope range.
   3. For each miu entry where we calculated the adjusted person days, multiply the adjusted person days with this slope.
2. Sum up the individual adjusted person day contributions for each MIU linked species per compartment id to get the total person days for that compartment.

# Treatment costs

Obtain costing for treatment

The cost model has the following parameters:

* Initial team size
* Initial team cost/day
* Follow-up team size
* Follow-up team cost/day
* Vehicle cost/day
* Fuel cost/hour
* Maintenance level
* User defined costs

The additional information will be needed for the costing to occur:

* Individual linked species entries form miu linked species excel file
* Density of each entry per that year of budget (from density algorithm)
* Prioritization values of the compartments (from priority algorithm)
* Normal (base) person days (from person day algorithm)
* Adjusted person days (from person day algorithm)
* Drive time from compartment file
* Budget amount
* Budget yearly escalation percentage

Iterate over the years 1 to end year:

For each year do the following:

Iterate through GIS shapefile:

1. For each compartment id do the following:
   1. Locate the compartment id in the compartment shapefile and obtain the cost code in the costing column
   2. Match the cost code in the mucp input file under the planning\_budgets spreadsheet
   3. In this way the costing model name is obtained
2. If the costing model name is inspection, then apply the inspection cost model parameters by:
   1. Iterating over the years 1 to 20 (or end year)
   2. Use inspection cost model found in support\_costing spreadsheet in the mucp input file. It contains a **user defined daily cost** with all other cost model parameters set to 0.
      1. For the current compartment id determine if it has a miu (and/or nbal)
      2. If there is no miu (and/or nbal) then use 0 for the compartment cost
      3. Else if there is a miu (and/or nbal) attached, then search through the miu linked species file and extract the entries with the miu compartment id
      4. Then for each entry found, use the following formula to determine the cost per miu linked species:
      5. Sum up the individual miu entries per compartment ID to get the inspection cost per compartment
   3. Go to the next compartment id (step 1)
3. Else if the costing model name is **not** Inspection:
   1. Check if all costing model parameters (ignore maintenance level) is 0:
      1. If all costing model parameters 0 then
      2. For the current compartment id determine if it has a miu (and/or nbal)
      3. If there is no miu (and/or nbal) then use 0 for the compartment cost
      4. Else if there is a miu (and/or nbal) attached, then search through the miu linked species file and extract the entries with the miu compartment id
      5. Use the adjusted person days (PDADJUSTED) as the cost for the individual miu linked species.
      6. Add the individual miu cost entries per compartment to get the cost of compartment
      7. Go to next compartment (Step 1)
   2. Else if any costing parameters are not 0 (ignore maintenance):
      1. Then follow the next set of rules to get the **total cost per individual MIU linked species, fuel compartment cost** and **total compartment cost**.
      2. First find cost for the individual linked species, for the current compartment id determine if it has a miu (and/or nbal)
      3. If there is no miu (and/or nbal) then use 0 for the compartment cost
      4. Else if there is a miu (and/or nbal) attached, then search through the miu linked species file and extract the entries with the miu compartment id
      5. Iterate through all miu linked species attached to the compartment
         1. If **year 1 and MIU only**, use the initial cost parameters and follow this formula:
         2. Note that if **initial team cost per day** or **initial team size** is 0 then set it to 1 for the calculation to work above.
         3. Else if **year 1 and miu with nbal**:
         4. Find nbal id in the nbal shapefile and determine if it is a follow up or an “Initial treatment”.
         5. If nbal treatment is **initial** then use the initial team and cost i.e.:
         6. Note that if **initial team cost per day** or **initial team size** is 0 then set it to 1 for the calculation to work above.
         7. Else if the treatment is **follow up**, then use the follow up team size and cost i.e. use the follow-up cost parameters
         8. Note that if **follow-up team cost per day** or **follow-up team size** is 0 then set it to 1 for the calculation to work above.
         9. **Else for any other year** treat it as a follow up i.e. use the follow-up cost parameters
         10. Note that if **follow-up team cost per day** or **follow-up team size** is 0 then set it to 1 for the calculation to work above.
      6. There is now a cost for each miu linked species for the specific compartment i.e. the **total cost per individual MIU linked species** was calculated
      7. (out of the if statements above regarding the year) Costing of fuel to compartment is an additional cost which needs to be calculated and distributed to each individual MIU linked species within the compartment. The fuel is independent of the MIU linked species and is a compartment attributed costing. Obtain the fuel cost as follows:
         1. Use the fuel cost per hour in the costing model parameters and perform the calculation for the compartment:
         2. To distribute into the individual linked miu species budgets, divide the **compartment fuel cost**, calculated above, by the **number of MIU individual entries** and add the cost to each **individual MIU linked species cost contributions**, to get the **total cost per individual MIU linked species** i.e e.g have 4 miu linked species for the current compartment with individual costs of R15, R20, R30 and R35 respectively, and fuel cost amounted to R40 for the compartment, then the cost which gets added onto the individual miu linked species cost is R40/4 = R10 that means each individual linked species costs become R15+10=R25, R20+10=R30, R30+10=R40 and R35+10=R45
      8. Each miu linked species now has its total cost
      9. Repeat from step 1 until all miu linked species have a cost attributed to them
4. Look at the miu linked species file: Distribution of species selected for specific budget. Once all costs are attributed to each miu linked species entry (whether it be a 0 for all costing parameters, inspection cost or a normal costing model), then assign to budgets as follows for optimal, budget 1,2,3 and 4:
   * 1. For the optimal budget do the following:
        1. Group the miu linked species according to compartment id
        2. For each compartment id, sum up the total cost per miu linked species (i.e. found above after you added the fuel cost per linked species) for all the linked species in that compartment
        3. This gives you the optimal cost for that compartment
        4. Repeat from 1 in this list until all compartments are finished
        5. If year 1, then density adjustments for each miu linked species occurs as an initial density reduction if there is no nbal attached to the current compartment
        6. Else if year 1 and nbal attached to miu, determine from nbal shapefile if it is an initial treatment then density adjustment for the compartment uses initial density reduction for density, else if the nbal is a follow up, then use the followup density reduction to obtain the current year density
        7. Since all compartments are cleared in the optimal budget there are no adjustments to person days i.e. no miu linked species person days are set to 0
     2. For the individual budgets with constrained budget amounts (i.e. budget 1,2,3 and 4), follow the selection process below to determine which individual linked species get selected for clearing and the adjustments for person days and density:
        1. Sort the compartments in descending order i.e highest to lowest priority. Iterate through the priority sorted compartments.
        2. Filter the miu linked species entries linked to the highest priority compartment, the higher the number, the higher the priority.
        3. If there are more than one compartment with the same priority, then group all the individual MIU entries for all those compartments together.
           1. For these entries, sort along the density (ascending, from smallest to largest)
           2. If there are multiple entries with the same density, sort along costing (ascending, from smallest to largest)
           3. This gives you a sorted list of individual miu linked species entries, based on highest priority, then lowest to highest density then lowest to highest costing
           4. Start the selection process by starting with the lowest density and lowest costing (if there are multiple density entries).
           5. If the cost can be subtracted from the current budget without the budget going less than R0, then use that miu linked species entry by subtracting it from the current budget. Do a reduction of density (if year 1 and miu only (or nbal with initial treatment) then it’s an initial density reduction, otherwise a follow up density reduction). Remove this entry from the current list of miu linked species entries (not permanently).
           6. Go to the next lowest density and lowest costing (if multiple density entries). If the cost can be subtracted from current budget, then select entry and subtract from the budget. Do a reduction of density (if year 1 and miu only (or nbal with initial treatment) then it’s an initial density reduction, otherwise a follow up density reduction). Remove this entry from the current list of miu linked species entries (not permanently).
           7. If subtracted and budget < R0, then do not use this miu entry, remove from the current list of miu linked species entries. Do a density adjustment by using the densification factor and set the person days to 0 for this miu linked species entry. Remove this entry from the current list of miu linked species entries (not permanently).
           8. Repeat algorithm from **step d** until there are no entries for this priority left.
        4. Go to next highest priority scoring compartment and repeat algorithm from **step 2** againuntil the budget cannot accommodate any other MIU entry subtraction.
        5. For obtaining the next year budget, use the current total budget and use simple interest formula i.e. F = P(1+in) where F is your next year budget, P your current year budget, I the interest rate in decimals and n is the number of years (1 in this case, because we do this once for every year), so formula is simplified to F = P(1+i). Note budget leftover from previous year is not carried to the next year.
   1. Iterate to the next year and repeat the algorithm from **Step 1** again for the following year (and note that only follow-up procedures are used instead of initial)

~~Once the selection process for the budgets are finished then iterate from step 1 for year 2,3,4…~~

~~Step 1: If all costing model parameters (irrelevant of maintenance level) is 0:~~

1. ~~Use the adjusted person days as the cost for the individual miu linked species.~~
2. ~~Add the individual cost entries per compartment to get the cost of compartment~~

~~Step 3: If non zero parameters in cost model, follow this set of rules to get the~~ **~~total cost per individual MIU linked species~~** ~~and~~ **~~total compartment cost~~**~~. This step is for individual linked species and the next step is an overall compartment costing distribution algorithm.~~

1. ~~If normal cost model do the following:~~
   1. ~~If~~ **~~year 1~~**~~, use the initial cost parameters and follow this formula:~~
      1. ~~Note that if~~ **~~initial team cost per day~~** ~~or~~ **~~initial team size~~** ~~is 0 then set it to 1 for the calculation to work above.~~
   2. ~~For the optimal budget, add the above individual entries per compartment to get the~~ **~~individual MIU linked species cost contributions,~~** ~~this will be used later when the fuel cost is added.~~
   3. ~~Else for~~ **~~year 2~~** ~~and beyond use the follow-up cost parameters:~~
      1. ~~Note that if~~ **~~follow-up team cost per day~~** ~~or~~ **~~follow-up team size~~** ~~is 0 then set it to 1 for the calculation to work above.~~
   4. ~~For the optimal budget, add the above individual entries per compartment to get the~~ **~~individual MIU linked species cost contributions,~~** ~~this will be used later when the fuel cost is added.~~
2. ~~Addition of fuel to compartment. The fuel is independent of the MIU linked species and is a compartment attributed costing.~~
   1. ~~Use the fuel cost per hour and perform the calculation for the compartment:~~
   2. ~~For the optimal budget, add this to the compartment cost.~~
   3. ~~For use with other distributed budgets, divide the~~ **~~compartment fuel cost~~** ~~by the~~ **~~number of MIU individual entries~~** ~~and add the cost to each~~ **~~individual MIU linked species cost contributions~~**~~, to get the~~ **~~total cost per individual MIU linked species~~**
3. ~~If calculating the~~ **~~optimal budget~~**~~, add the~~ **~~total cost per individual MIU linked species~~** ~~for all entries in that compartment to get the~~ **~~total cost for that compartment~~**
4. ~~For other budgets, follow the selection process in the subroutine below.~~

~~Step 4: Distribution of species selected for specific budget:~~

1. ~~Once the individual costing is obtained for each individual miu species (including the compartment fuel cost distributed into this cost), then follow the selection process to determine which individual linked species get selected for clearing:~~
   1. ~~Filter compartments on priority, the higher the number, the higher the priority.~~
   2. ~~If there are more than one compartment with the same priority, then group all the individual MIU entries together.~~
   3. ~~For the highest priority, sort along the density (from smallest to largest)~~
   4. ~~If there are multiple entries with the same density, sort along costing (from smallest to largest)~~
   5. ~~The selection process starts with the lowest density and lowest costing if multiple density entries.~~
   6. ~~If the cost can be subtracted from the current budget, then use that miu linked species entry.~~
   7. ~~Go to the next lowest density and lowest costing for this density if multiple density entries. If cost can be subtracted from current budget, then do so. If subtracted and its over the budget, then discard entry and repeat algorithm from~~ **~~step e~~** ~~until there are no entries for this priority left.~~
   8. ~~Go to next highest priority and repeat algorithm from~~ **~~step 4~~** ~~until the budget cannot accommodate any other MIU entry.~~
   9. ~~Set all the entries costing not used in the budget costing and person days to 0.~~
   10. ~~Furthermore, densify the density on those entries for the next year.~~
   11. ~~For obtaining the next year budget, use the current budget and use simple interest formula i.e. F = P(1+in) where F is your next year budget, P your current year budget, I the interest rate in decimal and n is the number of years (1 in this case), so formula is simplified to F = P(1+i). Note budget leftover from previous year is not carried to the next year.~~
   12. ~~Repeat the algorithm from Step 1 again for the following year (and note that follow-up procedures are used instead of initial)~~

# Flow

* For each entry in the species for the matched list from the MIU or NBAL linked species file data as appropriate:
  + Determine the **flow factor** by:
  + Obtain the age class:
    - If the age class is
      * Mature
      * Adult
      * Mixed
        + Then use 0 for the flow reduction parameter
    - If the age class is:
      * Young – select the flow reduction Select the correct flow reduction factor from the species attribute table in Support (Column Flow Young)
      * Seedling – select the flow reduction Select the correct flow reduction factor from the species attribute table in Support (Column Flow Seedling)
      * Coppice – select the flow reduction Select the correct flow reduction factor from the species attribute table in Support (Column Flow Coppice)

If the age class is blank or missing, treat it as mature

1. For each MIU (mapped invaded unit):
   * Start with year 1.
   * Obtain the MAR (mm/yr) for the mapping unit form the prioritization file
   * For each entry in MIU linked species file for the current compartment, obtain the Idenscode for the mapping unit
   * Obtain the Area for the mapping unit
   * Multiply the area, idenscode and MAR to get the “density of MAR”
   * Determine the riparian:
     + If MIU compartment only (no nbal and year 1 only) use initial density reduction factor otherwise for NBAL (and year 2 onward for MIU), use the follow-up density reduction factor. Special case, If the nbal has an initial treatment attached to it, then use the initial values for density reduction instead (for year 1 only).
     + If the mapping unit is dryland (l) then calculate the flow reduction (FR) (mm/yr) = Density of MAR x (100 – initial\_or\_follow-up\_density\_reduction\_factor)/100
     + If the mapping unit is riparian (r) then the dryland FR is adjusted as follows:
       - FR=FR x 1.5
   * Multiply the FR by flow factor i.e. FR = FR\*flow\_factor
   * Repeat this calculation for each species in the mapping unit
2. Sum the reductions for each of the species in the invaded mapped unit to get the total reduction per mapping unit per year (TR)
3. Convert back to a unit reduction by dividing the TR by 10 to get m3/ha/yr (UTR) for in invaded mapped unit
4. Select the next mapped invaded unit (repeat the procedure from step 1)
5. Continue until all invaded mapped units have been processed
6. For year 2 and beyond:
   * Use the FR per species calculated in previous iteration
   * Reduce on the FR using a fractional density i.e. FR = FR\*(100-followup\_density\_reduction)/100
   * Continue this calculation for all compartments
7. Iterate from step 6 for all years

Note: if there is no MAR in the prioritization file, then do not perform flow calculations, make them all 0.

1. ~~For each mapped invaded unit:~~
   * ~~Select the species, obtain its density (%cover) and the corresponding flow reduction factor (FRF) (see Table 1 for examples) taking account of whether growing conditions are optimal or not for~~ *~~Eucalyptus~~* ~~species,~~ *~~Pinus~~* ~~species and~~ *~~Prosopis~~* ~~species~~
   * ~~Identify the invaded mapping unit’s water status: dryland, riparian or groundwater~~
   * ~~Obtain the MAR (mm/yr) for the mapping unit~~
   * ~~Convert density to a proportion (density class midpoint ÷ 100)~~
   * ~~Calculate the flow reduction (FR) as follows:~~
     + ~~If the mapping unit is dryland FR (mm/yr) = FRF x Density x MAR~~
     + ~~If the mapping unit is riparian then the dryland FR is adjusted as follows:~~ 
       - ~~if the mapping unit biome type (BT) is grassland then FR=FR x 2.0~~
       - ~~if not FR=FR x 1.5~~
     + ~~If the mapping unit is groundwater then the FR=FR x 1.2~~
   * ~~Convert the calculated FR to a flow reduction in m~~~~3~~~~/yr: FRm3=FR x mapping unit area in ha x 10~~
   * ~~Repeat this calculation for each species in the mapping unit~~
2. ~~Sum the reductions for each of the species in the invaded mapped unit to get the total reduction per mapping unit per year (TR)~~
3. ~~Convert back to a unit reduction by dividing the TR by the area in ha to get m~~~~3~~~~/ha/yr (UTR) for in invaded mapped unit~~
4. ~~Select the next mapped invaded unit (repeat the procedure from step 1)~~
5. ~~Continue until all invaded mapped units have been processed~~

~~Notes:~~

* ~~For the miu and nbal linked species file, the Age column has the following options:~~
  + ~~Seedling~~
  + ~~Coppice~~
  + ~~Young~~
  + ~~Adult~~
  + ~~Mature~~
* ~~For flow regarding mature and adult, use the optimal and sub-optimal flow factors (Large mature adult plants)~~
* ~~For flow regarding coppice, young and seedling, use the specified flow factors for each of these types (for small growing and still establishing plants)~~

~~In order to propagate flow for the other budgeted years do the following.~~

~~Use the flow obtained for the miu or nbal at year 1. Multiply this value with 0.8 to obtain flow for year 2. Recursively repeat.~~

# Spelling errors to fix in input data reader file

#

NBAL\_linked\_species\_excel()

Has

self.miu\_id = self.data[nbal\_linked\_species\_excel\_headers[0]]

whereas it should be nbal\_id not miu\_id i.e.

self.nbal\_id = self.data[nbal\_linked\_species\_excel\_headers[0]]

#

NBAL\_shapefile()

Has

self.nbal\_ciontract\_id = self.data[[nbal\_shapefile\_headers[0],nbal\_shapefile\_headers[5]]]

there is a spelling error on contract i.e.

self.nbal\_contract\_id = self.data[[nbal\_shapefile\_headers[0],nbal\_shapefile\_headers[5]]]

#

Add all other fields for input in the data readers file function for:

class Compartment\_priority\_csv():

Here are all the fields that need to be present

aggression  
diversity  
density  
elevation  
erosion  
flood  
forage  
fuel  
invasion  
owner  
products  
quality  
rain  
riparian  
river  
runoff  
seepage  
situation  
slope  
soil  
status  
stress  
tourism  
treat  
veld\_age  
zone

Note that some fields are already there, mar is runoff and vegetation\_status is status, but these will be matched in the other tables so these can be overwritten:

ownership  
vegetation\_status  
veld\_age  
elevation  
rain  
mar

The headers will also need to be changed, note the order matters in the HEADERS file:

def compartment\_priority\_headers(self):

add them to this function. Remember pandas needs to try to read these columns but not break. If there is no column then skip this column and carry on the the next one

#

[https://scholar.sun.ac.za/bitstream/handle/10019.1/123841/boast\_cost\_2021.pdf?sequence=2&isAllowed=y](https://scholar.sun.ac.za/bitstream/handle/10019.1/123841/boast_cost_2021.pdf?sequence=2&isAllowed=y" \t "_blank)