Reproductive Allocation Calculations

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Chapter 1

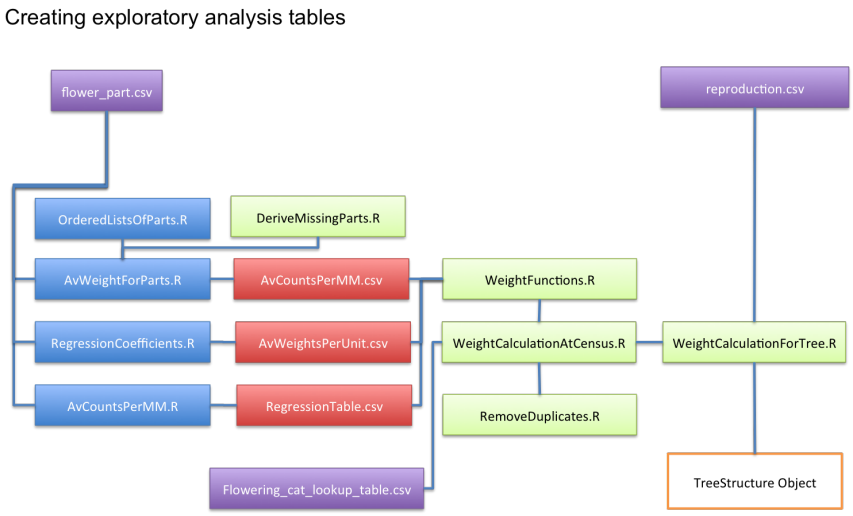
Software description

1.1 Purpose of software

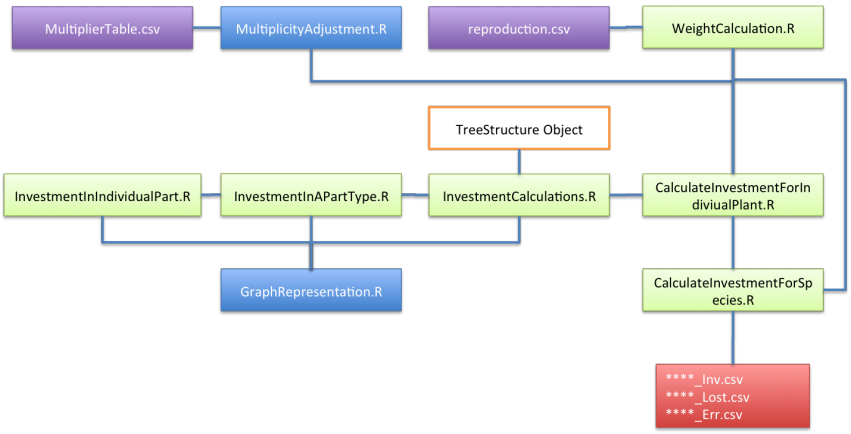
The goal of the code is to:

- Estimate reproductive investment from census data
- Estimate growth investment
- Determin Reproductive Allocation schedules for 14 species.

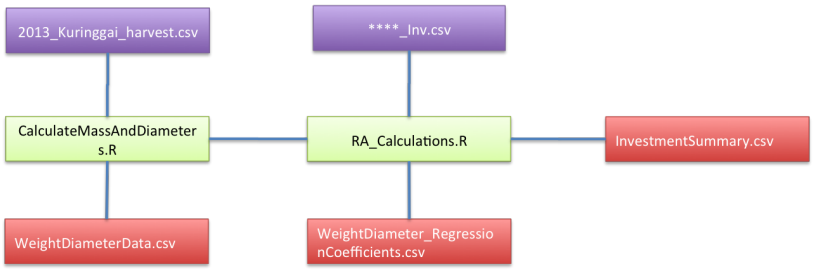
1.2 Structure of Software



Calculating Reproductive Allocation



Calculating Weight Investment and Reproductive Allocation



1.3 Listing of files

- Data Files
  - `flower_parts.csv` File containing measurements of weight, length, and dimensions for given species. The file is used to obtain the average weights of plant parts based on the count, length and dimension measurements of individual species at given times.
  - `reproduction.csv` File containing information about counts, lengths and dimensions (not weights) for individuals at different censuses.
  - `2013_Kuringgai_harvest.csv` File containing information sbout diameters and weight for the sampled trees.
  - `Flowering_cat_lookup_table.csv` File containing table describing the allowed parts of plants and the way they are measured.
  - `MultiplierTable.csv` File containing table describing the multiplicity of possible seed per plan part.
- R-functions' files
  - `WeightFunctions.R` - converts counts, lengths and dimensions to weights
  - `WeightCalculationAtCansus.R` - calculates weight of tree parts

  - `RemoveDumplicates.R` - merges multiple entries for the same tree parts
  - `DeriveMissingParts.R` - For particular species no measurements are provided/possible and they are being imputed with the values calculated by the script above.
  - `WeightCalculationsForTree.R` - calculates of weight dynamics for a tree along censuses
  - `InvestmentCalculations.R` - determines of investments of the plant along all censuses given a weight tree structure object
  - `InvestmentInAPartType.R` - calculates the investment in creation of a given type element at given census
  - `InvestmentInIndividualPart` - calculates the investment in creation of an **individual** of a given type at given census

- R-scripts
  - `AvWeightForParts.R` - calculates the average weights for the parts included in the flower_parts.csv file for a given species.
  - `AvCountsPerMM.R` - calculates the average density of counts per mm for a given species. Saves results in AvCountsPerMM.csv
  - `RegressionCoefficients.R` - Script determining the regression coefficients that are use to obtain weights of elements from their dimensions.
  - `GraphRepresentation.R` - Script containing the structure for each specie which describes part names, their progression, and carbon flow.
  - `OrderedListsOfParts.R` - Script containing the ordered part names. Used for construction of this document.
  - `RedoDocument.R` - Short script calling all functions which produce tables and plots used in this document.
  - `CalculateMassAndDiameter.R` -script calculating and saving masses and diameters for the individual plants (using data in `2013_Kuringgai_harvest.csv`)
  - `RA_Calculations.R` - script reading reproductive investment, growth investment and calculating total investment and RA.

- Plotting functions
  - `Plot_RAs` Function that plots and saves in a pdf RA for all the species on one plot.
  - `PlotIndividual_RA` Function that for each species creates a 3 panel plot with reproductive investment, growth investment and RA.

- Libraries used
  - `igraph` used for representing and manipulating plant graphs.
  - `stringr` used for some string manipulations.
  - `colorspace` used for defining HCL colours for plotting RAs.

1.4 Individual Functions Description

WeightFromCount (in WeightFunctions.R)

Given the count, species type and plant part the function returns a vector that contains the weight of each plant part.
Input parameters:

- `count` integer describing number of observed plant parts
- `species` character string defining the name of the species (as used in `flower_part.csv`) file
- `part` character sting corresponding to the name of the plant part

Output parameters:

- `w` vector of length `count` with weight of the plant part at each position.

WeightFromLength (in WeightFunctions.R)

Given the length of a body par, species type and plant part the function returns a vector that contains the weight of each plant part. The function uses the species specific relationship to estimate the count corresponding to the observed length.
Input parameters:

- `length` double describing the length of observed plant parts
- `species` character string defining the name of the species (as used in `flower_part.csv`) file
- `part` character sting corresponding to the name of the plant part

Output parameters:

- `w` vector with weight of the plant part at each position. The size of the vector is estimated using allometric relationship.

WeightCalculationsAtCensus

Given the census data from the measurement Excel spreadsheet the function creates a list which contains information about all existing parts, their counts, and weights.
Input parameters:

- `C` Data from a given census about an individual tree

Output parameters:

- `C_list` A list which elements are list that contain fields: `type` -part name, `m.type` - measurement type (count, length), `count` - number of such parts, `weight` - vector of weight for each part.

RemoveDuplicates

Checks the list describing tree at a given census and merges multiple fields for the same tree part. Input parameters:

- `C` List with the structure of output of `MeasurmentsToWeight` function.

Output parameters:

- `C_new` The same list with the fields for the same tree part merged. If there were two measurement types used for a given part the `m.type` is changed to `mixed`.

WeightCalculationsForTree

Given the information about particular individual tree the functions returns a list representing the growth development of the tree.
Input parameters:

- `Tree` Rows of data.frame in `reproduction.csv` corresponding to an individual tree from all censuses

Output parameters:

- `TreeList` A list which in the first element contains the tree id. The remaining 18 elements are 3 element lists with fields `pre.existing`, `new` and `total` describing the structure of the tree at each census. Each of the 3 lists is in the format corresponding to the result of `MeasurmentsToWeight` function.

AdjustForMultiplicity (in MultiplicityAdjustment.R)

Function `AdjustForMultiplicity` together with its help functions (`AdjustForMultiplicity_Census`,`AdjustForMultipl`
that given Tree Structure adjust counts and weights to take into account number of seeds per fruit/flower etc. Input parameters:

- `Tree` Tree structure with weights and individual ID of a plant (result of WeightCalculations-ForTree)

Input parameters:

- `Tree` Tree structure with weights and individual ID of a plant (result of WeightCalculations-ForTree), where counts are multiplied by multipliers and weights are divided.

InvestmentInIndividualPart

Given element name, its weight, allowed progression and the list of possible existing predecessors the function returns the investment that was made to grow the element from its previous form to the existing one. Input parameters:

- `Element` Name of element
- `TreeList_Pred` Tree structure (similar to the result of WeightCalculcations function) with possible predecessors. Its length determine the time point at which we are now.
- `Progression` Character vector defining the possible previous stages of the Element.

- `El_weight` Weight of the element.

Output parameter is a list containing 6 elements

- `TreeList_Pred` Updated list of possible predecessors with the used predecessor removed.
- `Invest` Calculated investment (using the path from element to it's predecessor, incorporating the carbon flow in case of division)
- `from` Selected predecessor's name
- `to` The same as `Element`
- `Census` Information at which census the transition to Element has been observed.
- `Count` 1.

Function description:

- Given the element, possible predecessor and history of development of the tree, the function performs a back search in history looking for matching Predecessor.
- After finding Predecessor the investment is calculated. The investment is defined as the difference between the Element mass and the proportion of the mass of Predecessor. If the path from Predecessor to the Element does not have any accessory tissue the proportion will be 1. Otherwise the side allocation of the carbon to the accessory tissue is taken into consideration.
- The predecessor is removed from the list of possible predecessors and the list is returned for further calculations.

InvestmentInAPartType

Given part name, tree structure, allowed progression and the tree structure of possible existing predecessors the function returns the investment that was made to grow the plant part of a given type. It also calculates the investment in all newly created elements of a given type. Input parameters:

- `TreeList` Tree structure (like the result of WeightCalculcations function) containing information about the plant. The length of the list determine current time point.
- `TreeList_Pred` Tree structure (like the result of WeightCalculcations function) with possible predecessors.
- `Element` Name of element
- `Progression` Character vector defining the possible previous stages of the Element.

Output parameter is a list containing 2 elements

- `TreeList_Pred` Updated list of possible predecessors with the used predecessors removed.
- `Invest` Data structure containing information about investment in creation/progression of all elements of a given type at a given time.

Function description:

- Function determines the census by calculating length of TreeList_Pred.

- First we check if there are new elements of given type at this time point. If yes, the investment in them is calculated as their weight.
- The function checks if there are pre.existing elements of that type. If yes, it checks how many they are and use function CalculateIndividualInvestment to find the investment made in them attaining the stat.
- *OBS!* Exception is made if at the first census we have a part that is pre.existing. It's mass is not to be counted as new since it was created outside the monitoring period, however, the information about it needs to be included as in later censuses it might develop resulting in carbon investment.

InvestmentCalculations

Given a tree structure along all censuses the history of investment is calculated. Input parameters:

- `TreeList` Tree structure (the result of WeightCalculcations function) containing information about the plant.

Output parameter:

- `Inv` Data frame containing information about investment in creation/progression of specific parts along all censuses.
- `Lost` Data frame containing information about lost parts.
- `Error` Data frame containing information about possible errors (missing predecessors to pre-existing species).

Function description:

- First the structure of the specie is determined and number of main paths is determined. Then for each of the main paths:
  - We determine the main progression line, and go backwards census by census along all elements in the main progression lines calculating the investment. If the line includes "x-or" parts (mostly aborted fruits,flowers) calculation along this lines is made as well.
  - After calculating main and "x-or" lines the list of possible predecessors is reset to all values and separate carbon investment is performed for each of the auxiliary tissue type.

CalculateInvestmentForIndividualPlane

Given the name (tag_ID) of the individual plant, calculations of reproductive investment are performed. Input parameters:

- `individual` String corresponding to tree ID in the reproduction spreadsheet

Output parameter is a list including 3 data frames

- `Inv` Data frame containing information about investment in creation/progression of specific parts along all censuses.
- `Lost` Data frame containing information about lost parts.
- `Error` Data frame containing information about possible errors (missing predecessors to pre-existing element).

CalculateInvestmentForSpecies

A wrapper around function `CalculateInvestmentForIndividualPlane` that given string specifying specie name calculates the investment for all individuals of the species and saves the result in csv files. Input parameters:

- `TreeList` Tree structure (the result of WeightCalculcations function) containing information about the plant.

The function does not return anything, however it saves 3 files(`****` stands for species name):

- `****_Inv` Information about investment in creation/progression of specific parts along all censuses for all the individuals.
- `****_Lost` Information about lost parts for all individuals.
- `****_Error` Information about possible errors (missing predecessors to preexisting element).

1.4.1 GraphRepresentation

Script `GraphRepresentatio.R` contains the definitions of the graph structures defining plant development. This structures mimic to a large extent the plant maps. Each specie is represented by `igraph` object and a data frame `Paths` defining main progression lines for the species.

The graph object consist of:

- Vertices with name being a part name. Each vertex is also coloured. The distinct progression lines have distinct colour. Moreover the final stages of the accessory tissues have colour with a number larger by 1 from the main path they belong to.
- Edges that connect the subsequent parts on the map. Each edge has a weight attribute defining how much of the carbon allocated the predecessor is being used for ancestor creation. If there are no accessory tissues created at this point of progression weight will be 1. If there is more than one ancestor the weights are set as the proportion of the ancestor mass to the sum of all ancestors. This is done at that point manually and needs to be adjusted if any new data will be collected.

An example of the graph for CEOR species is presented in Figure 1.1.

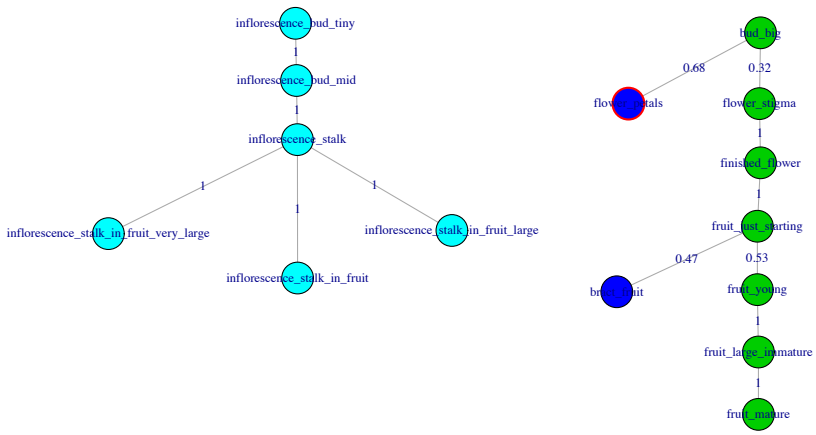
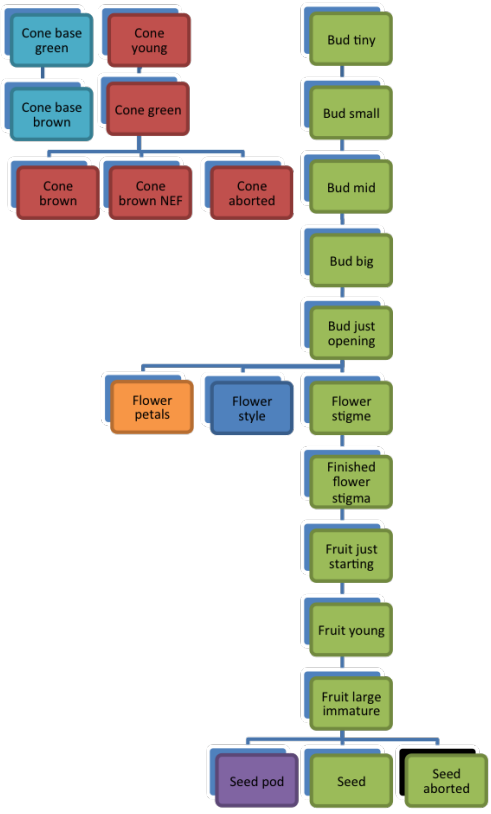


Figure 1.1: Graphical presentation of the `igraph` tree structure of plant map for COER.

Chapter 2

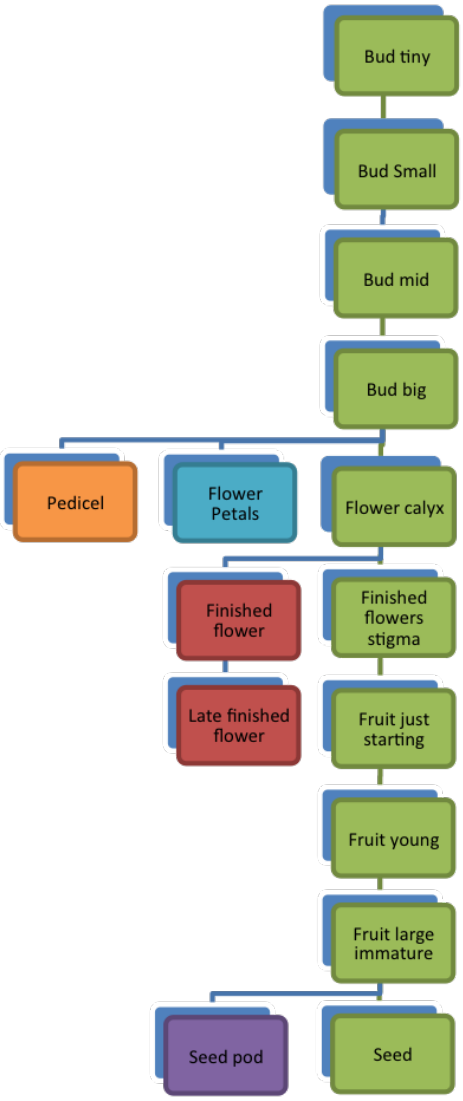
Species Average Weight Summary

2.1 BAER



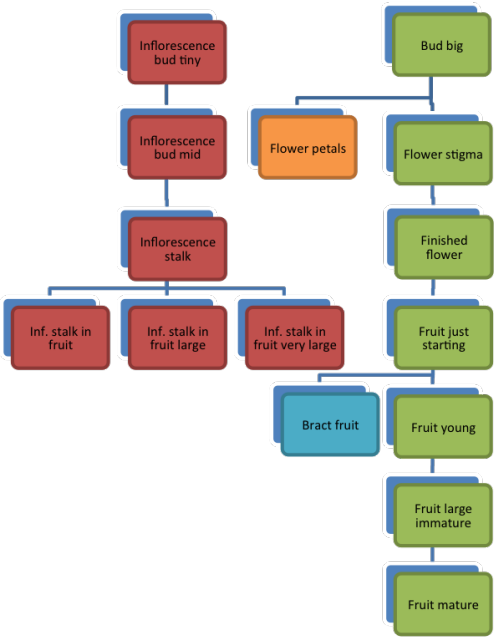
	species	part	n	av.weight
1	BAER	cone_base_green	30	316.93
2	BAER	cone_base_brown	13	360.76
3	BAER	cone_green	47	5910.92
4	BAER	cone_brown	8	47160.41
5	BAER	cone_brown_no_expanded_follicles	13	5800.80
6	BAER	cone_aborted	9	264.13
7	BAER	bud_tiny	14	2.87
8	BAER	bud_small	19	3.70
9	BAER	bud_mid	16	6.03
10	BAER	bud_big	19	7.05
11	BAER	bud_just_opening	24	9.54
12	BAER	flower_petals	16	6.85
13	BAER	flower_style	40	4.51
14	BAER	flower_stigma	9	1.53
15	BAER	finished_flower_stigma	10	9.67
16	BAER	fruit_just_starting	10	200.71
17	BAER	fruit_young	11	560.98
18	BAER	fruit_large_immature	10	1126.27
19	BAER	seed_pod	1	1200.00
20	BAER	seed	6	146.18
21	BAER	seed_aborted	1	92.95

2.2 BOLE



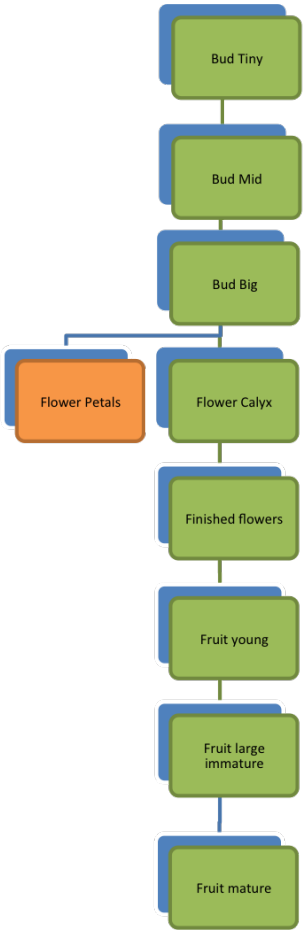
	species	part	n	av.weight
1	BOLE	bud_tiny	18	1.52
2	BOLE	bud_small	23	3.21
3	BOLE	bud_mid	30	6.01
4	BOLE	bud_big	22	8.70
5	BOLE	pedicel	20	1.60
6	BOLE	flower_petals	23	4.84
7	BOLE	flower_calyx	20	5.98
8	BOLE	finished_flower	10	4.93
9	BOLE	finished_flower_stigma	10	0.35
10	BOLE	late_finished_flower	9	6.93
11	BOLE	fruit_just_starting	22	1.24
12	BOLE	fruit_young	25	2.76
13	BOLE	fruit_large_immature	10	5.50
14	BOLE	seed_pod	6	6.19
15	BOLE	seed	56	5.75

2.3 COER



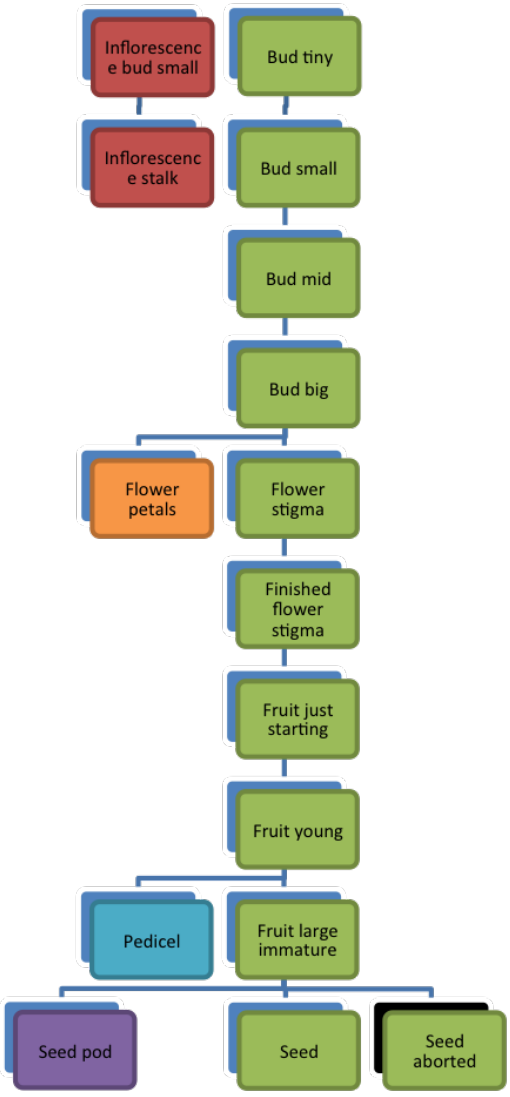
	species	part	n	av.weight
1	COER	inflorescence_bud_tiny	11	3.13
2	COER	inflorescence_bud_mid	9	9.49
3	COER	inflorescence_stalk	17	11.08
4	COER	bud_big	11	0.77
5	COER	inflorescence_stalk_in_fruit	64	22.06
6	COER	inflorescence_stalk_in_fruit_large	14	39.89
7	COER	inflorescence_stalk_in_fruit_very_large	11	50.36
8	COER	flower_petals	13	0.81
9	COER	flower_stigma		0.37
10	COER	finished_flower	10	0.83
11	COER	fruit_just_starting	19	1.18
12	COER	bract_fruit	20	0.83
13	COER	fruit_young	10	0.91
14	COER	fruit_large_immature	10	1.91
15	COER	fruit_mature	29	2.06

2.4 EPMI



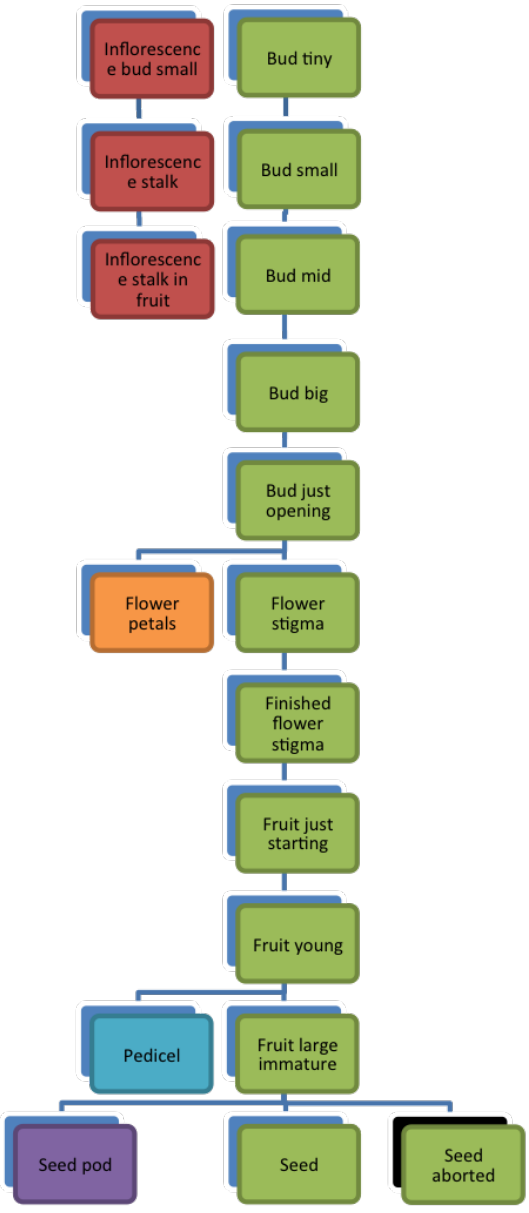
	species	part	n	av.weight
1	EPMI	bud_tiny	14	0.20
2	EPMI	bud_mid	15	0.62
3	EPMI	bud_big	12	1.17
4	EPMI	flower_petals	21	0.63
5	EPMI	flower_calyx	7	0.74
6	EPMI	finished_flower	10	0.88
7	EPMI	fruit_young	13	1.04
8	EPMI	fruit_large_immature	16	1.24
9	EPMI	fruit_mature	8	1.68

2.5 GRBU



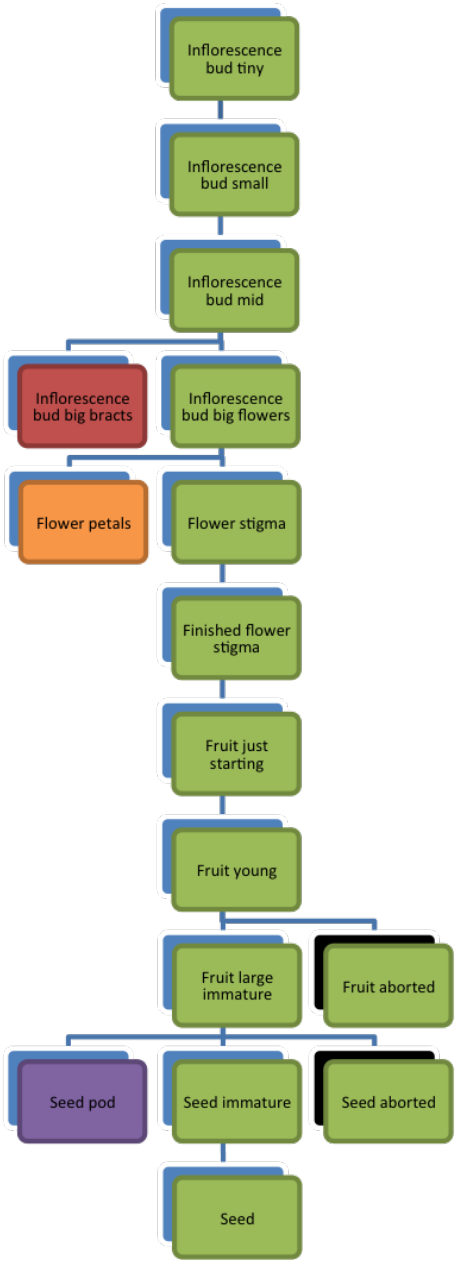
	species	part	n	av.weight
1	GRBU	inflorescence_bud_small	14	9.51
2	GRBU	inflorescence_stalk	4	17.60
3	GRBU	bud_tiny	13	2.03
4	GRBU	bud_small	11	3.23
5	GRBU	bud_mid	11	5.43
6	GRBU	bud_big	20	8.92
7	GRBU	flower_petals	13	6.50
8	GRBU	flower_stigma	13	10.79
9	GRBU	fruit_just_starting	22	13.44
10	GRBU	fruit_young	19	22.55
11	GRBU	pedicel	27	13.23
12	GRBU	fruit_large_immature	31	73.61
13	GRBU	seed_pod	62	164.02
14	GRBU	seed	30	53.45
15	GRBU	seed_aborted	14	25.10

2.6 GRSP



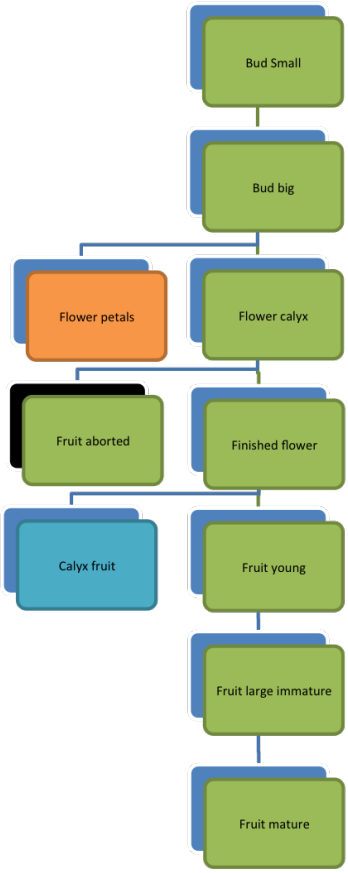
	species	part	n	av.weight
1	GRSP	inflorescence_bud_small	38	4.86
2	GRSP	inflorescence_stalk	46	7.32
3	GRSP	bud_tiny	27	0.41
4	GRSP	inflorescence_stalk_in_fruit	8	10.25
5	GRSP	bud_small	23	1.15
6	GRSP	bud_mid	19	2.08
7	GRSP	bud_big	16	4.34
8	GRSP	bud_just_opening	14	7.62
9	GRSP	flower_petals	24	5.29
10	GRSP	flower_stigma	21	4.15
11	GRSP	finished_flower_stigma	16	4.20
12	GRSP	fruit_just_starting	20	6.23
13	GRSP	fruit_young	11	9.69
14	GRSP	pedicel	6	6.00
15	GRSP	fruit_large_immature	43	55.10
16	GRSP	seed_pod	57	93.23
17	GRSP	seed_aborted	10	8.91
18	GRSP	seed	20	23.49

2.7 HATE



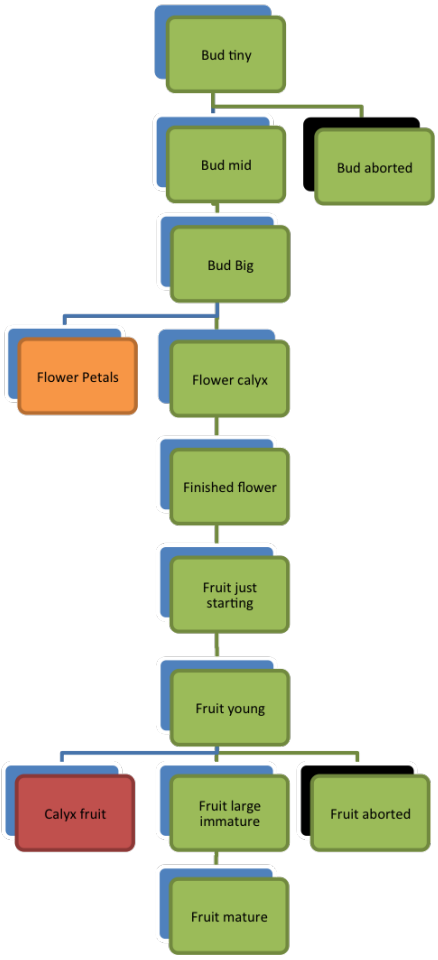
	species	part	n	av.weight
1	HATE	inflorescence_bud_tiny	12	3.66
2	HATE	inflorescence_bud_small	24	4.12
3	HATE	inflorescence_bud_mid	20	7.82
4	HATE	inflorescence_bud_big_bracts	13	8.16
5	HATE	inflorescence_bud_big_flowers	5	6.28
6	HATE	flower_petals	33	1.36
7	HATE	flower_stigma	37	1.08
8	HATE	finished_flower_stigma	12	1.37
9	HATE	fruit_just_starting	34	28.55
10	HATE	fruit_young	30	51.41
11	HATE	fruit_large_immature	13	176.66
12	HATE	fruit_aborted	9	102.60
13	HATE	seed_pod	212	369.59
14	HATE	seed_immature	74	5.09
15	HATE	seed_aborted	109	5.65
16	HATE	seed	83	12.67

2.8 HEPU



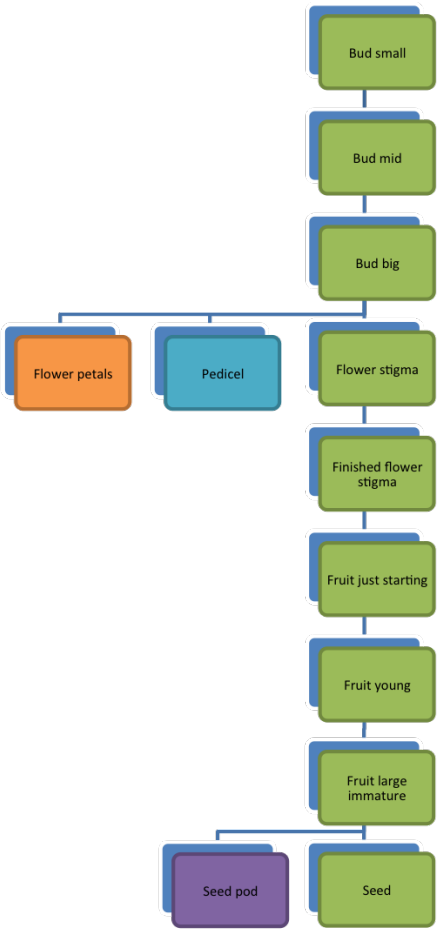
	species	part	n	av.weight
1	HEPU	bud_small	14	2.83
2	HEPU	bud_big	15	3.13
3	HEPU	flower_petals	16	2.51
4	HEPU	flower_calyx	30	2.20
5	HEPU	fruit_aborted	9	2.95
6	HEPU	finished_flower	16	2.75
7	HEPU	calyx_aborted_fruit		
8	HEPU	calyx_fruit	80	3.11
9	HEPU	fruit_young	23	1.85
10	HEPU	fruit_large_immature	20	2.63
11	HEPU	fruit_aborted	9	2.95
12	HEPU	fruit_mature	39	3.15

2.9 LEES



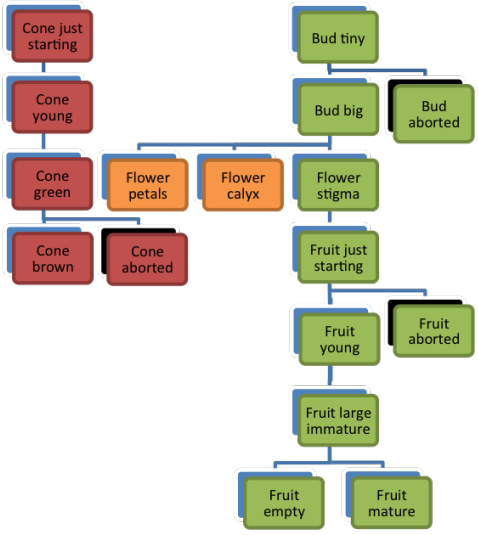
	species	part	n	av.weight
1	LEES	bud_tiny	21	0.64
2	LEES	bud_mid	7	1.10
3	LEES	bud_aborted	17	0.78
4	LEES	bud_big	16	1.34
5	LEES	flower_petals	19	0.58
6	LEES	flower_calyx	21	0.90
7	LEES	finished_flower	17	1.11
8	LEES	fruit_just_starting	30	1.24
9	LEES	fruit_young	10	2.18
10	LEES	calyx_fruit	25	0.81
11	LEES	fruit_large_immature	19	3.27
12	LEES	fruit_aborted	13	2.31
13	LEES	fruit_mature	36	3.87

2.10 PELA



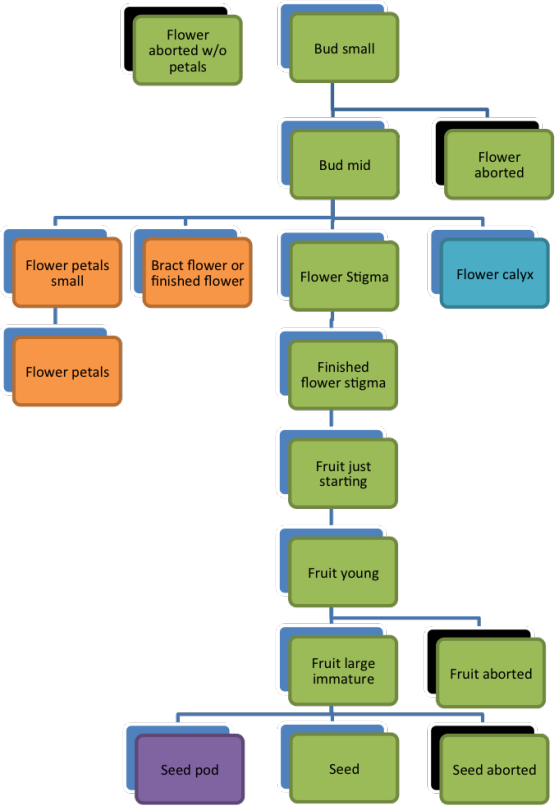
	species	part	n	av.weight
1	PELA	bud_small	12	8.08
2	PELA	bud_mid	11	12.87
3	PELA	bud_big	56	16.77
4	PELA	flower_petals	23	13.87
5	PELA	pedicel	51	2.65
6	PELA	flower_stigma	12	1.51
7	PELA	finished_flower_stigma	14	1.85
8	PELA	fruit_just_starting	17	2.45
9	PELA	fruit_young	27	7.14
10	PELA	fruit_large_immature	84	118.67
11	PELA	seed	44	121.03
12	PELA	seed_pod	43	167.19

2.11 PEPU



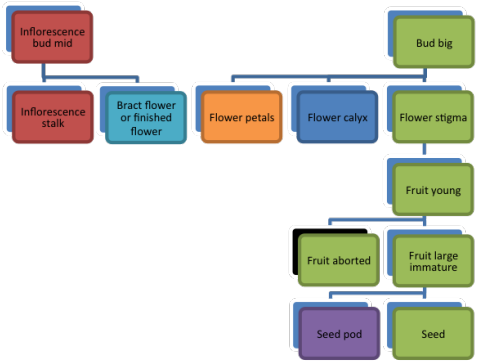
	species	part	n	av.weight
1	PEPU	cone_just_starting	10	48.32
2	PEPU	cone_young	4	80.12
3	PEPU	cone_green	14	882.46
4	PEPU	cone_brown	34	1807.26
5	PEPU	cone_aborted	4	554.52
6	PEPU	bud_tiny	1	2.00
7	PEPU	bud_big	12	7.63
8	PEPU	bud_aborted	1	3.00
9	PEPU	flower_petals	20	5.83
10	PEPU	flower_calyx	1	1.00
11	PEPU	flower_stigma	25	1.88
12	PEPU	fruit_just_starting	22	2.27
13	PEPU	fruit_young	1	3.00
14	PEPU	fruit_large_immature	1	3.40
15	PEPU	fruit_empty	423	4.06
16	PEPU	fruit_mature	161	6.50
17	PEPU	fruit_aborted	115	2.80

2.12 PHPH



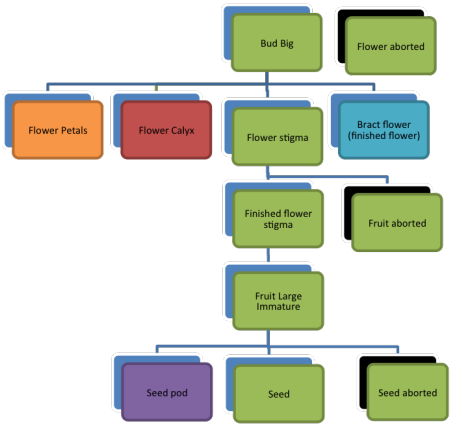
	species	part	n	av.weight
1	PHPH	bud_small	3	5.07
2	PHPH	bud_mid	19	5.87
3	PHPH	flower_petals_small	8	2.45
4	PHPH	flower_petals	22	2.91
5	PHPH	bract_flower_or_finished_flower	21	2.42
6	PHPH	flower_calyx	27	1.36
7	PHPH	flower_stigma	15	0.46
8	PHPH	flower_aborted	4	5.65
9	PHPH	flower_aborted_without_petals	19	3.86
10	PHPH	finished_flower_stigma	15	0.72
11	PHPH	fruit_just_starting	5	1.32
12	PHPH	fruit_young	11	1.93
13	PHPH	fruit_large_immature	27	3.86
14	PHPH	fruit_aborted	12	1.96
15	PHPH	seed_pod	39	2.91
16	PHPH	seed	31	2.74
17	PHPH	seed_aborted	22	0.91

2.13 PILI



	species	part	n	av.weight
1	PILI	inflorescence_bud_mid	5	4.77
2	PILI	inflorescence_stalk	24	2.63
3	PILI	bract_flower_or_finished_flower	39	8.72
4	PILI	bud_big	10	0.98
5	PILI	flower_calyx	10	0.27
6	PILI	flower_stigma		0.03
7	PILI	flower_petals	12	1.00
8	PILI	fruit_young	8	0.27
9	PILI	fruit_large_immature	14	0.76
10	PILI	fruit_aborted	13	0.47
11	PILI	seed_pod	14	0.45
12	PILI	seed	13	0.71

2.14 PUTU



	species	part	n	av.weight
1	PUTU	bud_big	10	6.41
2	PUTU	flower_petals	13	3.89
3	PUTU	flower_calyx	29	1.21
4	PUTU	bract_flower_or_finished_flower	39	1.34
5	PUTU	flower_stigma	10	1.24
6	PUTU	finished_flower_stigma	23	1.75
7	PUTU	flower_aborted	7	2.96
8	PUTU	fruit_large_immature	6	2.28
9	PUTU	fruit_aborted	10	1.37
10	PUTU	seed_pod	59	2.38
11	PUTU	seed	53	1.65
12	PUTU	seed_aborted	34	0.57

Chapter 3

Additional preliminary calculations

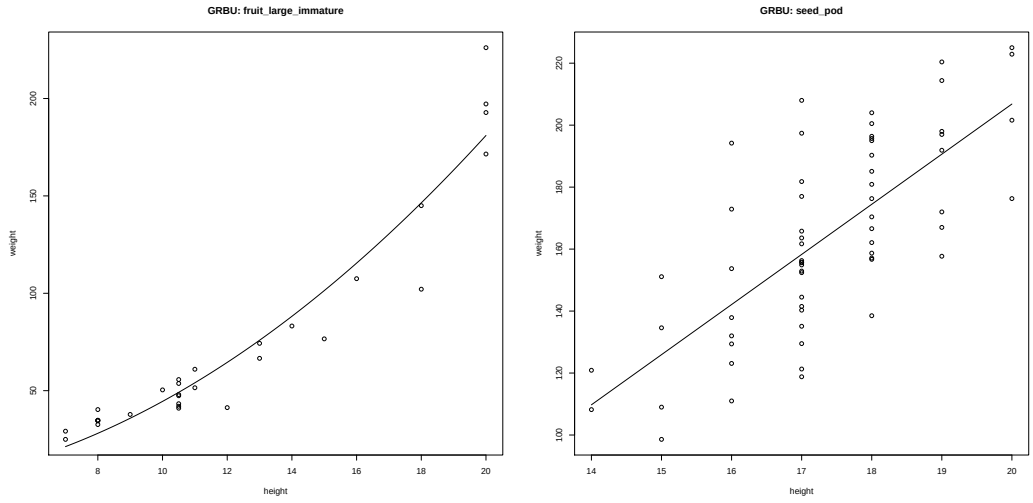
3.1 Average count/length values

	species	tot.count	AvCountPerMM
1	BAER	13030.38	5.17
2	EPMI	990.00	0.99
3	LEES	483.00	0.89

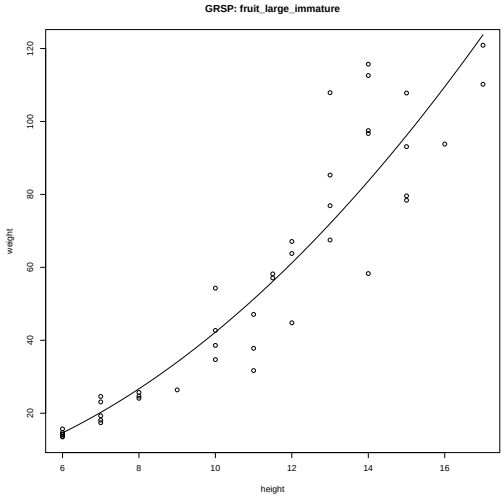
Figure 3.1: Table summarising the average number of elements per mm. To be used for calculations of mass based on the length for conversion to counts.

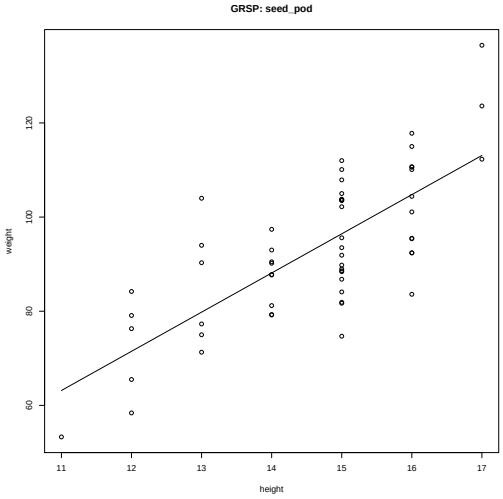
3.2 Regression Fits and Coefficients

GRBU

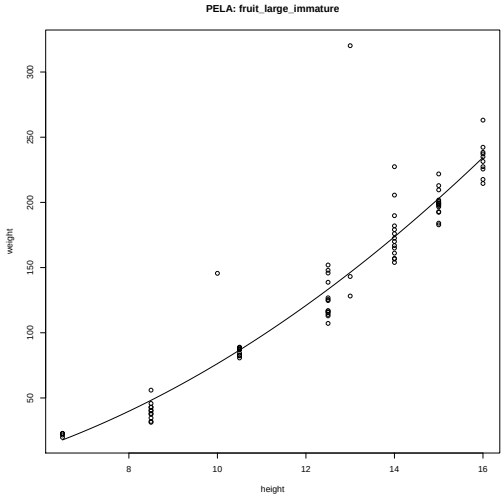


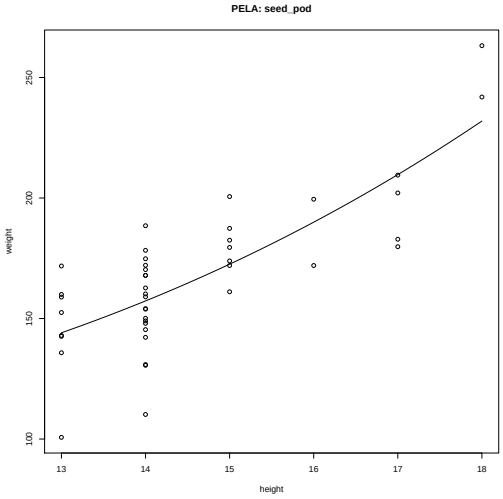
3.2.1 GRSP

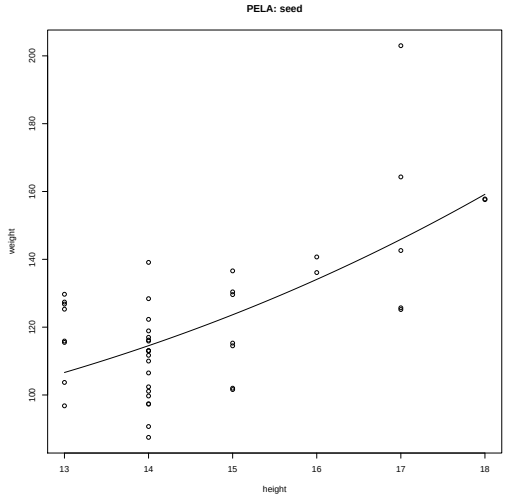




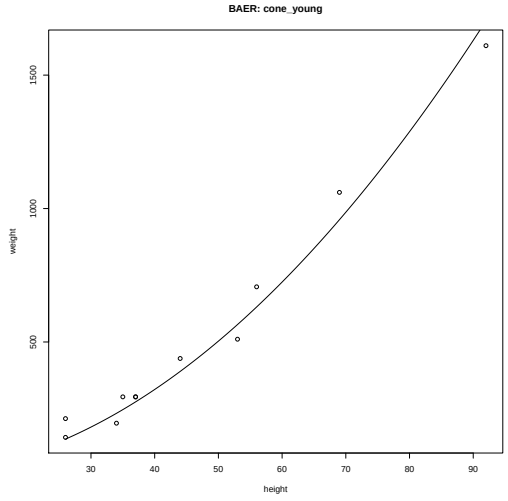
3.2.2 PELA

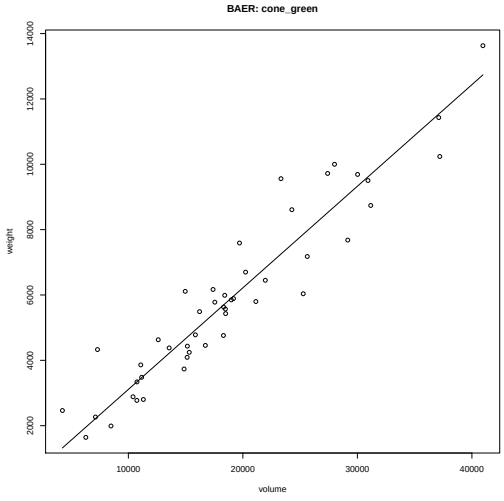


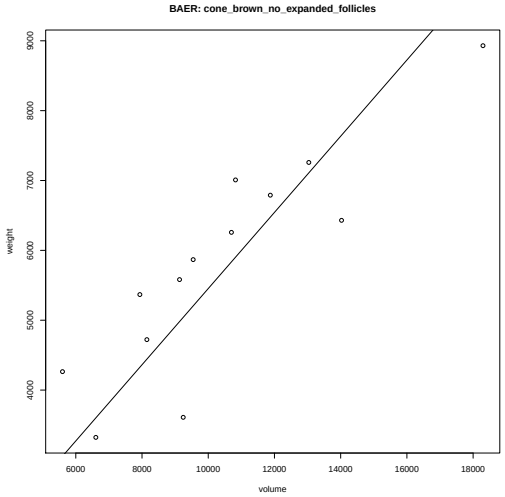


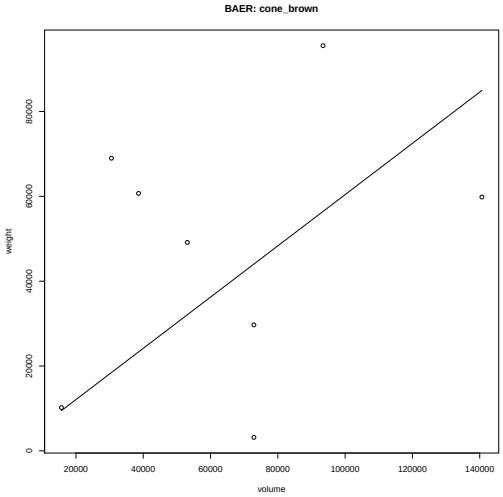

PELA: seed
weight
height
100
120
140
160
180
200
13
14
15
16
17
18

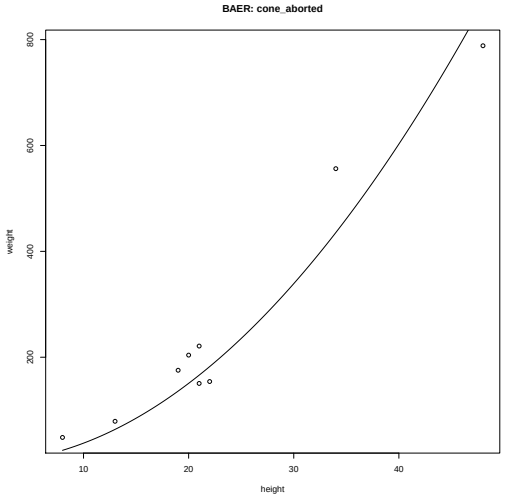
3.2.3 BAER

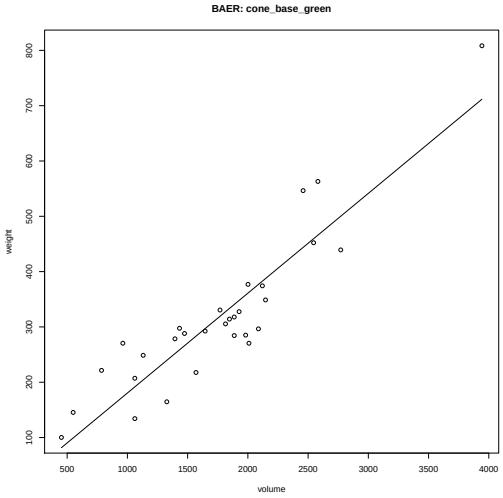

BAER: cone_young
weight
height
500
1000
1500
30
40
50
60
70
80
90

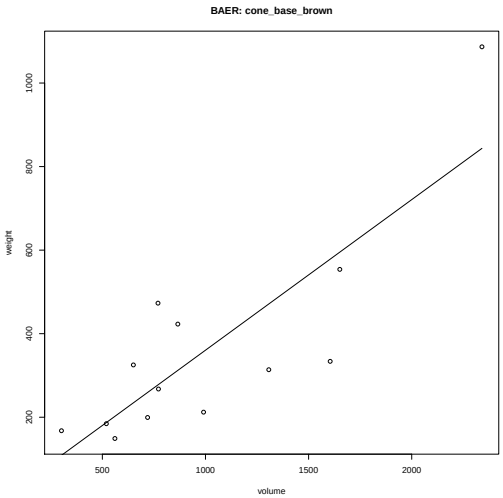

BAER: cone_green
weight
volume
2000
4000
6000
8000
10000
12000
14000
10000
20000
30000
40000


BAER: cone_brown_no_expanded_follicles
weight
volume
4000
5000
6000
7000
8000
9000
6000
8000
10000
12000
14000
16000
18000

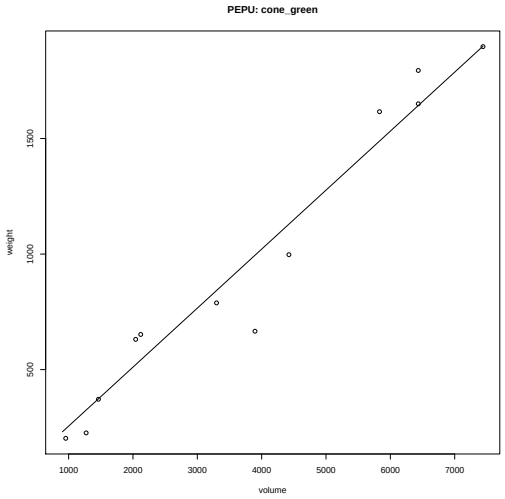

BAER: cone_brown
weight
volume
0
20000
40000
60000
80000
20000
40000
60000
80000
100000
120000
140000

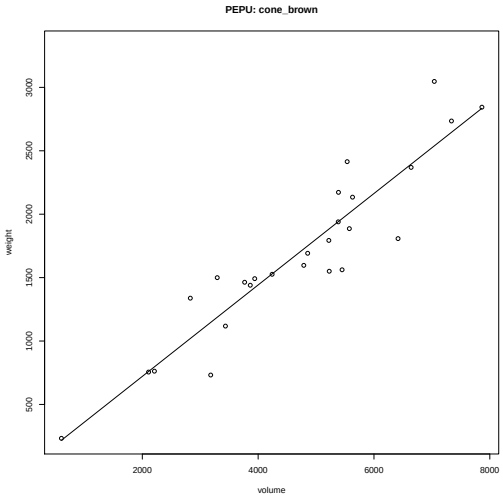

BAER: cone_aborted
weight
height
200
400
600
800
10
20
30
40

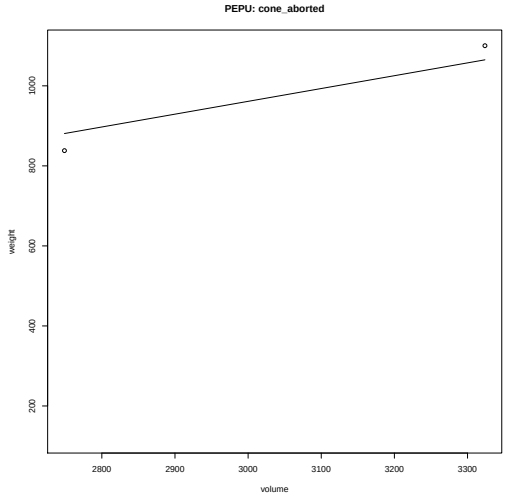

BAER: cone_base_green
weight
volume
100
200
300
400
500
600
700
800
500
1000
1500
2000
2500
3000
3500
4000


BAER: cone_base_brown
weight
volume
200
400
600
800
1000
500
1000
1500
2000

3.2.4 PEPU


PEPU: cone_green
weight
volume
500
1000
1500
1000
2000
3000
4000
5000
6000
7000


PEPU: cone_brown
weight
volume
500
1000
1500
2000
2500
3000
2000
4000
6000
8000


PEPU: cone_aborted
weight
volume
200
400
600
800
1000
2800
2900
3000
3100
3200
3300

3.2.5 Summary table for regression

	species	part	n	reg.type	reg.order	intercept	slope
1	GRBU	fruit_large_immature	31	quadratic_undecided	2.00	-1.02	0.46
2	GRBU	seed_pod	62	linear	1.00	-116.72	16.18
3	GRSP	fruit_large_immature	43	quadratic	2.00	-0.92	0.43
4	GRSP	seed_pod	57	linear	1.00	-28.35	8.32
5	PELA	fruit_large_immature	84	quadratic	2.00	-25.03	1.01
6	PELA	seed_pod	43	cubic	3.00	90.99	0.02
7	PELA	seed	44	cubic	3.00	74.87	0.01
8	BAER	cone_young	11	quadratic without intercept	2.00	0.00	0.20
9	BAER	cone_green	47	volume*density	1.00	0.00	0.31
10	BAER	cone_brown_no_expanded_follicles	13	volume*density	1.00	0.00	0.55
11	BAER	cone_brown	8	volume*density	1.00	0.00	0.60
12	BAER	cone_aborted	9	quadratic	2.00	0.00	0.38
13	BAER	cone_base_green	32	volume*density	1.00	0.00	0.18
14	BAER	cone_base_brown	13	volume*density	1.00	0.00	0.36
15	PEPU	cone_just_starting	10	No data	1.00	3.15	10.27
16	PEPU	cone_young	4	No data	1.00	-1.25	8.80
17	PEPU	cone_green	15	volume*density	1.00	0.00	0.26
18	PEPU	cone_brown	35	volume*density	1.00	0.00	0.36
19	PEPU	cone_aborted	4	volume*density	1.00	0.00	0.32

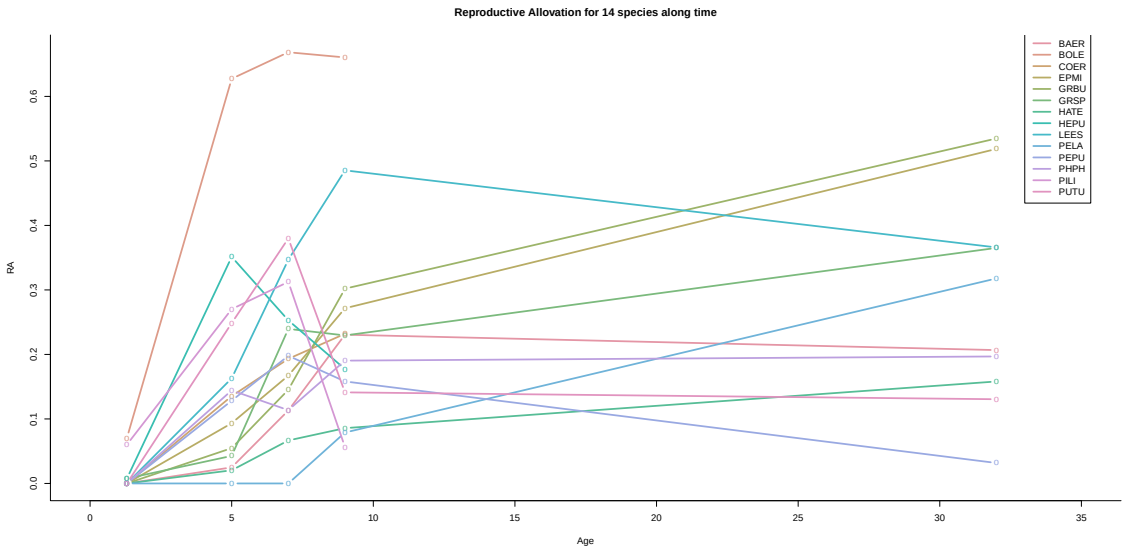
Figure 3.2: Table summarising the equations used to determine weights of individual plant parts by using their size.

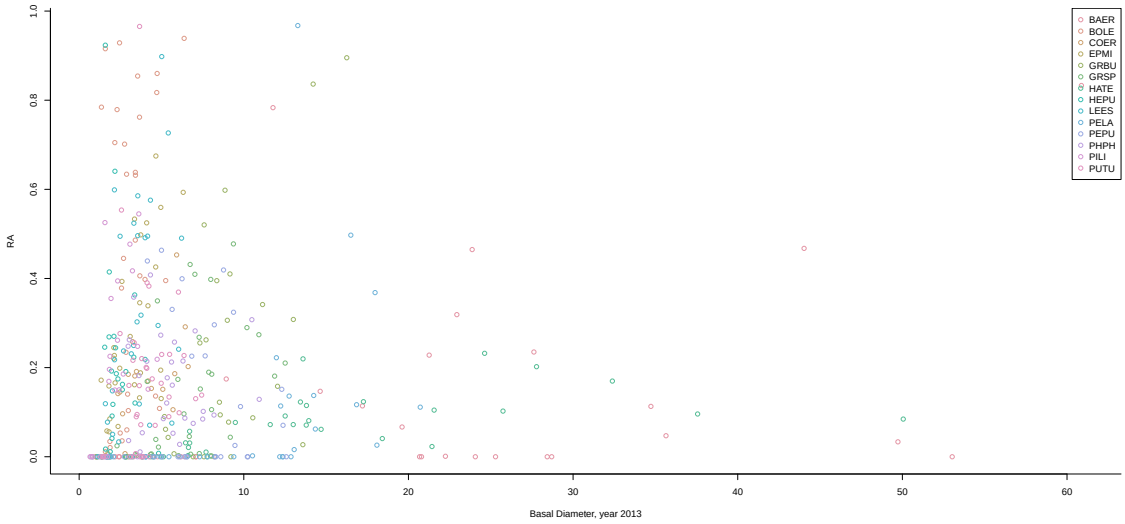
Chapter 4

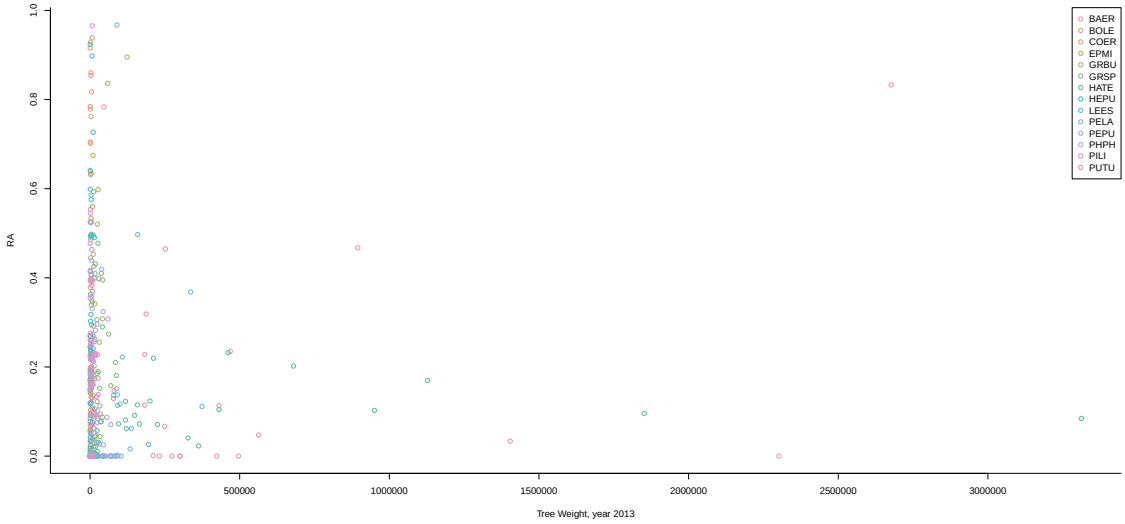
Preliminary results

4.1 Reproductive allocation results

4.1.1 Overview

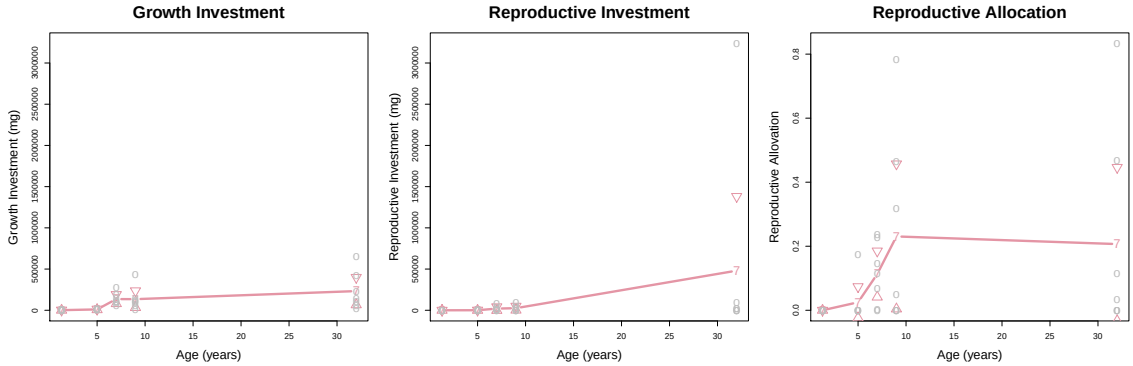


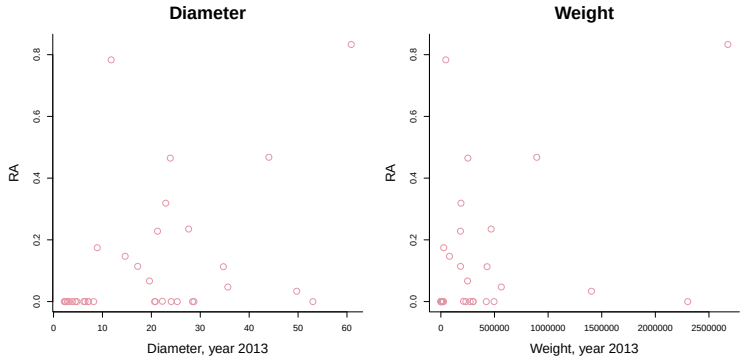

RA
Basal Diameter, year 2013
BAER
BOLE
COER
EPMI
GRBU
GRSP
HATE
HEPU
LEES
PELA
PEPU
PHPH
PILI
PUTU


RA
Tree Weight, year 2013
BAER
BOLE
COER
EPMI
GRBU
GRSP
HATE
HEPU
LEES
PELA
PEPU
PHPH
PILI
PUTU

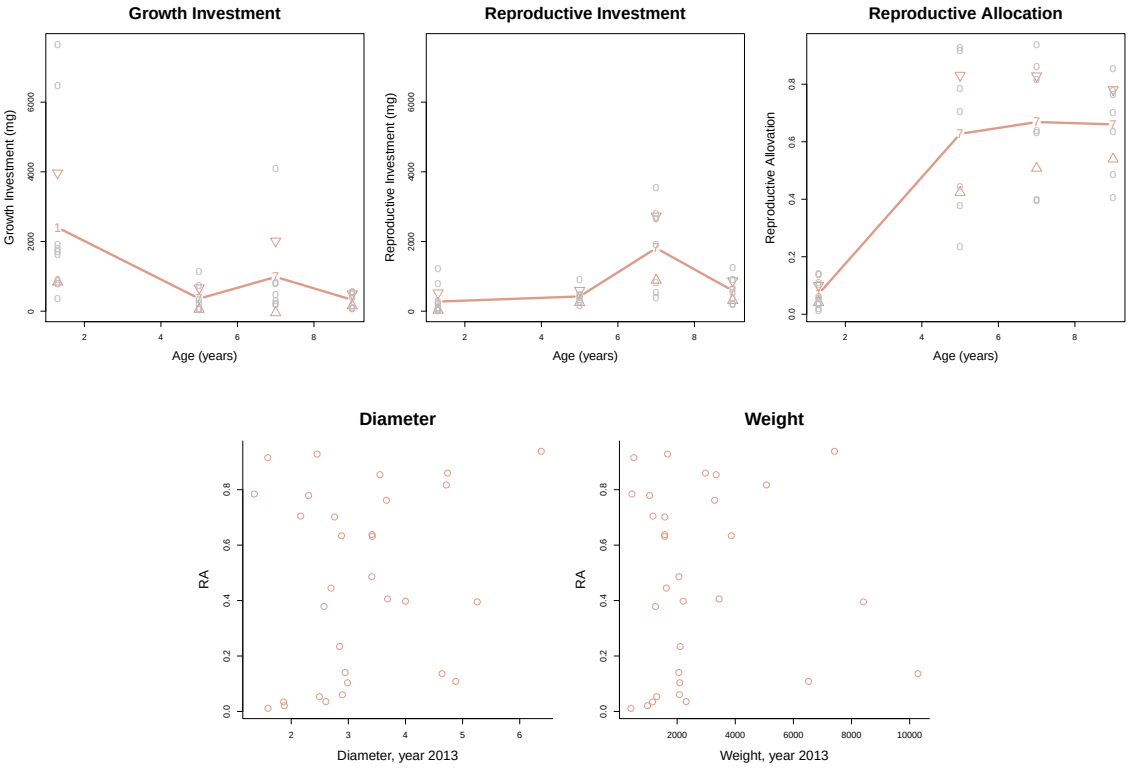
4.2 Individual species

4.2.1 BAER

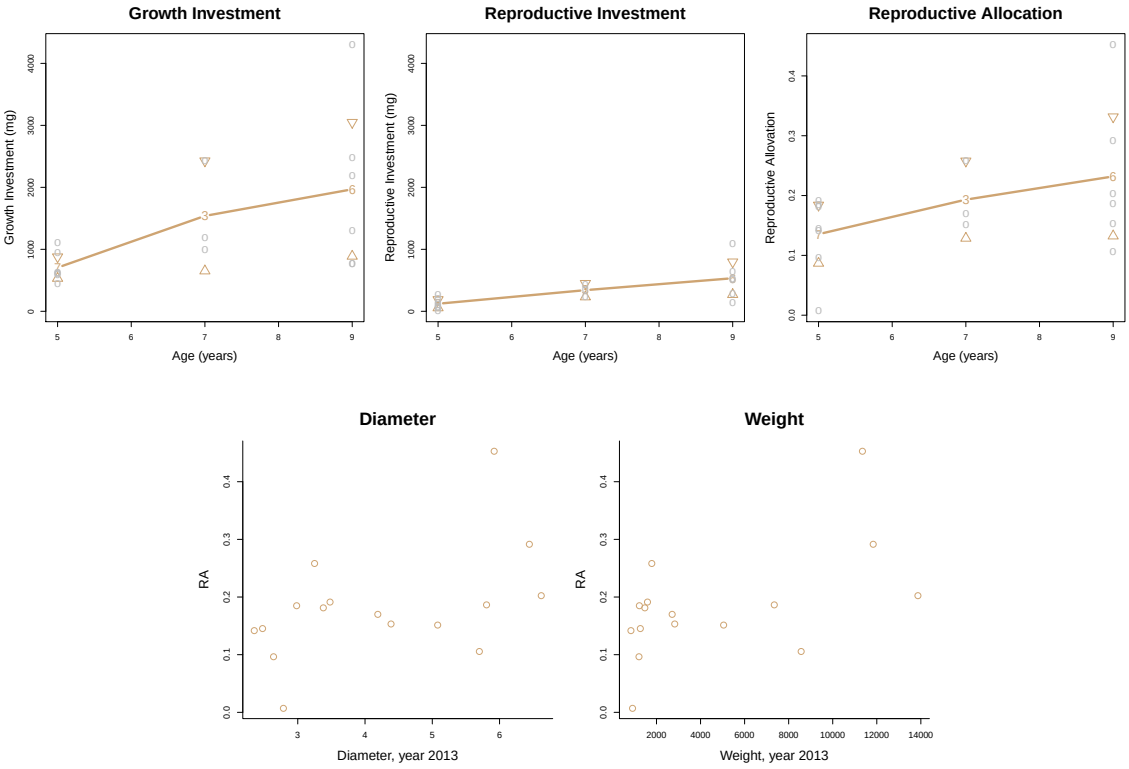




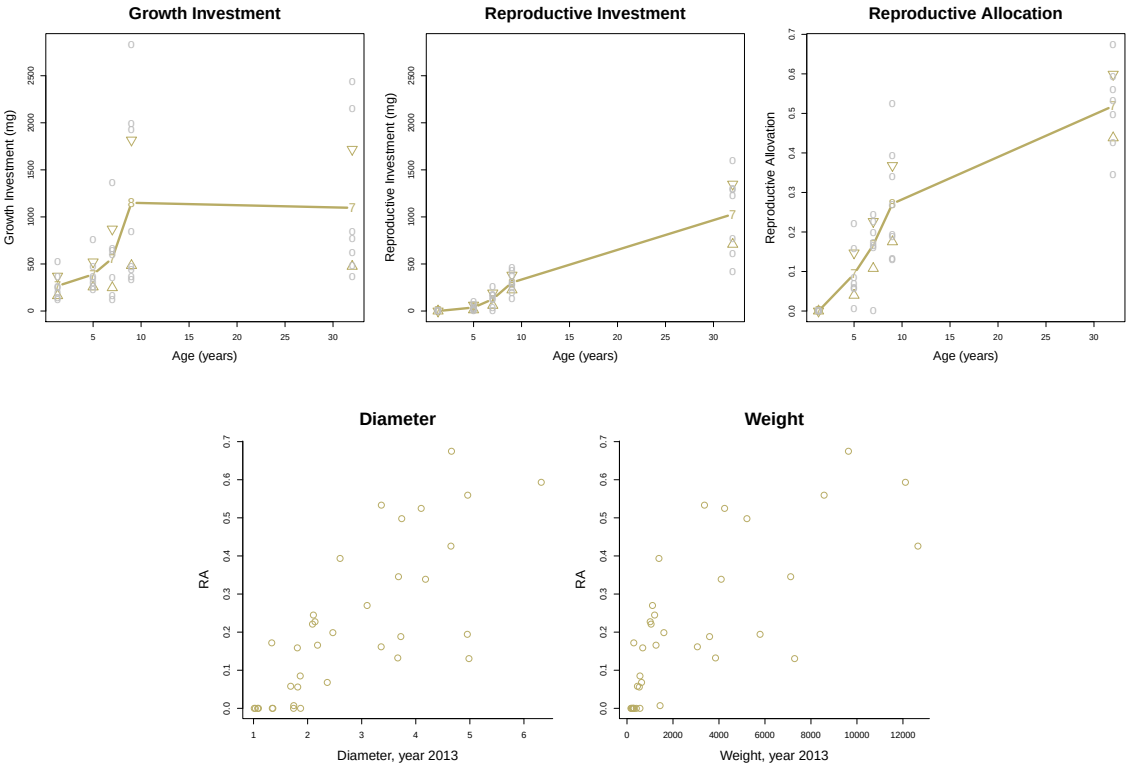
4.2.2 BOLE


Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)
Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013

4.2.3 COER

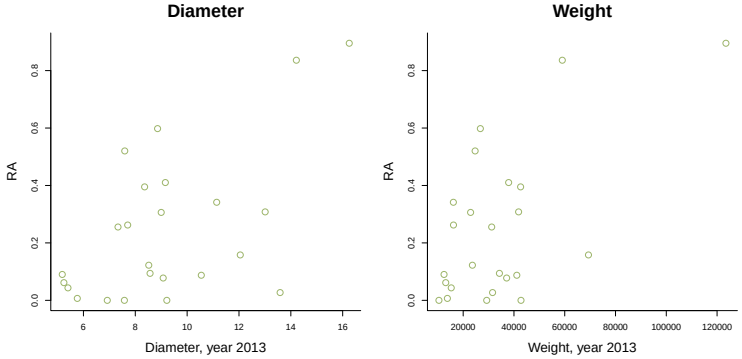

Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)
Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013

4.2.4 EPMI

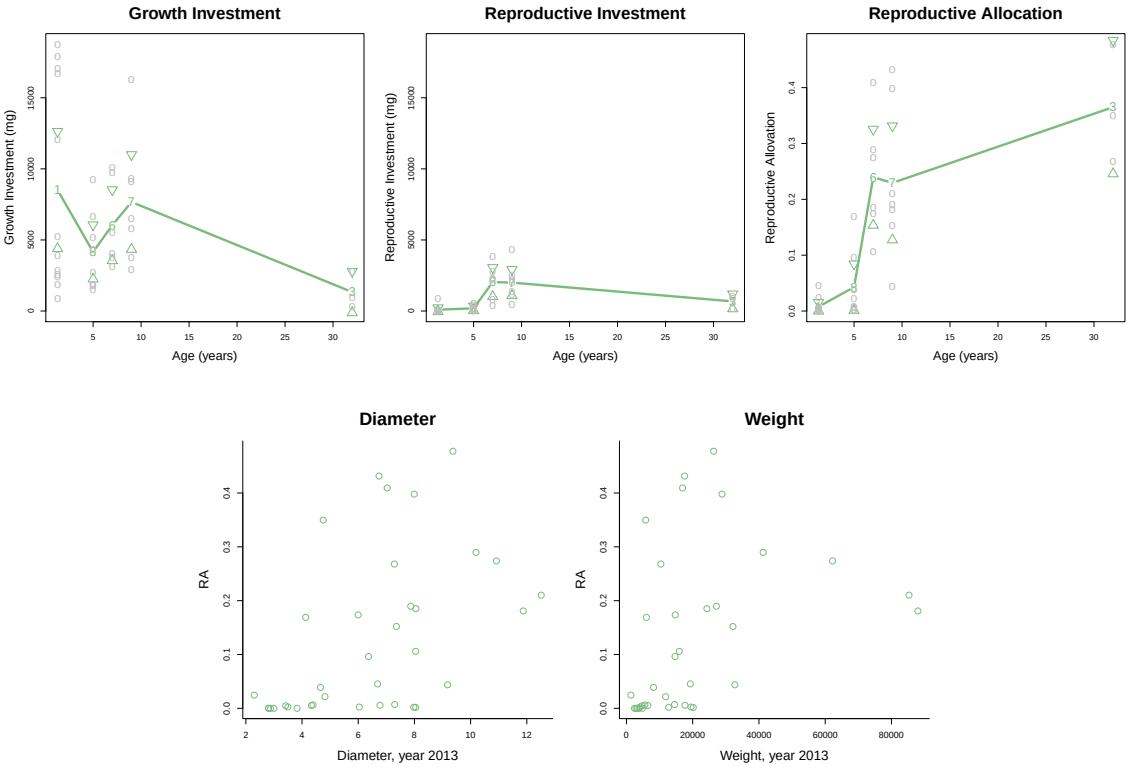

Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)
Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013

4.2.5 GRBU

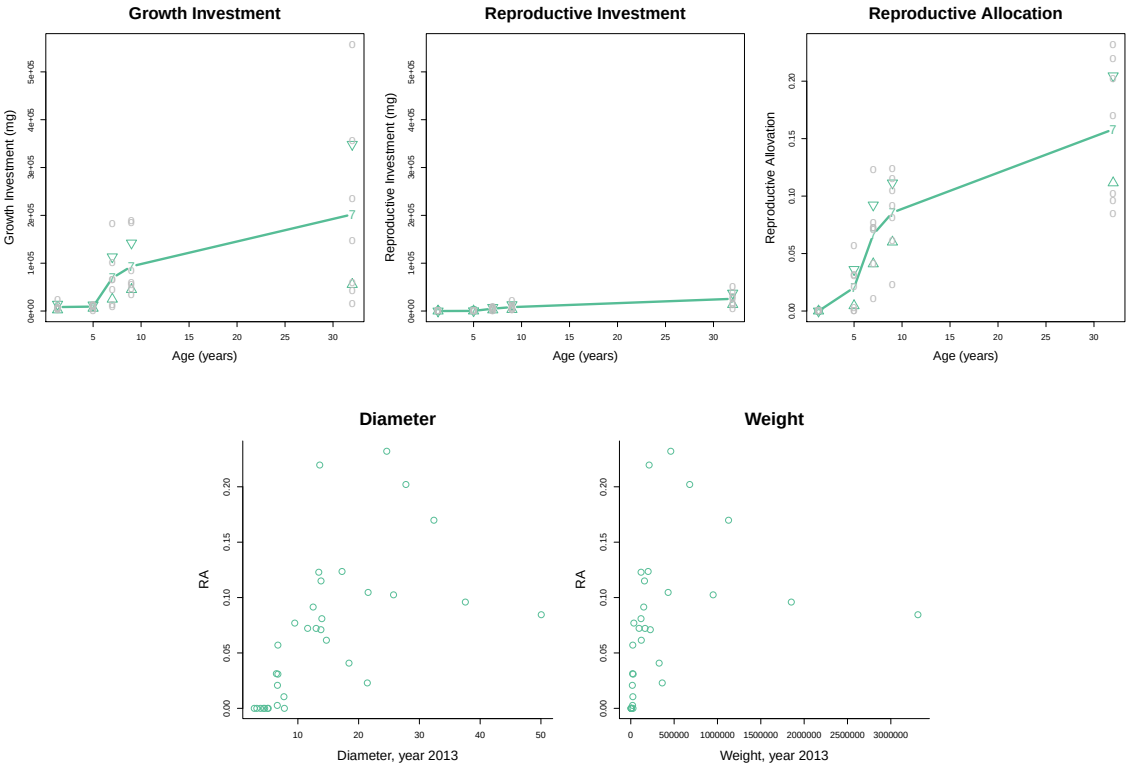
Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)


Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013

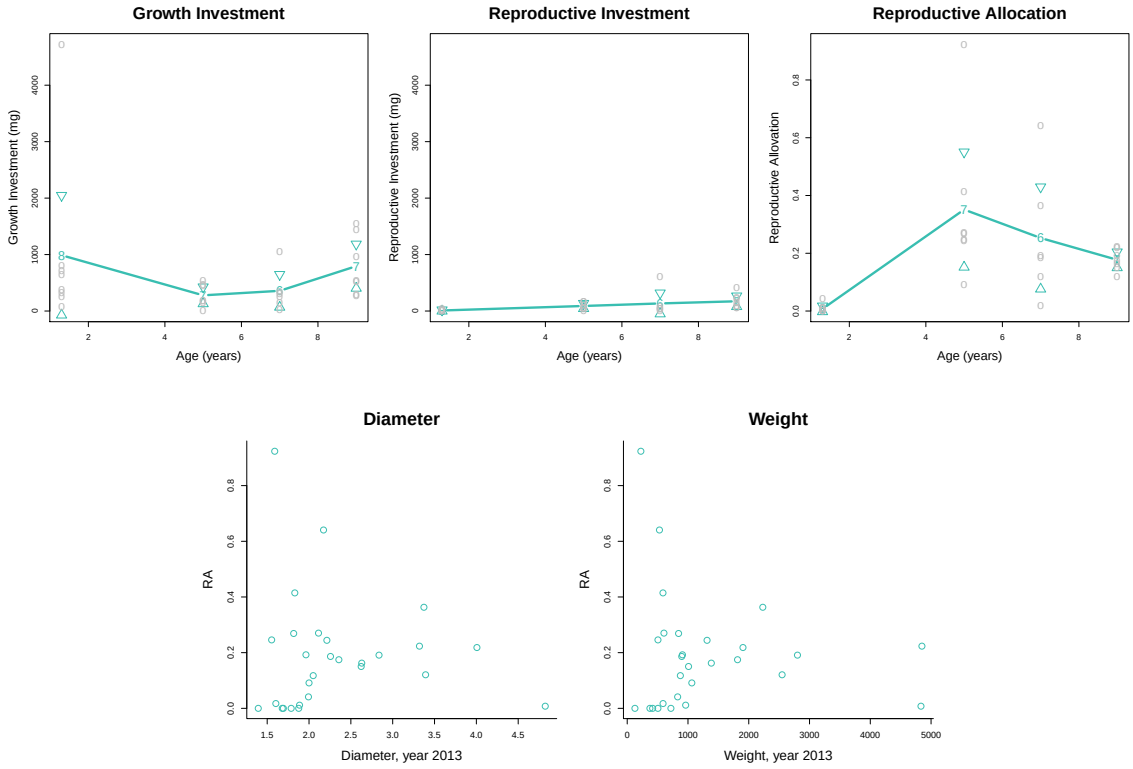
4.2.6 GRSP


Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)
Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013

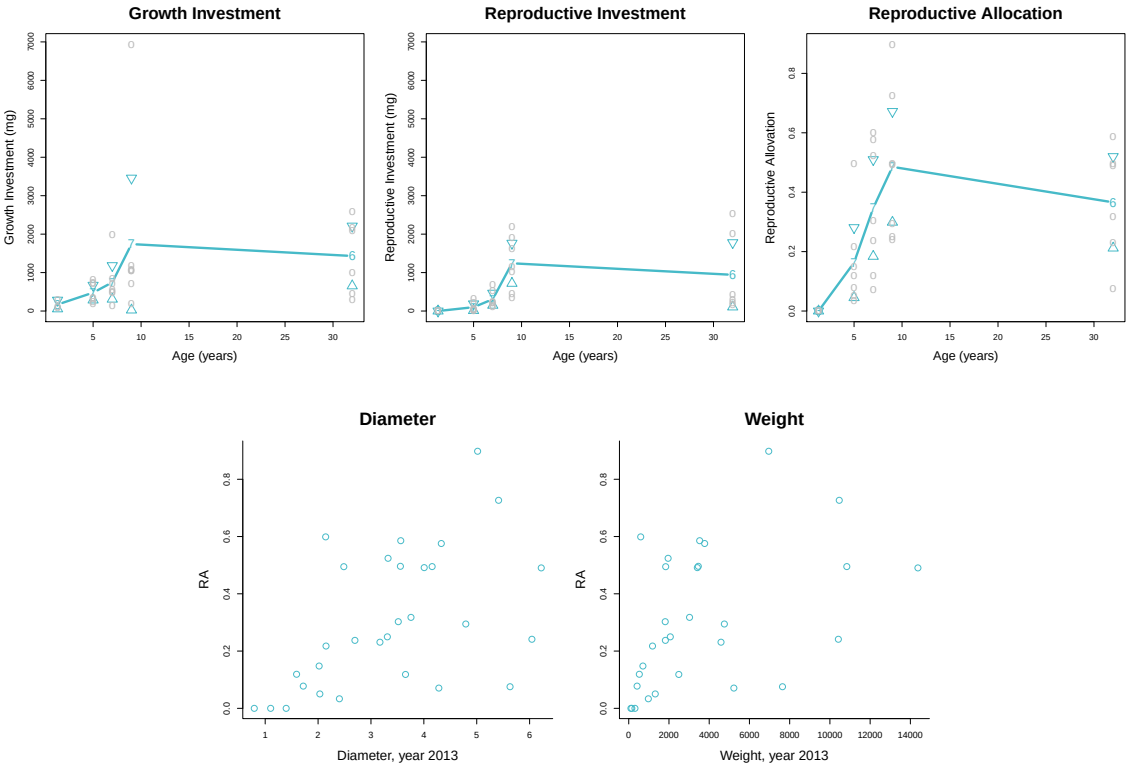
4.2.7 HATE


Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)
Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013

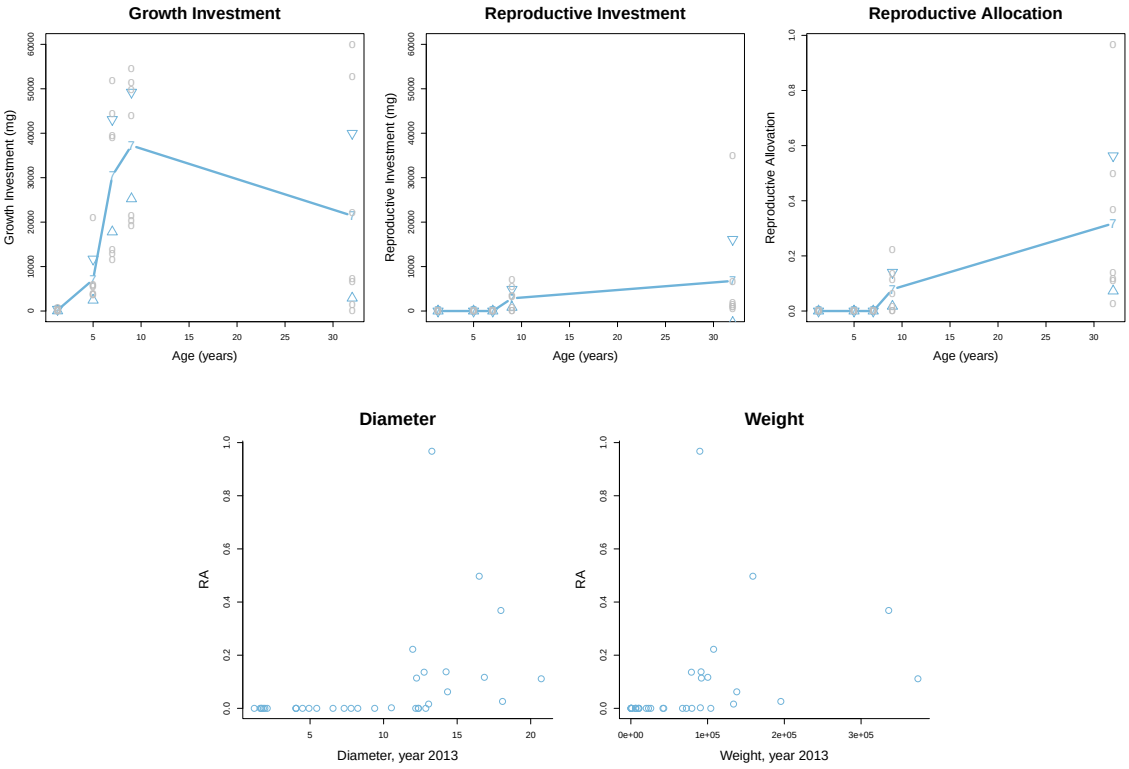
4.2.8 HEPU


Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)
Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013

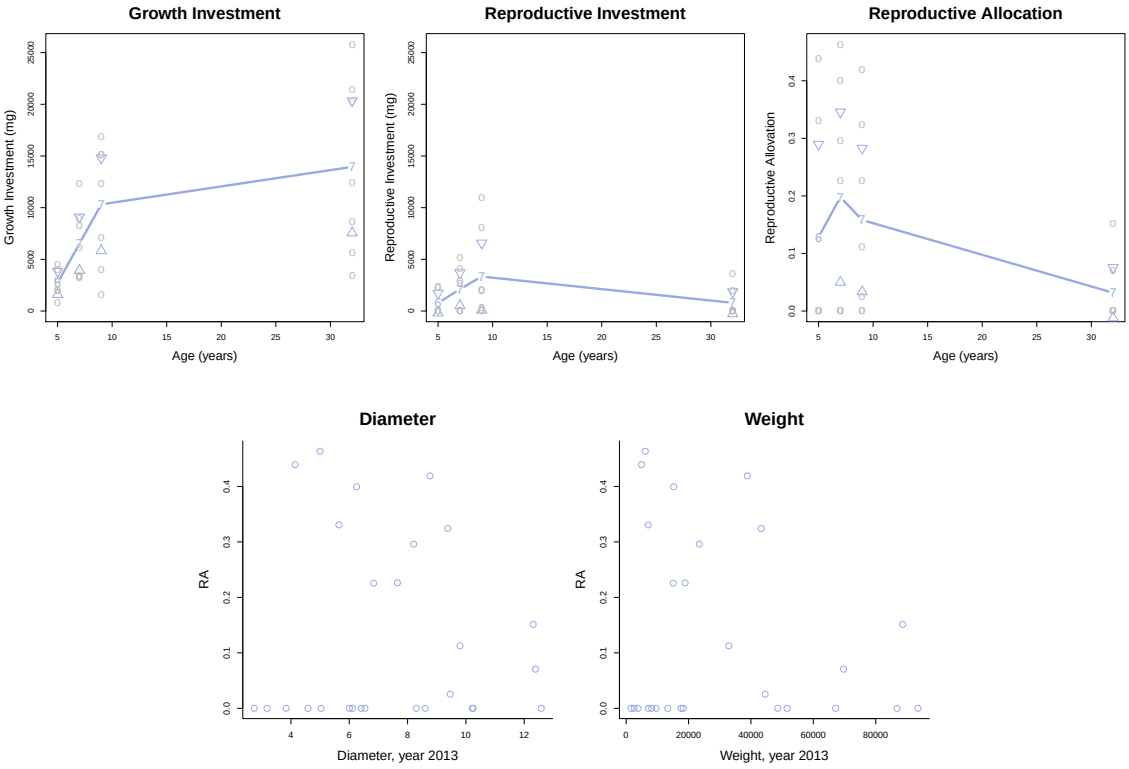
4.2.9 LEES


Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)
Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013

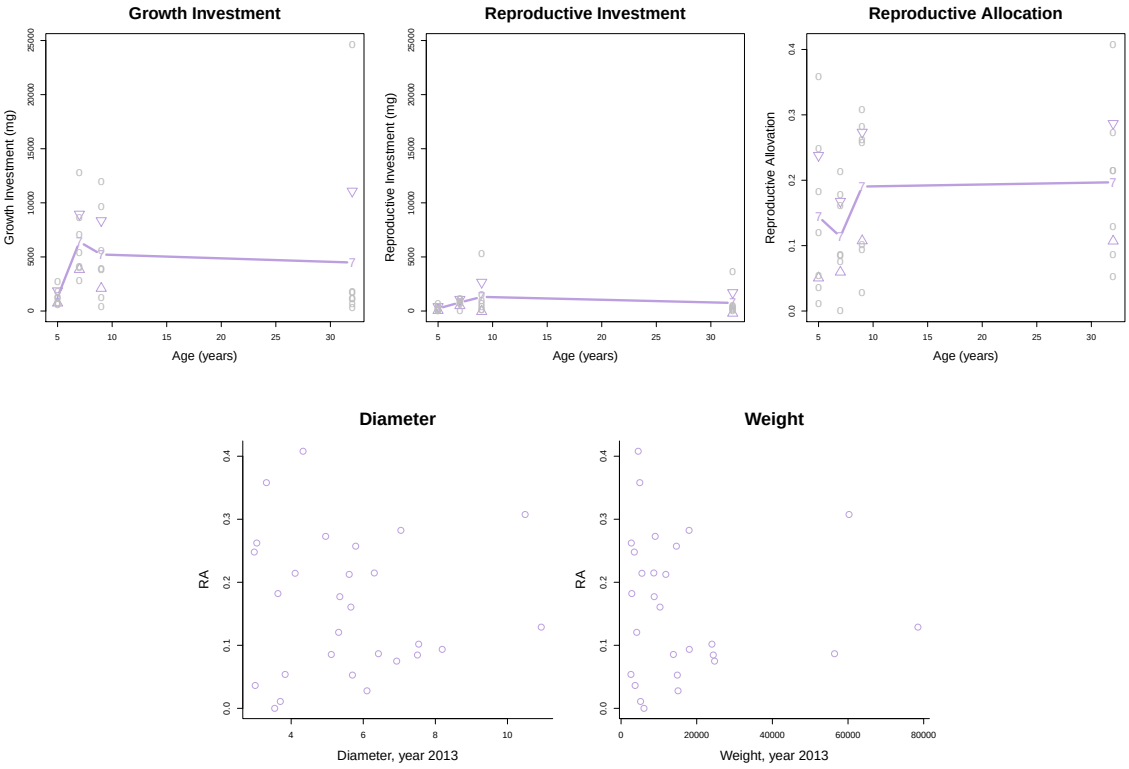
4.2.10 PELA


Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)
Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013

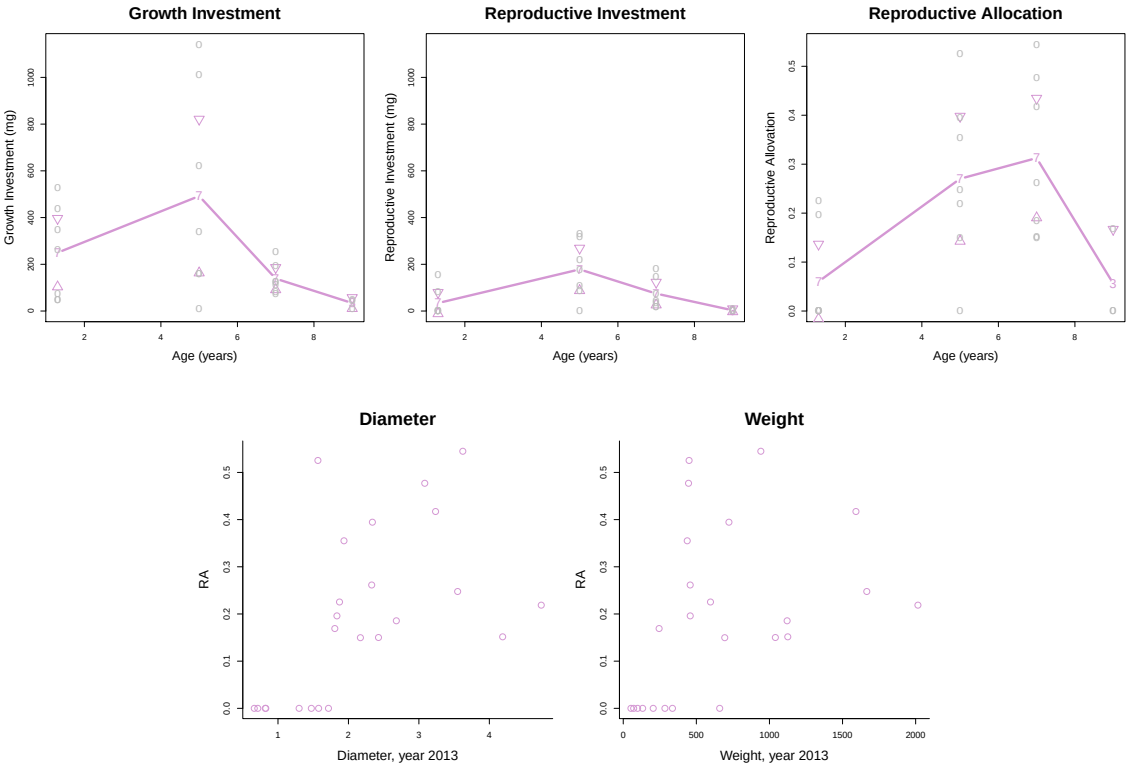
4.2.11 PEPU


Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)
Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013

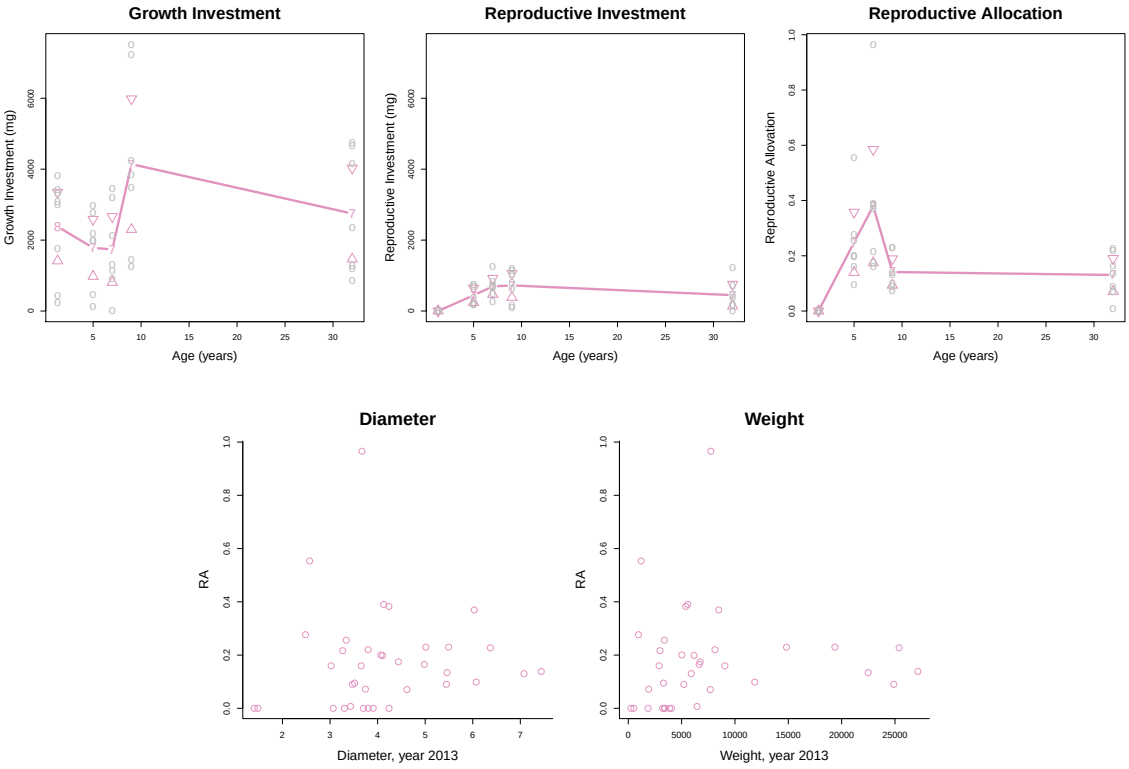
4.2.12 PHPH


Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)
Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013

4.2.13 PILI


Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)
Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013

4.2.14 PUTU


Growth Investment
Growth Investment (mg)
Age (years)
Reproductive Investment
Reproductive Investment (mg)
Age (years)
Reproductive Allocation
Reproductive Allocation
Age (years)
Diameter
RA
Diameter, year 2013
Weight
RA
Weight, year 2013