

# ESTIMATING ABOVE-GROUND BIOMASS IN CTFS PLOTS

R. CONDIT

SHORT-TITLE: Biomass END\_SHORT-TITLE

## CTFS BIOMASS PACKAGE

DESCRIPTION: This package provides a main function and a series of subroutines for calculating above-ground-biomass (AGB) from tree diameter. The base functions can be used with any tables having diameter and wood density for trees. The top-level functions are designed to CTFS R Analytical tables, and to consult the CTFS wood-density database, to fill in the agb column with the biomass (dry weight, in Mg) for each tree and stem.

The top level function is `biomass.CTFSdb`. It must be passed two tables, one with trees, the other with stems. These are the two standard CTFS R Analytical tables, described in the Data Format section. The function also requires the name of the CTFS wood-density table, available for download at <http://ctfs.arnarb.harvard.edu/Public/Datasets>.

Please note that the CTFS R Analytical Tables already have the agb column filled in, using this function and the default values for the Chave calculation (in the function `Chave.AGB`).  
END\_DESCRIPTION

0.1. **Sample calculations.** Here is a sample with BCI data, using the function `CTFSplot` (in the Utilities Package) to load the Full table and the Stem table.

```
> CTFSplot("bci", "full", census = 1)
[1] 7
> CTFSplot("bci", "stem", census = 1)
[1] 6
> attach_if_needed("biomass/wsg.ctfs.Rdata")
[1] 2
> args(biomass.CTFSdb)
function (RStemTable, RTreeTable, whichtable = "tree", dbhunit = "mm",
  plot = "bci", wsgdata = wsg.ctfs2, forest = "moist", ht.param = NULL,
  htmodel = predht.asym)
NULL
> newtable = biomass.CTFSdb(RStemTable = bci.stem1, RTreeTable = bci.full1, plot = "bci")
> head(newtable[, c("sp", "dbh", "agb")])
      sp dbh      agb
1 swars1  90 0.0426371077
2 hybapr  35 0.0028894861
3 aegipa  10 0.0001466688
4 beilpe   NA 0.0000000000
5 faraoc   NA 0.0000000000
6 hybapr   NA 0.0000000000
```

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```
> sum(newtable$agb)/50
```

```
[1] 411.0447
```

To run at Lambir:

```
> CTFSplot("lambir", "full", census = 1)
```

```
[1] 4
```

```
> CTFSplot("lambir", "stem", census = 1)
```

```
[1] 3
```

```
> newtable = biomass.CTFSdb(RStemTable = lambir.stem1, RTreeTable = lambir.full1, plot
```

```
> head(newtable[, c("sp", "dbh", "agb")])
```

	sp	dbh	agb
1	MEMECO	1.0	0.0001715131
2	ANI2DI	1.1	0.0001839861
3	DACRBM	1.3	0.0002307484
4	DRYOAR	1.3	0.0002705326
5	CANALL	1.4	0.0002329130
6	DIOSMI	1.5	0.0003842751

```
> sum(newtable$agb)/52
```

```
[1] 490.6625
```

**0.2. CTFS Wood Density table.** The calculations depend on the table `wsg.ctfs2` (attached from file `wsg.ctfs.Rdata`) having values of wood density for many CTFS species taken from the literature (assembled by Chave et al., thanks to Nate Swenson for the data). The table has columns with plot name, species code, and the species' wood density. One other important column is `idlevel`, which indicates whether the wood density value comes from the species itself, or from a mean for its genus or family.

To use the table, you must use one of the plot names included in the table and use the CTFS species codes.

The function `density.ind` matches species code and plot names in a table with species names and returns a vector of one density value per individual. If a species code is not found in the plot, the mean wood density for all other species in the plot is assigned to that species. If the plot is not found, however, nothing is assigned.

```
> colnames(wsg.ctfs2)
[1] "wsg"      "idlevel"  "site"     "sp"       "genus"    "species"  "genwood"  "famwood"  "sp"
> head(wsg.ctfs2[, c("site", "sp", "idlevel", "wsg")])
      site      sp idlevel      wsg
1 amacayacu abarbarb  genus 0.566750
2 amacayacu abarjupu species 0.585143
3 amacayacu abutgran  genus 0.450000
4 amacayacu acalcune  genus 0.300000
5 amacayacu aegicord  genus 0.656667
6 amacayacu aegiglan  genus 0.656667
> data.frame(table(wsg.ctfs2$site))
      Var1 Freq
1   amacayacu 1663
2         bci 1089
3 bukittimah  562
4     cardoso  116
5   changbai   53
6         crc   39
7     fushan  110
8     gutian  154
9 haliburton   18
10    hawaii   20
11     hkk    334
12     ituri  845
13  khaochong  609
14     korup  494
15    lambir 1641
16 laplanada  241
17 lienhuachih 145
18   luquillo  157
19    manaus  915
20  mosingto  265
21 mudumalai   74
```

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22	nanjenshan	129
23	palanan	335
24	pantree	2719
25	pasoh	937
26	serc	19
27	sinharaja	223
28	wabikon	38
29	wytham	23
30	xtbg	469
31	yasuni	1134

0.3. **Allometry.** The function `Chave.AGB` applies the equations given in Chave (2005, *Oecologia*) to estimate above-ground biomass (in Mg) for individual diameters. A wood density for each stem (or one single value) must be submitted. Check inside the function to see the parameter values.

```
> args(Chave.AGB)
```

```
function (dbh, density = 0.62, htparam = c(41.7, 0.057, 0.748),  
  heightmodel = predht.asym, forest = "moist")
```

```
NULL
```

```
> testdbh = c(1, 2, 5, 10, 20, 30, 50, 100, 200)
```

```
> AGBmoist = Chave.AGB(dbh = testdbh, density = 0.61, htparam = NULL, forest = "moist",
```

```
> AGBwet = Chave.AGB(dbh = testdbh, density = 0.61, htparam = NULL, forest = "wet")
```

```
> data.frame(testdbh, AGBwet, AGBmoist)
```

	testdbh	AGBwet	AGBmoist
1	1	1.767010e-01	1.362456e-01
2	2	7.627926e-01	6.607892e-01
3	5	6.504111e+00	6.572012e+00
4	10	3.588317e+01	4.073561e+01
5	20	2.004350e+02	2.556408e+02
6	30	5.391914e+02	7.361778e+02
7	50	1.804600e+03	2.684672e+03
8	100	8.354351e+03	1.396356e+04
9	200	3.249528e+04	6.102064e+04

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0.4. **Appendix.** Output created by

```
> Sweave("~/programs/CTFSRpackage/biomass.CTFSdb.Rnw")
> system("htlatex biomass.CTFSdb.tex")
> system("pdflatex biomass.CTFSdb.tex")
> system("mv biomass.CTFSdb* ~/programs/CTFSRpackage/biomass")
> system("mv ~/programs/CTFSRpackage/biomass/biomass.CTFSdb.html ~/programs/CTFSRpackage/biomass")
> system("cp ~/programs/CTFSRpackage/biomass/* /var/www/Public/CTFS_RPackage/files/tutorials/04_appendix/CTFSdb.html")
```