

HARVEST.for -- Version 1.0

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GENERALIZED PROGRAM FLOW OF HARVEST.for

```
main()
{
    readsp() - read names of potential tree species (contained in
species.tab).
    readmas() - read species-specific biomass coefficients
(contained in massin.tab).
    readtap() - read species-specific taper coefficients (contained
in taperou.tab).
    readhgt() - read species-specific hgt-diameter coefficients
(contained in richin.tab).
    readcof() - read other species-specific parameters used in
computations (contained in params.tab).
```

```

queue for parameter settings*
  [set lower and upper limits]

for lower to upper limit -> stump height
  for lower to upper limit -> min. tree diameter
    for lower to upper limit -> top diameter
      for lower to upper limit -> slope
        for each possible tree species (max of 30)
          for each possible tree diameter class (max of 400)
            /* calculate mass of bole, branches, leaves, roots
*/
                /* calculate stump mass */
                /* calculate mass of top loss */
                /* calculate % decay of bole */
                /* calculate % breakage of bole*/
            next diameter class
          next tree species
        write results to disk file
      next slope
    next top diameter
  next min. tree diameter
next stump height
}

```

QUEUES

Main queue for program control and selection of harvest parameters

Select Option:

- 1 - Mod Stump Hgt (m)
- 2 - Mod Top Diam. (cm)
- 3 - Mod Min Diam. (cm)
- 4 - Mod Slope (deg)

- 5 - Mod Stand Age (yrs)

[If using single-aged stand]

- 6 - Select file containing stand table [filename]
- 7 - Generate stand table
- 8 - Use command file
- 9 - Execute

- 10 - Exercise functions
- 11 - Exit to DOS Shell
- 12 - Quit

Queue displayed in GENESIS() [option 7]

- Select Option:
- 1 - Normal Distribution
 - 2 - Negative Exponential
 - 3 - Positive Exponential
 - 4 - One Line at a Time
 - 5 - Exit to DOS Shell
 - 6 - Quit

Queue displayed in EXERCISE() [option 10]

- Select Option:
- 1 - function DECAY
 - 2 - function BREAKAGE
 - 3 - Exit to DOS Shell
 - 4 - Quit

DESCRIPTION OF SUBROUTINES AND FUNCTIONS

Subroutines

subroutine AGG() - aggregates discrete distribution of stems into 5-cm size classes

subroutine DUMP() - dumps select results to output files

subroutine DOSCMD() - handles transition to and from the DOS shell

subroutine EXERCISE() - exercises select functions

subroutine GENESIS() - creates a stand table

subroutine GETAGE() - queues for stand age

subroutine READCOF() - reads parameters specific to harvest.for

subroutine READHGT() - reads coefficients for dbh-height allometry

subroutine READMAS() - reads biomass coefficients

subroutine READSP() - reads species list

subroutine READTAB() - reads stand tables

subroutine READTAP() - read taper coefficients

subroutine RMASS(speciesid,dbh_cm,total,thebole,other) - calculates mass. Returns total, thebole, and other in Mg.
 thebole = stem wood + stem bark
 other = root + foliage + live & dead branches
 total = thebole+other

subroutine SPECIES() - queues for species name

Functions

real function BASAREA(dbh_cm) - returns basal area in m²

real function BREAKAG(dbh_cm,slope_degrees,Brmax,b5,b6) - returns % breakage of bole. Brmax, b5, and b6 from params.tab.

real function DECAY(age,Dmax,b3,b4) - returns % decay of bole. Dmax, b3, b4 are from params.tab.

real function DIAMBOL(speciesid,dbh_cm,h_m,hgt_m) - returns diameter of a bole at height hgt_m.

real function HEIGHT(dbh_cm,speciesid) - returns height in m

real function ROOTMAS(dbh_cm) - returns root mass in Mg using BIOLIB Eq. #6 for PSme

real function SPECID(sp) - returns species id number

real function STUMPD(dbh_cm, stump height_m,b2) - returns stump diameter in cm. b2 is from params.tab.

real function STUMPV(stump height_m,stump top diameter_m, ba top_m2, ba bottom_m2, form factor, slope_degrees) - returns stump volume in m3.

real function TOPF(speciesid,dbh_cm, top diameter_cm, debug) - returns volume in m3 of bole from the specified top diameter to the top of the tree.

real function VOL(speciesid,dbh_cm,hgt_m, upper hgt_m,lower hgt_m) - returns volume of a bole (m3) between specified lower and upper height using Kozak's taper equation.

FILES ASSOCIATED WITH HARVEST.for
 =====

PARAMETER FILES:

1. MASSIN.TAB - biomass coefficients
 Coefficients correspond to b0 and b1 for foliage, live branch, dead branch, stem bark, and stem wood.

Coefficients were derived from BIOLIB and were based on the following list provided by Gody Spycher, 2 July, 1991. Number refers to equation number in BIOLIB.

STUDYID	Species	Total Foliage [BFT]	Live Branch [BBL]	Dead Branch [BBD]	Stem Bark [BSB]	Stem Wood [BSW]
OHJA	ABAM	23 ABAM	24 ABAM	545 TSHE	319 ABAM	318 ABAM
OHJA	ABCO	23 ABAM	24 ABAM	545 TSHE	379 ABCO	378 ABCO
OHJA	ABGR	23 ABAM	24 ABAM	545 TSHE	379 ABCO	378 ABCO
OHJA	ABLA2	23 ABAM	24 ABAM	545 TSHE	397 ABLA	396 ABLA
OHJA	ABPR	27 ABPR	28 ABPR	3 PSME	251 ABPR	252 ABPR
OHJA	ACMA	428 ACMA	32 ACMA	33 ACMA	35 ACMA	34 ACMA
OHJA	ALRU	272 ALRU	274 ALRU	422 ALRU	275 ALRU	276 ALRU

OHJA	ARME	40	CACH	41	CACH	431	ARME	44	CACH	43	CACH
OHJA	CACH	40	CACH	41	CACH	42	CACH	44	CACH	43	CACH
OHJA	CADE3	1	PSME	2	PSME	3	ABAM	385	CADE	384	CADE
OHJA	CONU	272	ALRU	274	ALRU	422	ALRU	275	ALRU	276	ALRU
OHJA	PILA	66	PILA	67	PILA	60	PINUS	391	PILA	390	PILA
OHJA	PIMO	66	PILA	67	PILA	60	PINUS	391	PILA	390	PILA
OHJA	PSME	1	PSME	2	PSME	3	PSME	343	PSME	342	PSME
OHJA	QUGA	40	CACH	41	CACH	42	CACH	44	CACH	43	CACH
OHJA	RHPU	272	ALRU	274	ALRU	422	ALRU	275	ALRU	276	ALRU
OHJA	TABR	8	TSHE	18	TSHE	545	TSHE	349	TSHE	348	TSHE
OHJA	THPL	46	CEDAR	47	CEDAR	3	PSME	400	THPL	399	THPL
OHJA	TSHE	8	TSHE	18	TSHE	545	TSHE	340	TSHE	348	TSHE
OHJA	TSME	14	TSME	15	TSME	16	TSME	340	TSME	339	TSME

Other Species not included on list

Species	Total Foliage [BFT]	Live Branch [BBL]	Dead Branch [BBD]	Stem Bark [BSB]	Stem Wood [BSW]					
ABAM	19	ABIES	20	ABIES	545	TSHE	379	ABCO	21	ABIES
BEPA	272	ALRU	274	ALRU	422	ALRU	275	ALRU	276	ALRU
CHNO							325	CHNO	324	CHNO
LAOC	1	PSME	2	PSME	3	PSME	343	PSME	342	PSME
PICO	63	PICO	64	PICO	3	PSME	412	PICO	411	PICO
PIEN	465	PISI	466	PISI	3	PSME	415	PIEN	414	PIEN
PIJE							388	PIJE	387	PIJE
PIPO	70	PIPO	703	PIPO	72	PIPO	316	PIPO	315	PIPO
PISI	465	PISI	466	PISI	3	PSME	310	PISI	309	PISI
SEGI							394	SEGI	393	SEGI

ROOT MASS EQUATION FOR PSME (#6) (used for all species)

$$\text{Root Mass (g)} = \exp(2.2117) * \text{DBH(cm)}^{**2.6929}$$

2. PARAMS.TAB - parameters specific to HARVEST.for (Harmon 1993)
3. RICHINA.TAB - height-dbh coefficients. Version 15 July 93 (Garman 1993)
4. SPECIES.TAB - list of possible species
5. TAPEROU.TAB - taper coefficients for outside bark *
* Garman, Unpubl. Coefficients were derived from TV009 data set and from Kozak et al. (1969), Taper functions and their application in forest inventory. The Forestry Chronicle, 45:278-283.

SUBSTITUTIONS/NEEDS FOR SPECIES PARAMETERS

NEED: m-mass, t-taper, h-height coefficients

ABam
ABco
ABgr
ABla
ACma (t - derived from Kozak's inside Bark equ.)
ALru (t - derived from Kozak's inside Bark equ.)
BEpa (m t h -> subst. ALru)
CHno m h
LAoc (m t h -> subst. PSme)
LBde
Pico (m -> subst. PSme for dead branch)
PIen (m -> subst. PSme for dead branch)
Pimo (t -> from Kozak's inside Bark equ.)
PIpo
Pisi (m -> subst. PSme for dead branch)
POtr (m, h --> ALru), (t -> from Kozak's inside Bark equ.)
POtr (m, h --> ALru), (t -> from Kozak's inside Bark equ.)
PSme
THpl
TShe

DATA FILES:

1. STAND1.DAT - Type I (Single aged, single species)
"Age=80---SI=1, based on MCARDLE AND MYER Table 11"
2. STAND2.DAT - Type II (Multiple species and ages)

OUTPUT FILES:

STAND TABLE
Data File= data\newosp

species	age	dbh	#
ABam	470	5	1.00
ALru	470	5	13.00
PSme	470	5	28.00
THpl	470	5	5.00
TShe	470	5	12.00
ACma	470	10	1.00
ALru	470	10	22.00

PSme	470	10	39.00
THpl	470	10	4.00
TShe	470	10	15.00
ACma	470	15	2.00
ALru	470	15	10.00
PSme	470	15	35.00
THpl	470	15	2.00
TShe	470	15	17.00
ACma	470	20	2.00
ALru	470	20	6.00
PSme	470	20	23.00
TShe	470	20	14.00
ACma	470	25	2.00
ALru	470	25	3.00
PSme	470	25	20.00
TShe	470	25	11.00
ACma	470	30	1.00
ALru	470	30	1.00
PSme	470	30	11.00
TShe	470	30	9.00
ACma	470	35	1.00
PSme	470	35	7.00
THpl	470	35	1.00
TShe	470	35	7.00
ACma	470	40	1.00
PSme	470	40	8.00
THpl	470	40	1.00
TShe	470	40	8.00
PSme	470	45	9.00
TShe	470	45	9.00
PSme	470	50	9.00
TShe	470	50	4.00
PSme	470	55	8.00
THpl	470	55	1.00
TShe	470	55	3.00
PSme	470	60	5.00
TShe	470	60	2.00
PSme	470	65	5.00

TShe	470	65	2.00
PSme	470	70	3.00
TShe	470	70	1.00
PSme	470	75	5.00
TShe	470	75	1.00
PSme	470	80	1.00
THpl	470	80	1.00
TShe	470	80	1.00
PSme	470	85	2.00
TShe	470	85	1.00

PSme	470	90	2.00
TShe	470	90	1.00
PSme	470	95	3.00
TShe	470	95	1.00
TShe	470	100	1.00
PSme	470	105	3.00
PSme	470	110	2.00
PSme	470	115	2.00
PSme	470	120	5.00
PSme	470	125	4.00
PSme	470	130	4.00
PSme	470	135	2.00
PSme	470	140	2.00
PSme	470	145	3.00
PSme	470	150	4.00
PSme	470	155	1.00
PSme	470	160	1.00
PSme	470	165	1.00
PSme	470	170	1.00
PSme	470	175	1.00
PSme	470	185	1.00
PSme	470	190	1.00

PARAMETER LIST

	From	To	Step
Stump Hgt (m)	0.450	6.000	1.000
Top Diam. (cm)	13.000	13.000	13.000
Min Diam. (cm)	20.000	20.000	20.000
Slope (deg)	0.000	45.000	45.000

Stand Age (yrs) 470.

Min. Stump Height (m) 0.450
Min. Top Diam. (cm) = 13.000
Min. DBH (cm) = 20.000
Slope (degrees) = 0.000

	Total	Non-Merch	(Root)	Bole	Stump	Top
Decay	Breakage					
	1262.2530	380.6811	272.3265	881.5716	26.6052	3.9419
137.6169	67.9451	Mg/unit area				
	100.0000	30.1589	21.5746	69.8411	2.1078	0.3123
10.9025	5.3828	% of Total				
				100.0000	3.0179	0.4471
15.6104	7.7073	% of Bole				

Whips

Adjusted

Decay	Breakage	7.5746
132.4804	65.8288	Mg/unit area
10.4956	5.2152	% of Total
15.0278	7.4672	% of Bole

UNADJUSTED

ADJUSTED

Total Residual Mass (Mg) =	616.7902	Total
Residual Mass (Mg) =	609.5375	
Total Residual/Total Mass (%) =	48.86	Total
Residual/Total Mass (%) =	48.29	
Total Above Grnd. Residual (Mg) =	344.4637	Total
Above Grnd. Residual (Mg) =	337.2109	
Total Above G. Res./Total Above G. Mass (%) =	34.80	Total
Above G. Res./Total Above G. Mass (%) =	34.06	
Bole Residual (Mg) (Stump+Top+Decay+Breakage) =	236.1091	Bole
Residual (Mg) (Stump+Top+Decay+Breakage) =	228.8564	
Bole Residual/Bole Mass (%) =	26.78	Bole
Residual/Bole Mass (%) =	25.96	

 Min. Stump Height (m) 0.450
 Min. Top Diam. (cm) = 13.000
 Min. DBH (cm) = 20.000
 Slope (degrees) = 45.000

	Total	Non-Merch	(Root)	Bole	Stump	Top
Decay	Breakage					
	1262.2530	380.6811	272.3265	881.5716	65.4772	3.9419
137.6169	135.8902	Mg/unit area				
	100.0000	30.1589	21.5746	69.8411	5.1873	0.3123
10.9025	10.7657	% of Total				
				100.0000	7.4273	0.4471
15.6104	15.4145	% of Bole				

Whips

Adjusted

Decay	Breakage	7.5746
126.7764	125.3851	Mg/unit area
10.0437	9.9334	% of Total
14.3807	14.2229	% of Bole

UNADJUSTED

ADJUSTED

Total Residual Mass (Mg) =	723.6072	Total
Residual Mass (Mg) =	702.2617	
Total Residual/Total Mass (%) =	57.33	Total
Residual/Total Mass (%) =	55.64	
Total Above Grnd. Residual (Mg) =	451.2807	Total
Above Grnd. Residual (Mg) =	429.9352	
Total Above G. Res./Total Above G. Mass (%) =	45.59	Total
Above G. Res./Total Above G. Mass (%) =	43.43	
Bole Residual (Mg) (Stump+Top+Decay+Breakage) =	342.9262	Bole
Residual (Mg) (Stump+Top+Decay+Breakage) =	321.5806	
Bole Residual/Bole Mass (%) =	38.90	Bole
Residual/Bole Mass (%) =	36.48	

Total --> above and below ground mass
 Non-Merch --> live and dead branches, leaves, roots, and
 whips
 (Root) --> coarse-root portion of Non-Merch
 Bole --> stem wood and bark (includes stump, top, decay, &
 breakage)
 Stump --> remaining stumps
 Top --> remaining tops
 Decay --> Bole decay
 Breakage --> Bole breakage
 Whips --> mass of Boles with dbh smaller than the min.
 criteria
 Total Residual Mass --> Non-Merch + Stump + Top + Decay +
 Breakage
 Total Above Grnd. Residual Mass --> Total Residual - (Root)
 Bole Residual Mass --> Stump + Top + Decay + Breakage

UNADJUSTED & ADJUSTED --> Residual Mass is the summation of Non-Merch, Top, Stump, Decay, and Breakage.

Unadjusted values are where Decay and Breakage are based on the total mass of the Bole [above ground portion]. Mass loss owing to these two factors is not proportionally distributed between Top and Stump;

Decay and Breakage loss are not subtracted from Bole mass before calculating the other. In extreme cases

where Decay and Breakage are extensive, it is possible for Residual Mass to exceed Total Mass.

Adjusted values are where Decay and Breakage are based on the Bole Mass after adjusting for mass loss from Stumps and Tops. Decay loss is subtracted from adjusted Bole Mass before calculating the breakage, thus adjusted values should never exceed 100% of the total bole mass.

DATA I/O

Input

Data can be input via the interactive queues or via a command file.

Example Command File

```
outfile -stand file - 1 for Type I, 2 for Type II stand format -
stump min max step (mms),top mms ,dbh mms,
slope mms, species
mul data\newy65      2    .45 .45 .45    13 13 13    20 20 20    0
45 45  PSme
mul data\newy65.n    2    .45 .45 .45    13 13 13    20 20 20    0
45 45  PSme
mul0 data\newy65     2    1   1   1     30 30 30    40 40 40    0
45 45  PSme
mul0 data\newy65.n   2    1   1   1     30 30 30    40 40 40    0
45 45  PSme
```

The first line is merely annotation regarding the format of the script file, but must be included in each script file. Output (containing tabular listing of results) and input files are specified followed by the stand-table type (1 or 2). Following are parameter values specifying minimum and maximum values and the step (=increment) value for stump (m), top (cm), dbh (cm), and slope (degrees). Species designation is always required but is only used when running with a type 1 stand table. Output data are concatenated to the designated output file.

Output

Output are in two forms. Tabulation of results (q.v. OUTPUT, Pg. 15) are presented in the primary output file designed interactively or via the script noted above. Select data are also output in a format facilitating ease of import into graphical packages, primarily Harvard Graphics. Files Tres, Ares, Bres correspond to total residual, above ground residual, and bole residual (stump + top + decay + breakage), respectively. A suffix of "p" indicates that values are percentages; an "m" indicates mass (Mg/ha). Stump.p contains percentage of residual stump mass in total above ground mass. Top.p contains percentage of residual top bole mass plus whip bole mass resulting from the minimum top diameter limit (i.e., dbh < minimum top diameter) in total above ground mass. Whip.p contains percentage of all whips in whips + Merchantable boles. DWhip.p contains percentage of whips resulting from the minimum diameter limit (i.e., dbh < minimum diameter) in total above ground mass. The file, Above.m, contains the total above ground mass. NMerch.p contains the percentage of above ground mass represented by above-ground non merchantable residual (branches, leaves, & whips). All data correspond to adjusted values. These files are created each run and will contain output from each of the operations specified in the command file. These files must not be present prior to performing a run. If they do, error messages will queue the operator to rename or delete them before output of the current run are exported.

ANALH() is an analysis routine that will strip select data from the tabular output files for use in graphical packages.

NOTES:

BRf (% breakage) and Df (% decay) were derived from volume (cubic) measures. In HARVEST(), we reduce the bole mass instead of the volume. But because the mass equation is the product of volume and density, we are in effect reducing volume.