QAQC Updates

Bruce D. Marron
LANDIS-II Upgrades Project

I.   PWL43-QAQCDeadBiomass-20170215

```
Title: QAQC of Extension-Biomass-Harvest/issues/13  (dead biomass)
Project Description: LANDIS-II upgrades/corrections
Project ID: 2016SoE021
Author: bmarron
Origin Date: 16 Feb 2017
Final Date: 26 Feb 2017


############
QAQC Results
############

1. Extension-Biomass-Harvest (running NECN succession) DOES output differences in
==> TotalBiomassHarvested (column 7) as reported by the (harvest)
    "summary_log_output.csv"
==> SOMTC (column 6), C_SOM1surf (column 25) and C_SOM1soil (column 26) as
            reported by the "NECN_succession_log.csv"


2. QAQC tests used the prescription below and varied the percentages in the
   "CohortsRemoved SpeciesList" LANDIS-II runs were made with 15%, 25%, and 95%.

Prescription SelectiveNorthernHardwood
    StandRanking     Economic
>>Species  EconomicRank  Minimum Age
>>-------  ------------  -----------
    acerrubr    60        45
    acersacc    100            5
    betualle    100       50
    fraxamer    60        40


    SiteSelection PatchCutting 10%  1  << ha


    CohortsRemoved SpeciesList
>>Species Selection
>>----------------
acerrubr    1-400 (15%)
acersacc    1-40 (15%)   45-100 (15%) 105 (15%)
betualle    1-400 (15%)
fraxamer    1-400 (15%)


3. The direction and magnitude of change appears to be what would be expected for
   "TotalBiomassHarvested",
==> 25%-15%: large positive values
==> 25%-95%: very large negative values
==> 95%-15%: very large positive values

4. The direction and magnitude of change appears inconsistent for "C_SOM1surf" and
   "C_SOMsoil",
==> 25%-15%: small decimal negative values
==> 25%-95%: small integer negative values
==> 95%-15%: small integer positive values




##################################
```

```
Extension-Biomass-Harvest/issues/13
"dead biomass issue"
#####################################
Japan issue == dead biomass issue == partial harvesting changing the amount of dead
woody material issue
https://github.com/LANDIS-II-Foundation/Extension-Biomass-Harvest/issues/13


a. affected
==> https://github.com/LANDIS-II-Foundation/Extension-Biomass-Harvest
==> https://github.com/LANDIS-II-Foundation/Library-Biomass-Cohort
==> https://github.com/LANDIS-II-Foundation/Library-Leaf-Biomass-Cohort
==> some of the harvest libraries.


##########
QAQC prep
###########

a. Per Rob, Testing of BiomasHarvest-v2.dll should be done
   w/ NECN extension ("LANDIS-II NECN Succession 4.2-setup.exe")


a1. standardize and restructure NECN repo


a2. VS re-build of NECN
C:\Users\bmarr\Desktop\New_folder_WorkingNECN\Extension-NECN-Succession\src\bin\debug\Landis.Extension.Succession.NetEcosystemCarbonNitrogen.
========== Build: 1 succeeded, 0 failed, 0 up-to-date, 0 skipped ==========


a3. modify "LANDIS-II_NECN_Succession_v4.2.iss"
==> add all *.gis
==> restructure to std template


a4. Run "LANDIS-II_NECN_Succession_v4.2.iss" and build new installer
==> "LANDIS-II NECN Succession 4.2-setup.exe"


a5. uninstall
==> Biomass Harvest Extension v3.1
==> NetEcosystemCN Succession v4.1.1


a6. install
==> "LANDIS-II Biomass Harvest 3.2-setup.exe"
==> "LANDIS-II NECN Succession 4.2-setup.exe"



b. run stock "scenario.txt" with stock "biomass-harvest_NECN_Prescriptions.txt"

b1. modify "scenario.txt"
==> rename "biomass Harvest" initialization file
    "biomass-harvest_NECN_Prescriptions.txt"
==> set random number seed
==> standardize


b2. modify "biomass-harvest_NECN_Prescriptions.txt"
==> Error at line 62 of file "biomass-harvest_NECN_Prescriptions.txt":
        Error reading input value for Age Range:
           "60" is not a valid percentage for partial thinning:
             Value does not start with "("

==> change percentages in "Prescription SelectiveNorthernHardwood"
==> change the "PRESCRIPTION IMPLEMENTATION" schedule
==> set random number seed
==> standardize


"scenario.txt" ==>
=====================================================================================
```

```
LandisData  Scenario
Duration  30

Species    species.txt

Ecoregions      ./ecoregions-2regions.txt
EcoregionsMap   ./ecoregions.gis

CellLength  100 << meters, 100 x 100 m = 1 ha


>> ----------------------
>> SUCCESSION EXTENSIONS
>> ----------------------

>>  Succession Extension      Initialization File
>>  --------------------      -------------------
     "NetEcosystemCN Succession" NECN-succession.txt


>> ------------------------
>> DISTURBANCE EXTENSIONS
>> ------------------------

>>  Disturbance Extensions    Initialization File
>> ---------------------     -------------------
>>"Base Fire" base-fire.txt
"Biomass Harvest" biomass-harvest_NECN_Prescriptions.txt


>>   DisturbancesRandomOrder  yes  << optional parameter; default = no

>> -----------------------
>> OTHER EXTENSONS
>> ---------------------

>>  Other Extensions         Initialization File
>> ----------------         ------------------
>>    "Output Cohort Stats"    cohort-stats.output.txt


RandomNumberSeed  147  << optional parameter; default = the seed is
                         << randomly generated using the current time

===============================================================================================



"biomass-harvest_NECN_Prescriptions.txt" ==>
===============================================================================================
LandisData  "Biomass Harvest"

Timestep    5

ManagementAreas  "./management.gis"
Stands       "./stand.gis"



>> ------------------------
>> HARVEST PRESCRIPTIONS
>> ------------------------

Prescription MaxAgeClearcut
    StandRanking  MaxCohortAge
    SiteSelection  Complete
    CohortsRemoved  ClearCut


Prescription    AspenClearcut
    StandRanking    Economic
```

```
>>  Species  Economic Rank  Minimum Age
>>  -------  -------------  -----------
     poputrem    100            40

    MinimumAge   35
    SiteSelection CompleteStandSpread 40 50
    CohortsRemoved ClearCut


Prescription SelectiveNorthernHardwood
    StandRanking     Economic
>>Species  EconomicRank  Minimum Age
>>-------  ------------  -----------
    acerrubr    60          45
    acersacc    100          5
    betualle    100         50
    fraxamer    60          40

    SiteSelection PatchCutting 10%  1  << ha

    CohortsRemoved SpeciesList
>>Species Selection
>>----------------
acerrubr    1-400 (25%)
acersacc    1-40 (25%)   45-100 (5%) 105 (65%)
betualle    1-400 (25%)
fraxamer    1-400 (25%)



Prescription    OakPatchCutting
    StandRanking MaxCohortAge
    MinimumAge   60
    StandAdjacency 10
    AdjacencyType  StandAge
    AdjacencyNeighborSetAside 10

   ForestTypeTable
>>InclusionRule ageRange %Cells species
>>  --------------------------------
Forbidden 1-131 (60%) acersacc
Required 100-450 (20%) querrubr

    SiteSelection PatchCutting 75% 50

    CohortsRemoved SpeciesList
>>Species Selection
>>-------  ---------
abiebals  All
querrubr  AllExceptOldest
pinubank  All



>> ----------------------------------
>> PRESCRIPTION IMPLEMENTATION
>> ----------------------------------

    HarvestImplementations
>>Mgmt Area Prescription Harvest Area BeginTime EndTime
>>  ---------  -----------  -----------   ----------  --------
1 SelectiveNorthernHardwood 10%
3 SelectiveNorthernHardwood 10% 0        10
3 SelectiveNorthernHardwood 20% 10       30
>>1 MaxAgeClearcut 5% 0 15
>>1 MaxAgeClearcut 10% 15 30
>>3 AspenClearcut 5%
>>2 OakPatchCutting 30%



>> ------------
```

```
>> OUTPUTS
>> ----------

PrescriptionMaps    harvest/prescripts-{timestep}.img
BiomassMaps         harvest/biomass-removed-{timestep}.img
EventLog            harvest/biomass-harvest-event-test-log.csv
SummaryLog      harvest/summary-log.csv


====================================================================================



b3. LANDISII run complete
LANDIS-II 6.2 (beta release 1)
Loading scenario from file "scenario.txt" ...
Initialized random number generator with seed = 278,834,935
Loading species data from file "species.txt" ...
Loading ecoregions from file "./ecoregions-2regions.txt" ...
Initializing landscape from ecoregions map "./ecoregions.gis" ...
...........
...........
Ageing cohorts ...
% done:   0%  10%  20%  30%  40%  50%  60%  70%  80%  90%  100%
          |----|----|----|----|----|----|----|----|----|----|
Progress: ++++++++++++++++++++++++++++++++++++++++++++++++++
dataset created: necn/ag_npp-30.gis
dataset created: necn/nee-30.gis
Model run is complete.
Press any key to continue . . .
```

```
c. check outputs in R

open "harvest/summary_log.csv" in R ==>
> summary_log_output <- as.matrix(setNames(summary_log[, c(2,4,6,7)], NULL))

Col2==ManagementArea
Col4==HarvestedSites
Col6==TotalCohortsPartialHarvest
Col7==TotalBiomassHarvested

       [,1] [,2] [,3]     [,4]
 [1,]    1  289 1825   782.85
 [2,]    3  199  996   412.54
 [3,]    1  293 1843   761.53
 [4,]    3  196  957   427.54
 [5,]    1  306 1876   818.76
 [6,]    3  202  970   475.68
 [7,]    1  310 1818   915.78
 [8,]    3  212  964   528.62
 [9,]    1  307 1555   925.63
[10,]    3  206  831   549.47
[11,]    1  293 1541  1211.17
[12,]    3  204  894   771.52


open "NECN_succession_log" in R ==>
> NECN_succession_log_output <- as.matrix(setNames(NECN_succession_log[, c(3,6,25,26)], NULL))

Col3==EcoregionIndex
Col6==SOMTC
Col25==C_SOM1surf
Col26==C_SOM1soil

        [,1]    [,2]  [,3]   [,4]
 [1,]     0 17164.4 785.5 3363.3
 [2,]     1 15394.7 818.0 2947.8
 [3,]     0 17532.7 806.2 3434.7
```

```
 [4,]    1 15921.3 848.7 3051.9
 [5,]    0 17882.3 819.2 3503.9
 [6,]    1 16418.4 866.4 3152.7
 [7,]    0 18226.3 832.7 3572.9
 [8,]    1 16915.1 888.3 3254.4
 [9,]    0 18545.7 838.6 3638.9
[10,]    1 17374.2 896.6 3351.6
[11,]    0 18844.9 843.3 3702.5
[12,]    1 17807.1 905.0 3446.2
[13,]    0 19123.7 845.3 3762.6
[14,]    1 18213.8 909.2 3536.2
```

```
###########################
QAQC using Biomass Harvest
###########################


Biomass Harvest v3.1 LANDIS-II Extension âĂŞ User Guide (p. 5)
"When SpeciesList is specified for the CohortsRemoved parameter in a prescription, the user may specify a percentage after any individual age

CohortsRemoved SpeciesList
acersacc 1-40(50%) 50(65%) 65-70 71-107(15%)

The default percentage is 100%. If no parenthetical biomass removal values are given, the Biomass Harvest extension will behave identically t


a. modify prescriptions for QAQC and sync with scenario.txt


a1i. modify "biomass-harvest_NECN_Prescriptions.txt"
==> "biomass-harvest_NECN_QAQCPrescription1.txt"

"biomass-harvest_NECN_QAQCPrescription1.txt" ==>
=================================================================================
LandisData  "Biomass Harvest"


Timestep    5

ManagementAreas  "./management.gis"
Stands         "./stand.gis"



>> ------------------------
>> HARVEST PRESCRIPTIONS
>> ------------------------


Prescription SelectiveNorthernHardwood
    StandRanking    Economic
>>Species  EconomicRank  Minimum Age
>>-------  ------------  -----------
     acerrubr    60           45
     acersacc    100               5
     betualle    100          50
     fraxamer    60           40

    SiteSelection PatchCutting 10%  1  << ha

    CohortsRemoved SpeciesList
>>Species Selection
>>----------------
acerrubr    1-400 (15%)
acersacc    1-40 (15%)   45-100 (15%) 105 (15%)
betualle    1-400 (15%)
fraxamer    1-400 (15%)
```

```
>> ---------------------------------
>> PRESCRIPTION IMPLEMENTATION
>> ---------------------------------

    HarvestImplementations
>>Mgmt Area Prescription Harvest Area BeginTime EndTime
>>  ---------    -----------    -----------    ----------  --------
1 SelectiveNorthernHardwood 10%
3 SelectiveNorthernHardwood 10% 0         10
3 SelectiveNorthernHardwood 20% 10         30


>> ------------
>> OUTPUTS
>> ----------

PrescriptionMaps    harvest/prescripts-{timestep}.img
BiomassMaps         harvest/biomass-removed-{timestep}.img
EventLog            harvest/biomass-harvest-event-test-log.csv
SummaryLog      harvest/summary-log.csv


==============================================================================================


a1ii. modify "scenario.txt"
==> "scenario_QAQC1.txt"

"scenario_QAQC1.txt" ==>
==============================================================================================
LandisData  Scenario
Duration   30

Species    species.txt

Ecoregions       ./ecoregions-2regions.txt
EcoregionsMap    ./ecoregions.gis

CellLength  100 << meters, 100 x 100 m = 1 ha


>> ----------------------
>> SUCCESSION EXTENSIONS
>> ----------------------

>>  Succession Extension     Initialization File
>>  --------------------     -------------------
    "NetEcosystemCN Succession" NECN-succession.txt


>> -------------------------
>> DISTURBANCE EXTENSIONS
>> -------------------------

>>  Disturbance Extensions    Initialization File
>>  ----------------------    -------------------
>>"Base Fire" base-fire.txt
"Biomass Harvest" biomass-harvest_NECN_QAQCPrescription1.txt


>>   DisturbancesRandomOrder  yes  << optional parameter; default = no

>> ------------------------
>> OTHER EXTENSONS
>> ---------------------

>>  Other Extensions         Initialization File
>>  ----------------         ------------------
>>    "Output Cohort Stats"    cohort-stats.output.txt
```

```
RandomNumberSeed  147  << optional parameter; default = the seed is
                            << randomly generated using the current time


================================================================================


a1iii. run "scenario_QAQC1" check QAQC outputs in R

open "harvest/summary_log.csv" in R ==>
> QAQC_summary_log_output1 <- as.matrix(setNames(summary_log[, c(2,4,6,7)], NULL))


Col2==ManagementArea
Col4==HarvestedSites
Col6==TotalCohortsPartialHarvest
Col7==TotalBiomassHarvested

        [,1] [,2] [,3]      [,4]
  [1,]    1  289 1825   888.99
  [2,]    3  199  996   461.34
  [3,]    1  293 1843   894.39
  [4,]    3  196  957   477.18
  [5,]    1  306 1876   959.80
  [6,]    3  202  970   524.88
  [7,]    1  310 1818  1054.82
  [8,]    3  212  964   583.18
  [9,]    1  307 1555  1066.99
 [10,]    3  206  831   605.27
 [11,]    1  293 1541  1506.76
 [12,]    3  204  894   915.90




open "NECN_succession_log" in R ==>
> QAQC_NECN_succession_log_output1 <- as.matrix(setNames(NECN_succession_log[, c(3,6,25,26)], NULL))

Col3==EcoregionIndex
Col6==SOMTC
Col25==C_SOM1surf
Col26==C_SOM1soil


        [,1]     [,2]  [,3]   [,4]
  [1,]    0 17164.4 785.5 3363.3
  [2,]    1 15394.7 818.0 2947.8
  [3,]    0 17532.8 806.2 3434.7
  [4,]    1 15921.3 848.7 3051.9
  [5,]    0 17882.6 819.2 3504.0
  [6,]    1 16418.6 866.4 3152.8
  [7,]    0 18226.8 832.8 3573.0
  [8,]    1 16915.4 888.3 3254.5
  [9,]    0 18546.3 838.7 3639.0
 [10,]    1 17374.5 896.7 3351.6
 [11,]    0 18845.7 843.3 3702.6
 [12,]    1 17807.5 905.0 3446.3
 [13,]    0 19124.7 845.5 3762.7
 [14,]    1 18214.3 909.3 3536.3






a2i. modify "biomass-harvest_NECN_Prescriptions.txt"
==> "biomass-harvest_NECN_QAQCPrescription2.txt"

"biomass-harvest_NECN_QAQCPrescription2.txt" ==>
================================================================================
LandisData  "Biomass Harvest"
```

```
Timestep    5

ManagementAreas  "./management.gis"
Stands          "./stand.gis"



>> ------------------------
>> HARVEST PRESCRIPTIONS
>> ------------------------

Prescription SelectiveNorthernHardwood
    StandRanking    Economic
>>Species  EconomicRank  Minimum Age
>>-------  ------------  -----------
    acerrubr    60          45
    acersacc    100             5
    betualle    100         50
    fraxamer    60          40

    SiteSelection PatchCutting 10%  1  << ha

    CohortsRemoved SpeciesList
>>Species Selection
>>----------------
acerrubr    1-400 (95%)
acersacc    1-40 (95%)   45-100 (95%) 105 (95%)
betualle    1-400 (95%)
fraxamer    1-400 (95%)




>> ---------------------------------
>> PRESCRIPTION IMPLEMENTATION
>> ---------------------------------

    HarvestImplementations
>>Mgmt Area Prescription Harvest Area BeginTime EndTime
>> ---------    -----------    -----------    ----------  --------
1 SelectiveNorthernHardwood 10%
3 SelectiveNorthernHardwood 10% 0        10
3 SelectiveNorthernHardwood 20% 10       30


>> ------------
>> OUTPUTS
>> ----------

PrescriptionMaps    harvest/prescripts-{timestep}.img
BiomassMaps         harvest/biomass-removed-{timestep}.img
EventLog            harvest/biomass-harvest-event-test-log.csv
SummaryLog    harvest/summary-log.csv


===============================================================================================



a2ii. modify "scenario.txt"
==> "QAQCscenario2.txt"

"QAQCscenario2.txt" ==>
===============================================================================================
LandisData  Scenario
Duration  30

Species   species.txt
```

```
Ecoregions        ./ecoregions-2regions.txt
EcoregionsMap     ./ecoregions.gis

CellLength  100 << meters, 100 x 100 m = 1 ha


>> ----------------------
>> SUCCESSION EXTENSIONS
>> ----------------------

>>  Succession Extension      Initialization File
>>  --------------------      -------------------
     "NetEcosystemCN Succession" NECN-succession.txt



>> ------------------------
>> DISTURBANCE EXTENSIONS
>> ------------------------

>>  Disturbance Extensions    Initialization File
>> ---------------------     -------------------
>>"Base Fire" base-fire.txt
"Biomass Harvest" biomass-harvest_NECN_QAQCPrescription2.txt


>>   DisturbancesRandomOrder  yes  << optional parameter; default = no

>> -----------------------
>> OTHER EXTENSONS
>> ----------------------

>>  Other Extensions          Initialization File
>> ----------------          ------------------
>>    "Output Cohort Stats"    cohort-stats.output.txt


RandomNumberSeed  147  << optional parameter; default = the seed is
                           << randomly generated using the current time

====================================================================================================



a2iii. run "scenario_QAQC2" check QAQC outputs in R

open "harvest/summary_log.csv" in R ==>
> QAQC_summary_log_output2 <- as.matrix(setNames(summary_log[, c(2,4,6,7)], NULL))

Col2==ManagementArea
Col4==HarvestedSites
Col6==TotalCohortsPartialHarvest
Col7==TotalBiomassHarvested

      [,1] [,2] [,3]    [,4]
 [1,]    1  289 1921 5670.28
 [2,]    3  199 1067 2942.56
 [3,]    1  293 1843 5718.16
 [4,]    3  196  957 3050.12
 [5,]    1  306 1876 6116.60
 [6,]    3  202  970 3343.08
 [7,]    1  310 1818 6720.89
 [8,]    3  212  964 3712.35
 [9,]    1  307 1631 6799.65
[10,]    3  206  861 3858.38
[11,]    1  293 1689 9578.03
[12,]    3  204  952 5821.41


open "NECN_succession_log" in R ==>
> QAQC_NECN_succession_log_output2 <- as.matrix(setNames(NECN_succession_log[, c(3,6,25,26)], NULL))
```

```
Col3==EcoregionIndex
Col6==SOMTC
Col25==C_SOM1surf
Col26==C_SOM1soil


        [,1]    [,2]  [,3]    [,4]
 [1,]     0 17164.4 785.5 3363.3
 [2,]     1 15394.7 818.0 2947.8
 [3,]     0 17536.4 807.2 3435.3
 [4,]     1 15926.1 850.0 3052.6
 [5,]     0 17889.4 820.5 3505.1
 [6,]     1 16427.3 868.0 3154.2
 [7,]     0 18236.8 834.3 3574.7
 [8,]     1 16928.1 890.1 3256.6
 [9,]     0 18560.0 840.4 3641.4
[10,]     1 17391.0 898.5 3354.5
[11,]     0 18862.3 844.9 3705.6
[12,]     1 17827.7 906.9 3450.0
[13,]     0 19145.1 847.4 3766.5
[14,]     1 18240.9 912.0 3541.1
```

```
b. evaluate process differences

---- (harvest) summary_log_output -------------------------------------------------------

biomass-harvest_NECN_Prescriptions ==> 25% harvested
biomass-harvest_NECN_QAQCPrescription1 ==> 15%     ''
biomass-harvest_NECN_QAQCPrescription2 ==> 95%     ''

(harvest) summary_log_output ==>
Col2==ManagementArea
Col4==HarvestedSites
Col6==TotalCohortsPartialHarvest
Col7==TotalBiomassHarvested

25%-15% ==>
test1a <- summary_log_output - QAQC_summary_log_output1
test1a

       [,1] [,2] [,3]    [,4]
 [1,]     0    0    0  387.54
 [2,]     0    0    0  213.32
 [3,]     0    0    0  342.25
 [4,]     0    0    0  224.83
 [5,]     0    0    0  362.86
 [6,]     0    0    0  254.50
 [7,]     0    0    0  431.67
 [8,]     0    0    0  282.99
 [9,]     0    0   76  438.29
[10,]     0    0   30  297.56
[11,]     0    0  148  420.52
[12,]     0    0   58  325.50


25%-95% ==>
test1b <- summary_log_output - QAQC_summary_log_output2
test1b

test1b
       [,1] [,2] [,3]     [,4]
 [1,]     0    0  -96 -4393.75
 [2,]     0    0  -71 -2267.90
```

```
 [3,]    0    0    0 -4481.52
 [4,]    0    0    0 -2348.11
 [5,]    0    0    0 -4793.94
 [6,]    0    0    0 -2563.70
 [7,]    0    0    0 -5234.40
 [8,]    0    0    0 -2846.18
 [9,]    0    0    0 -5294.37
[10,]    0    0    0 -2955.55
[11,]    0    0    0 -7650.75
[12,]    0    0    0 -4580.01


95%-25% ==>
test1c <- QAQC_summary_log_output2 - QAQC_summary_log_output1
test1c

      [,1] [,2] [,3]     [,4]
 [1,]    0    0   96  4781.29
 [2,]    0    0   71  2481.22
 [3,]    0    0    0  4823.77
 [4,]    0    0    0  2572.94
 [5,]    0    0    0  5156.80
 [6,]    0    0    0  2818.20
 [7,]    0    0    0  5666.07
 [8,]    0    0    0  3129.17
 [9,]    0    0   76  5732.66
[10,]    0    0   30  3253.11
[11,]    0    0  148  8071.27
[12,]    0    0   58  4905.51


---- NECN_succession_log ------------------------------------------------------
biomass-harvest_NECN_Prescriptions ==> 25% harvested
biomass-harvest_NECN_QAQCPrescription1 ==> 15%    ''
biomass-harvest_NECN_QAQCPrescription2 ==> 95%    ''

Col3==EcoregionIndex
Col6==SOMTC
Col25==C_SOM1surf
Col26==C_SOM1soil

25%-15% ==>
test2a <- NECN_succession_log_output - QAQC_NECN_succession_log_output1
test2a

      [,1] [,2] [,3] [,4]
 [1,]    0  0.0  0.0  0.0
 [2,]    0  0.0  0.0  0.0
 [3,]    0 -0.1  0.0  0.0
 [4,]    0  0.0  0.0  0.0
 [5,]    0 -0.3  0.0 -0.1
 [6,]    0 -0.2  0.0 -0.1
 [7,]    0 -0.5 -0.1 -0.1
 [8,]    0 -0.3  0.0 -0.1
 [9,]    0 -0.6 -0.1 -0.1
[10,]    0 -0.3 -0.1  0.0
[11,]    0 -0.8  0.0 -0.1
[12,]    0 -0.4  0.0 -0.1
[13,]    0 -1.0 -0.2 -0.1
[14,]    0 -0.5 -0.1 -0.1


25%-95% ==>
test2b <- NECN_succession_log_output - QAQC_NECN_succession_log_output2
test2b

      [,1]  [,2] [,3] [,4]
 [1,]    0   0.0  0.0  0.0
 [2,]    0   0.0  0.0  0.0
 [3,]    0  -3.7 -1.0 -0.6
 [4,]    0  -4.8 -1.3 -0.7
```

```
 [5,]    0  -7.1 -1.3 -1.2
 [6,]    0  -8.9 -1.6 -1.5
 [7,]    0 -10.5 -1.6 -1.8
 [8,]    0 -13.0 -1.8 -2.2
 [9,]    0 -14.3 -1.8 -2.5
[10,]    0 -16.8 -1.9 -2.9
[11,]    0 -17.4 -1.6 -3.1
[12,]    0 -20.6 -1.9 -3.8
[13,]    0 -21.4 -2.1 -3.9
[14,]    0 -27.1 -2.8 -4.9


95%-15% ==>
test2c <- QAQC_NECN_succession_log_output2 - QAQC_NECN_succession_log_output1
test2c

      [,1] [,2] [,3] [,4]
 [1,]    0  0.0  0.0  0.0
 [2,]    0  0.0  0.0  0.0
 [3,]    0  3.6  1.0  0.6
 [4,]    0  4.8  1.3  0.7
 [5,]    0  6.8  1.3  1.1
 [6,]    0  8.7  1.6  1.4
 [7,]    0 10.0  1.5  1.7
 [8,]    0 12.7  1.8  2.1
 [9,]    0 13.7  1.7  2.4
[10,]    0 16.5  1.8  2.9
[11,]    0 16.6  1.6  3.0
[12,]    0 20.2  1.9  3.7
[13,]    0 20.4  1.9  3.8
[14,]    0 26.6  2.7  4.8
```

II. PWL50-QAQC-SalvageLoggingBiomassHrvst-20170226

```
Title: QAQC of salvage logging w/ NECN and BiomassHarvest
Project Description: LANDIS-II upgrades/corrections
Project ID: 2016SoE021
Author: bmarron
Origin Date: 26 Feb 2017
Final Date: 26 Feb 2017


############
QAQC Results
############


1. Extension-Biomass-Harvest (running NECN succession and Base Fire) DOES recognize
    the new StandRanking prescription, "TimeSinceDisturbance" set with the
    "TimeSinceLastFire" parameter (ie, no LANDIS-II runtime errors)


2. The new StandRanking prescription, "TimeSinceDisturbance" set with the
   "TimeSinceLastFire" parameter outputs NO HARVEST DATA with either
==> Extension-Biomass-Harvest (running NECN succession and Base Fire)
     ==> Extension-Base-Harvest (running AgeOnly succession and Base Fire)


3. The parameter, "TimeSinceLastFire" was run with
TimeSinceLastFire=1
TimeSinceLastFire=90
   NO HARVEST DATA was obtained with either parameter setting


4. The prescription to test for salvage logging used the simplest SiteSelection
    option (ie, "Complete") and the simplest CohortsRemoved option (ie, "ClearCut")


5. To verify that LANDIS-ii was correctly processing runs using
    Extension-Biomass-Harvest (running NECN succession and Base Fire), two runs were
    realized using the StandRanking prescription, "MaxCohortAge." Harvest data was
    obtained in both cases.
```

```
#######################
salvage logging issue
#######################
https://github.com/LANDIS-II-Foundation/Extension-Base-Harvest/issues/1
https://github.com/LANDIS-II-Foundation/Library-Harvest-Mgmt/pull/6
https://github.com/LANDIS-II-Foundation/Library-Harvest-Mgmt/pull/7


a. affected
==> Landis.Library.HarvestManagement-v2.dll
==> Landis.Library.BiomassHarvest-v2.dll
==> Landis.Extension.BaseHarvest-3.0.dll
==> Landis.Extension.BiomassHarvest-3.2.dll



b. see "PWL42a_RepoStd-LibHrvstMngmnt_20170215.txt"
==> re-built "Landis.Library.HarvestManagement-v2.dll"



c. see "PWL44_RepoStd-ExtBaseHrvst_20170216.txt"
==> std repo and rebuild .dll

1. uninstall BaseHarvest extension from LANDIS (using Windows Control Panel)
2. clone BaseHarvest repo to desktop (local)
3. make changes to .csproj and .cs files
4. re-build the .dll in VS
5. make changes to .iss file
6. compile .iss file in Inno Script Studio and generate a new installer
7. re-install BaseHarvest extension



d. see "PWL45_RepoStd-ExtBiomassHrvst_20170217.txt"
==> std repo and rebuild .dll

1. uninstall BiomassHarvest extension from LANDIS (using Windows Control Panel)
2. clone BiomassHarvest repo to desktop (local)
3. make changes to .csproj and .cs files
4. re-build the .dll in VS
5. make changes to .iss file
6. compile .iss file in Inno Script Studio and generate a new installer
7. re-install BiomassHarvest extension





###################
pre-QAQC set up
###################


a. QAQC algorithm for salvage logging testing
==> use BiomassHarvest with Extension-NECN-Succession
==> manipulate combos of three, (3) Biomass Harvest Precriptions:
*MaxAgeClearcut
*SalvageLogger1
*SalvageLogger2
==> evaluate outcome data

b. modify "scenario.txt" in Extension-NECN-Succession
==> create "scenario_SalvageLog_QAQC1.txt"

c. modify "biomass-harvest_Prescriptions.txt"
==> create "biomass-harvest_SalvageLog_QAQCPrescription.txt"

d. rename and standardize "base-fire.txt"
==> "base-fire_NECN.txt"


"scenario_SalvageLog_QAQC1.txt" ==>
=============================================================================================
```

```
LandisData  Scenario

Duration   30

Species    species.txt

Ecoregions      ./ecoregions-2regions.txt
EcoregionsMap   ./ecoregions.gis

CellLength  100 << meters, 100 x 100 m = 1 ha



>> -----------------------
>> SUCCESSION EXTENSIONS
>> -----------------------

>>  Succession Extension      Initialization File
>>  --------------------      -------------------
    "NetEcosystemCN Succession" NECN-succession.txt



>> -------------------------
>> DISTURBANCE EXTENSIONS
>> -------------------------

>>  Disturbance Extensions    Initialization File
>> ----------------------     -------------------
"Base Fire" base-fire_NECN.txt
"Biomass Harvest" biomass-harvest_SalvageLog_QAQCPrescription.txt



>>   DisturbancesRandomOrder  yes  << optional parameter; default = no



>> -----------------------
>> OTHER EXTENSONS
>> ---------------------

>>  Other Extensions          Initialization File
>> ----------------          -------------------
>>    "Output Cohort Stats"     cohort-stats.output.txt


 RandomNumberSeed  147  << optional parameter; uncomment for reproducibilty tests
                          << default is a RandomNumberSeed generated using the current time
==========================================================================================



"biomass-harvest_SalvageLog_QAQCPrescription.txt" ==>
==========================================================================================
LandisData  "Biomass Harvest"


Timestep    5

ManagementAreas  "./management.gis"
Stands       "./stand.gis"



>> -------------------------
>> STAND SELECTION CRITERION
>> -------------------------
>>1) IF avgtime of fire in a stand >= TimeSinceLastFire
>>   THEN stand IS NOT selected

>>2) IF avgtime of fire in a stand < TimeSinceLastFire
>>   THEN stand IS selected
```

```
>> ----------------------------------------
>> HARVEST PRESCRIPTIONS
>> ----------------------------------------


Prescription MaxAgeClearcut
    StandRanking  MaxCohortAge
    SiteSelection  Complete
    CohortsRemoved  ClearCut


Prescription SalvageLogger1
    StandRanking TimeSinceDisturbance
    TimeSinceLastFire 90
    SiteSelection     Complete
    CohortsRemoved    ClearCut


Prescription SalvageLogger2
    StandRanking TimeSinceDisturbance
    TimeSinceLastFire 1
    SiteSelection     Complete
    CohortsRemoved    ClearCut


>> ----------------------------------------
>> PRESCRIPTION IMPLEMENTATION
>> ----------------------------------------


    HarvestImplementations
>>Mgmt Area Prescription Harvest Area BeginTime EndTime
>>-------------------------------------------------
>>1 SalvageLogger1 50%
>>1 SalvageLogger2 50%
1 MaxAgeClearcut 5% 0 15
>>1 MaxAgeClearcut 10% 15 30


>> --------------
>> OUTPUTS
>> --------------


PrescriptionMaps    harvest/harvest-prescripts-{timestep}.img
BiomassMaps         harvest/harvest-biomass-removed-{timestep}.img
EventLog            harvest/harvest-biomass-event-test-log.csv
SummaryLog      harvest/harvest-summary-log.csv
===========================================================================================


"base-fire_NECN.txt" ==>
===========================================================================================
LandisData  "Base Fire"

Timestep  5

>> ---------------
>> FIRE REGIONS
>> ---------------

>> Fire        Map ___ Event Size ___    Ignition
>> region      Code Mean  Min    Max    Prob.      k
>> ---------   ----------  ----   ----   --------  --------
    MN101       1  100    4      400    0.1      100
    MN102       2  200    6      600    0.1       50

InitialFireRegionsMap "./ecoregions.gis"


>> ---------------
```

```
>> FIRE TABLES
>> ---------------

  DynamicFireRegionTable  << Optional parameter
>>Year FileName  (this line always commented out)
  20 ecoregions.gis  << If table is not active, comment out this line


  FuelCurveTable
>>             Severities (in increasing order)
>> Ecoregion   S1   S2   S3   S4   S5
>> --------------------------------
    MN101       10   20   50   70   120
    MN102        5   15   20   -1   -1


  WindCurveTable
>>             Severities (in decreasing order)
>> Ecoregion   S5   S4   S3   S2   S1
>> --------------------------------
    MN101       -1   -1    1   10   20
    MN102        1    5   15   20   30


  FireDamageTable
>> Cohort Age      FireSeverity -
>> % of longevity   FireTolerance
>> --------------   --------------
     20%                 -2
     50%                 -1
     85%                  0
    100%                  1


>> ---------------
>> OUTPUTS
>> -------------
MapNames    fire/severity-{timestep}.img
LogFile     fire/fire-event-test-log.csv
SummaryLogFile  fire/summary-log.csv

===============================================================================================




###################
QAQC salvage logging
###################


a. (LANDIS-II) QAQC run1
==> "NECN-succession.txt"
==> "base-fire_NECN.txt"
==> "biomass-harvest_SalvageLog_QAQCPrescription.txt"
    HarvestImplementations
>>Mgmt Area Prescription Harvest Area BeginTime EndTime
>>-------------------------------------------------
>>1 SalvageLogger1 50%
>>1 SalvageLogger2 50%
1 MaxAgeClearcut 5% 0 15
>>1 MaxAgeClearcut 10% 15 30



a1. QAQCrun1 "harvest/harvest_summary_log.csv" in R
open "harvest/harvest_summary_log.csv" in R ==>
> QAQCrun1_harvest_summary_log_output <- as.matrix(setNames(harvest_summary_log[, c(2,4,5,7)], NULL))

Col2==ManagementArea
Col4==HarvestedSites
```

```
Col5==TotalCohortsCompleteHarvest
Col7==TotalBiomassHarvested


     [,1] [,2] [,3]     [,4]
[1,]    1  436 2144   932.15
[2,]    1  305 1518 13796.49
[3,]    1  337 1404 28784.21
```

```
a2. QAQCrun1 "NECN_succession_log.csv" in R
open "NECN_succession_log.csv" in R ==>
> QAQCrun1_NECN_succession_log_output <- as.matrix(setNames(NECN_succession_log[, c(3,6,25,26)], NULL))

Col3==EcoregionIndex
Col6==SOMTC
Col25==C_SOM1surf
Col26==C_SOM1soil


      [,1]    [,2]  [,3]   [,4]
 [1,]    0 17164.4 785.5 3363.3
 [2,]    1 15394.7 818.0 2947.8
 [3,]    0 15697.7 239.8 3187.4
 [4,]    1 14057.3 219.2 2818.0
 [5,]    0 14739.6 205.5 3019.9
 [6,]    1 13192.3 175.3 2685.8
 [7,]    0 13733.4 151.1 2836.4
 [8,]    1 12467.1 176.9 2552.6
 [9,]    0 12645.8 125.8 2606.8
[10,]    1 11583.8 131.9 2382.0
[11,]    0 11633.8 109.0 2387.1
[12,]    1 10644.4  95.2 2190.8
[13,]    0 10694.0  94.2 2179.5
[14,]    1  9686.3  64.0 1989.0
```

```
a3. QAQCrun1 "fire/summary-log.csv" in R
open "fire/summary-log.csv" in R ==>
> QAQCrun1_fire_summary_log_output <- as.matrix(setNames(summary_log[ ,1:5], NULL))

Col==Time
Col2==TotalSitesBurned
Col3==TotalNumberEvents
Col4==MN101
Col5==MN102


     [,1] [,2] [,3] [,4] [,5]
[1,]    5 9104  318 1635 7469
[2,]   10  769  515   77  692
[3,]   15 1496  779  147 1349
[4,]   20 2212  884  139 2073
[5,]   25 2092  853  133 1959
[6,]   30 1765  868  135 1630
```

```
b. (LANDIS-II) QAQC run2
==> "NECN-succession.txt"
==> "base-fire_NECN.txt"
==> "biomass-harvest_SalvageLog_QAQCPrescription.txt"
    HarvestImplementations
>>Mgmt Area Prescription Harvest Area BeginTime EndTime
>>-------------------------------------------------
>>1 SalvageLogger1 50%
>>1 SalvageLogger2 50%
1 MaxAgeClearcut 5% 0 15
1 MaxAgeClearcut 10% 15 30
```

```
b1. QAQCrun2 "harvest/harvest_summary_log.csv" in R
open "harvest/harvest_summary_log.csv" in R ==>
> QAQCrun2_harvest_summary_log_output <- as.matrix(setNames(harvest_summary_log[, c(2,4,5,7)], NULL))

Col2==ManagementArea
Col4==HarvestedSites
Col5==TotalCohortsCompleteHarvest
Col7==TotalBiomassHarvested


      [,1] [,2] [,3]     [,4]
[1,]    1  436 2144   932.15
[2,]    1  305 1518 13796.49
[3,]    1  933 3441 72965.38
[4,]    1  632 1350 39601.56
[5,]    1  622 1137 43281.59
[6,]    1   22   25   872.76


b2. QAQCrun2 "NECN_succession_log.csv" in R
open "NECN_succession_log.csv" in R ==>
> QAQCrun2_NECN_succession_log_output <- as.matrix(setNames(NECN_succession_log[, c(3,6,25,26)], NULL))

Col3==EcoregionIndex
Col6==SOMTC
Col25==C_SOM1surf
Col26==C_SOM1soil


       [,1]     [,2]  [,3]   [,4]
 [1,]     0 17164.4 785.5 3363.3
 [2,]     1 15394.7 818.0 2947.8
 [3,]     0 15697.7 239.8 3187.4
 [4,]     1 14057.3 219.2 2818.0
 [5,]     0 14739.6 205.5 3019.9
 [6,]     1 13192.3 175.3 2685.8
 [7,]     0 13615.1 107.1 2831.4
 [8,]     1 12431.0 165.9 2549.8
 [9,]     0 12203.5  35.1 2550.3
[10,]     1 11467.7 111.0 2366.3
[11,]     0 10840.4   5.2 2257.4
[12,]     1 10418.6  60.3 2158.2
[13,]     0  9624.7   0.4 1983.0
[14,]     1  9373.7  35.8 1933.7


b3. QAQCrun2 "fire/summary-log.csv" in R
open "fire/summary-log.csv" in R ==>
> QAQCrun2_fire_summary_log_output <- as.matrix(setNames(summary_log[ ,1:5], NULL))

Col==Time
Col2==TotalSitesBurned
Col3==TotalNumberEvents
Col4==MN101
Col5==MN102


      [,1] [,2] [,3] [,4] [,5]
[1,]     5 9104  318 1635 7469
[2,]    10  769  515   77  692
[3,]    15 1496  779  147 1349
[4,]    20 1964  887   46 1918
[5,]    25 1705  917   34 1671
[6,]    30  936  847    0  936
```

```
c. (LANDIS-II) QAQC run3
==> "NECN-succession.txt"
==> "base-fire_NECN.txt"
```

```
==> "biomass-harvest_SalvageLog_QAQCPrescription.txt"
    HarvestImplementations
>>Mgmt Area Prescription Harvest Area BeginTime EndTime
>>------------------------------------------------
1 SalvageLogger1 50%
>>1 SalvageLogger2 50%
>>1 MaxAgeClearcut 5% 0 15
>>1 MaxAgeClearcut 10% 15 30



c1. QAQCrun3 "harvest/harvest_summary_log.csv" in R
open "harvest/harvest_summary_log.csv" in R ==>
> QAQCrun3_harvest_summary_log_output <- as.matrix(setNames(harvest_summary_log[, c(2,4,5,7)], NULL))

Col2==ManagementArea
Col4==HarvestedSites
Col5==TotalCohortsCompleteHarvest
Col7==TotalBiomassHarvested

NO DATA!!!
0 observations of 76 variables


c2. QAQCrun3 "NECN_succession_log.csv" in R
open "NECN_succession_log.csv" in R ==>
> QAQCrun3_NECN_succession_log_output <- as.matrix(setNames(NECN_succession_log[, c(3,6,25,26)], NULL))

Col3==EcoregionIndex
Col6==SOMTC
Col25==C_SOM1surf
Col26==C_SOM1soil

        [,1]    [,2]  [,3]   [,4]
 [1,]      0 17164.4 785.5 3363.3
 [2,]      1 15394.7 818.0 2947.8
 [3,]      0 15903.6 273.7 3223.3
 [4,]      1 14069.4 221.3 2820.1
 [5,]      0 15424.3 308.5 3141.4
 [6,]      1 13244.6 184.5 2694.5
 [7,]      0 14997.5 306.7 3057.9
 [8,]      1 12569.8 189.2 2570.9
 [9,]      0 14563.7 292.1 2966.8
[10,]      1 11700.7 138.7 2404.4
[11,]      0 13968.6 245.7 2845.5
[12,]      1 10766.8  99.5 2215.6
[13,]      0 13267.8 206.0 2700.3
[14,]      1  9791.4  63.5 2011.8


c3. QAQCrun3 "fire/fire-summary-log.csv" in R
open "fire/fire-summary-log.csv" in R ==>
> QAQCrun3_fire_summary_log_output <- as.matrix(setNames(fire_summary_log[ ,1:5], NULL))

Col==Time
Col2==TotalSitesBurned
Col3==TotalNumberEvents
Col4==MN101
Col5==MN102

      [,1] [,2] [,3] [,4] [,5]
[1,]     5 9104  318 1635 7469
[2,]    10  776  515   80  696
[3,]    15 1570  758  181 1389
[4,]    20 2467  908  242 2225
[5,]    25 2269  877  290 1979
[6,]    30 2008  883  263 1745
```

```
d. (LANDIS-II) QAQC run4
==> "NECN-succession.txt"
==> "base-fire_NECN.txt"
==> "biomass-harvest_SalvageLog_QAQCPrescription.txt"
    HarvestImplementations
>>Mgmt Area Prescription Harvest Area BeginTime EndTime
>>-----------------------------------------------
>>1 SalvageLogger1 50%
1 SalvageLogger2 50%
>>1 MaxAgeClearcut 5% 0 15
>>1 MaxAgeClearcut 10% 15 30
```

```
d1. QAQCrun4 "harvest/harvest_summary_log.csv" in R
open "harvest/harvest_summary_log.csv" in R ==>
> QAQCrun4_harvest_summary_log_output <- as.matrix(setNames(harvest_summary_log[, c(2,4,5,7)], NULL))

Col2==ManagementArea
Col4==HarvestedSites
Col5==TotalCohortsCompleteHarvest
Col7==TotalBiomassHarvested

NO DATA!!!
0 observations of 76 variables
```

```
d2. QAQCrun4 "NECN_succession_log.csv" in R
open "NECN_succession_log.csv" in R ==>
> QAQCrun4_NECN_succession_log_output <- as.matrix(setNames(NECN_succession_log[, c(3,6,25,26)], NULL))

Col3==EcoregionIndex
Col6==SOMTC
Col25==C_SOM1surf
Col26==C_SOM1soil

        [,1]     [,2]   [,3]    [,4]
 [1,]     0 17164.4 785.5 3363.3
 [2,]     1 15394.7 818.0 2947.8
 [3,]     0 15903.6 273.7 3223.3
 [4,]     1 14069.4 221.3 2820.1
 [5,]     0 15424.3 308.5 3141.4
 [6,]     1 13244.6 184.5 2694.5
 [7,]     0 14997.5 306.7 3057.9
 [8,]     1 12569.8 189.2 2570.9
 [9,]     0 14563.7 292.1 2966.8
[10,]     1 11700.7 138.7 2404.4
[11,]     0 13968.6 245.7 2845.5
[12,]     1 10766.8  99.5 2215.6
[13,]     0 13267.8 206.0 2700.3
[14,]     1  9791.4  63.5 2011.8
```

```
d3. QAQCrun4 "fire/fire-summary-log.csv" in R
open "fire/fire-summary-log.csv" in R ==>
> QAQCrun4_fire_summary_log_output <- as.matrix(setNames(fire_summary_log[ ,1:5], NULL))

Col==Time
Col2==TotalSitesBurned
Col3==TotalNumberEvents
Col4==MN101
Col5==MN102

       [,1] [,2] [,3] [,4] [,5]
[1,]     5 9104  318 1635 7469
[2,]    10  776  515   80  696
[3,]    15 1570  758  181 1389
[4,]    20 2467  908  242 2225
[5,]    25 2269  877  290 1979
[6,]    30 2008  883  263 1745
```

References