

	2024-5				2024-6				2024-7				2024-8				2024-9				2024-10			
	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42
<b>Remote sensing of global biodiversity</b> Write perspectives paper <b>Working Groups</b> <b>BIEN 3</b> fix disk space leak that fills the disk (...) fix bug that causes joining on (...) narrow down the cause of the (...) fix geovalidation duplicated rows CSV to XML mappings for NYBG, SALVIAS CSV-XML-database mapping script XML to database conversion script (merged (...)) VegX-VegBank mapping look for formal mapping mechanism benchmark tests for database loading list of milestones VegBank metadata query mechanism mapping inversion script find plot data source provider to work (...) provide benchmark queries for NYBG data Direct mapping from native salvias_plots (...) Request new data dump of specimen data (...) Try to find source of DwCA (DwC Archives) (...) Mapping from NVS to VegX and VegBIEN TurboVeg data RAINFOR data Make changes to VegBIEN schema Mapping from VegBIEN to original VegBank Complete full dataset imports to VegBIEN (...)	<b>Remote sensing of global biodiversity</b> New 0%  <b>BIEN 3</b>																							

Complete full-dataset validations for (...)  
Acquire additional plot data sets from (...)  
Acquire additional specimen data sets (...)  
do a direct transfer of some public (...)  
mapping and export utility from VegBank (...)  
automated build process  
Decouple VegBIEN from VegBank and map (...)  
Finish importing SALVIAS data  
Import full NYBG data  
Import CTFS data  
Import TurboVeg data  
Direct mapping from VegX to VegBIEN  
decide whether to switch to VegX 1.5.2  
Update statistics/lists of user-defined (...)  
Convert user-defined VegX fields to (...)  
Convert user-defined VegBIEN fields (...)  
get access to raw CTFS data  
map NYBG data  
NYBG validations  
map CTFS data  
generic MOU template to request data  
look into Clio  
get raw data rather than flat file exports (...)  
make website user-protected  
DwC extension to VegX  
use VegX's individualOrganismObservation/relatedItem (...)  
switch to VegX 1.5.3  
add traits table to VegBIEN  
which DarwinCore attributes do we want (...)  
Look into using Sybase Powerbuilder (...)  
create VegBIEN ERD  
VegBIEN table renames  
put together samples of SALVIAS data (...)  
have "schema showdown"

<p> put together definitions of abstract (...)  create verbal descriptions of edge cases  make DwC_BIEN schema  integrate TNRS into VegBIEN  contact John about GNRS/georeferencing  integrate GNRS into VegBIEN  add georeferencing support to schema  revise milestones  1st draft of schema  make ERD of full schema  implement methods in VegBIEN  list of fields and method attributes (...)  create way to represent methods hierarchically (...)  add terms from previous versions of (...)  list of deliverables for next week (2/6-2/10)  implement morphospecies using a scoped (...)  support subplot events that link to (...)  make shortlist of 1st-level fields a (...)  make shortlist of 1st-level fields a (...)  retrieve taxonomic hierarchy in analytical (...)  refactor VegX  get Univ of Arizona DwC data  get TEAM VegX data  get CTFS data dictionary  create ERD of final schema  formalize proposed changes to VegX  talk to Nick about proposed changes (...)  map all specimens data in raw_data  mechanism to export VegBIEN data to (...)  ask NYBG for direct access to server  create automated feedback mechanism  convert VegBank data dictionary to database (...)  prototype tree traversal algorithm  implement mechanism to determine which (...) </p>	<p>Resolved 100%</p>
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load Canadensys data  
count how many duplicates between Canadensys (...)  
Finish translating XML functions to (...)  
Reimplement row-based logging mechanism (...)  
Reload DB using column-based import  
Load all plots data  
aggregating validations of imports  
import CTFS data using JOINS from DB (...)  
test restoring of import backups  
back up staging tables  
test backing up entire DB  
fix deadlock in INSERT IGNORE replacement  
timeout ANALYZE queries  
optimize JOINS on existing rows  
cast all untyped literals as text using (...)  
verify database contents as part of (...)  
add column-based import to automated (...)  
cluster vegbien tables periodically  
update summarizing queries for current (...)  
change summarizing queries to use vegbien (...)  
test that querying the DB uses the unique (...)  
use driver-native autocommit mode instead (...)  
map all VegX sources to stems table  
data provider feedback: propagate srcs (...)  
don't display warning when nullable (...)  
name backups according to svn revision (...)  
allow an input to appear multiple times (...)  
reverse XPath so that they start with (...)  
move issue tracker comments to wiki (...)  
column-based import: avoid most exceptions (...)  
underline all to do items in meetings (...)  
rename/delete and recreate public schema (...)  
give everyone their own account on vegbien  
source terms from old versions of DwC (...)

add make actions so new dependent maps (...)  
 replace accessioncodes with datasource\_id+sourceaccessioncode  
 use \_merge instead of \_alt to avoid (...)  
 use svn to figure out when a map file (...)  
 develop map spreadsheet -> header override (...)  
 allow putting specimens data directly (...)  
 automate adding a new table to an existing (...)  
 translate README.TXT to wiki page  
 rename staging table columns according (...)  
 support installing staging tables directly (...)  
 track data provider's citation requirements (...)  
 add unit-conversion mechanism  
 change import.stats.xls to use field (...)  
 add indexes for the analytical\_db\_view (...)  
 add separate datasource table rather (...)  
 create examples of taxonomic names to (...)  
 add definitions to columns in "green (...)  
 map example terms into the taxonomic (...)  
 when lower rank has name concatenated (...)  
 find out which datasources won't allow (...)  
 make place\* tables use a structure similar (...)  
 fix deadlock when multiple testers (...)  
 get analytical\_stem\_view to use merge (...)  
 integrate creation of analytical DB (...)  
 remove benign errors from the data provider (...)  
 add covering indexes on fkeys  
 move VegCore data dictionary to a phpPgAdmin-accessible (...)  
 make VegBIEN ID fields plain-text instead (...)  
 flatten the mappings  
 refactor VegBIEN to use VegCore terms  
 make all VegBIEN column names globally (...)  
 partition the TaxonDetermination table (...)  
 automatically adjust staging tables (...)  
 automap the analytical DB columns

mechanism to manually override the CSV (...)  
put all wiki attachments in svn  
merge the datasources' mappings into (...)  
use views instead of map spreadsheets (...)  
replace all fields of type text with (...)  
in sql\_gen.EnsureNotNull, use ARRAY[] (...)  
automap each word \*in\* a VegCore term (...)  
mechanism to dynamically autopopulate (...)  
enable running all the import steps (...)  
support TNRS-matching names in "", insted (...)  
autodetect column mismatches  
rename columns by name, not position  
auto-prepend table name to columns  
re-run TNRS on mis-scrubbed names  
make tests use their own public schema  
data provider feedback tables: include (...)  
standardize taxon ranks to a common (...)  
fix slowness in \_taxonlabel\_set\_parent\_id()  
remove dependencies on the development (...)  
    enable schema changes to be made (...)  
    move test DB to vegbiendev VM  
grant bien\_read access to publishable (...)  
grant bien\_read access to validation (...)  
fix crow's foot notation in ERD  
add limit on the # of parallel import (...)  
have import scripts regularly check (...)  
fix Postgres bug that causes query planner (...)  
remove dependencies on Mac  
schedule regular pg\_dump backups of (...)  
fix Ubuntu 14.04 upgrade bug that prevents (...)  
add MySQL public user to allow accessing (...)  
troubleshoot rsync verification errors  
generate the source-general derived (...)  
in aggregating validations pipeline, (...)



<p>Provide shared server access to 50-100GB (...)</p> <p>Produce global fused DEM layer</p> <p>Produce global slope layer</p> <p>Produce global aspect layer</p> <p>Produce global flow accumulation layer</p> <p>Confirm with Project Scientists: CGIAR (...)</p> <p>Evaluate existing E&amp;O AML scripts</p> <p>Establish file organization and possible (...)</p> <p>Validate fused DEM at SRTM/ASTER boundary</p> <p>Good News: JPL provides comprehensive (...)</p> <p>Organize and document SRTM input DEM (...)</p> <p>Organize and document ASTER input DEM (...)</p> <p>Producing, formatting and extracting (...)</p> <p>Test and compare the GAM method on several (...)</p> <p>Decide on a map projection for the Oregon (...)</p> <p>Integrate spatial variables and structure (...)</p> <p>Assemble monthly mean MODIS LST values (...)</p> <p>Assemble monthly mean TRMM precipitation (...)</p> <p>Insert DEM adaptive smoothing procedure (...)</p> <p>Identify Focal Regions</p> <p>OR-GAM predictions-model assessment (...)</p> <p>Capturing LST spatial structure using (...)</p> <p>Effect of sampling on GAM: hold out (...)</p> <p>Assemble all GHCN data into a single (...)</p> <p>Scope out workflow for calculating monthly (...)</p> <p>Process MOD06_L2 Cloud data</p> <p>Explore Landcover - LST interactions</p> <p>Assessment of results in the context (...)</p> <p>Develop stratified station sampling (...)</p> <p>Estimate total storage size of daily (...)</p> <p>Add buffer to station subsetting algorithm</p> <p>Climatic Stationarity</p> <p>Methods comparison</p> <p>Facilitate raster buffering across antimeridian</p>	<p>Closed 100%</p> <p>In Progress 100%</p> <p>New 0%</p> <p>New 0%</p> <p>New 0%</p> <p>Resolved 100%</p> <p>In Progress 30%</p> <p>Rejected 100%</p> <p>Closed 70%</p> <p>Rejected 100%</p> <p>In Progress 80%</p>
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<p><b>Interpolation of temperatures in the (...)</b></p> <p><b>MODIS Cloud Mask - landcover interaction</b></p> <p><b>DEM Evaluation</b></p> <p><b>Create Global Grid for Interpolation</b></p> <p><b>Run interpolation over tiles for North (...)</b></p> <p><b>Generate Global Monthly Median (Climatologies) (...)</b></p> <p><b>Run interpolation over all five case (...)</b></p>	
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