

## Developing the flora of Okanogan County, Washington

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Polepick Mountain, near Twisp, Okanogan County, spring, 2011.

This report describes procedures and data structures used to process a database of plant taxa and voucher collections used as the basis of the flora of Okanogan County, Washington.

The Okanogan flora can be accessed at:

<http://www.okanogan1.com/botany/flora/Okanogan-flora-wooten.pdf>

This document is available online at:

<http://www.okanogan1.com/botany/flora/Flora-database-Wooten.pdf>

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## 2. Background

The goal of the Okanogan County Flora project is to maintain a list of plant taxa occurring within Okanogan County, Washington. This list has a number of potential uses. It can be used to map invasive species; develop restoration projects; develop ecology guides; document the location and habitat requirements for rare or economically valuable plants; or as an aid in completing sets of herbarium vouchers for the county.

The plants in the flora are identified by unique scientific names that ensure each authored taxon was validly published under the rules of the International Code of Botanical Nomenclature (ICBN; McNeill and others 2006). Where a plant has two or more potential synonyms, only one of these can be the accepted name. The accepted name is resolved by a published authority, which ultimately will be the Flora of North America (FNA 1993+), when it is complete. Until that flora is complete, there is an online authority available as the PLANTS database (USDA, NRCS 2008+). PLANTS was initially developed through the work of Kartesz (1998). The PLANTS database contains taxa for the United States, Canada, and Greenland.

Beginning in 1992, the Okanogan flora project used the database from Kartesz (1998) and early versions of PLANTS (USDA, NRCS 2008+) to verify the accepted names of available plant lists and herbarium records. During this process, a number of scripts were developed to trap errors in the PLANTS database, which were periodically sent to USDA staff. Since the late 1990s, the Okanogan County Flora Project found and corrected over 2,000 errors in the PLANTS database that were forwarded to the PLANTS database

development team.

The PLANTS website also includes lists of plant species occurring within each of the states. The Washington state list was downloaded and matched with the list of corrected records from the full list of North American plants. The Washington state list was updated with a list of Okanogan County plants, DXWA2T (Wooten 2004+; superceded by this document). The dictionary is referred to here as the “DXWA” or “DX” database. The updated Washington list was used as the dictionary for the compilation of the Okanogan County flora.

The parsed and restructured Washington database dictionary is used as a cross-reference for plant survey lists, including the compiled flora for Okanogan County. Plant lists are processed through script 01VEG, which is a menu-driven suite of scripts within Borland Paradox for DOS. The scripts are capable of importing and exporting data, converting names between authorities, generating herbarium labels, and generating reports that list nomenclatural statistics, collection name, date, location, and plant characteristics such as habit and habitat.

To generate a flora, the scripts cross-reference entered names with those in the dictionary to generate a report. The scripts sequentially apply taxonomic and nomenclatural rules to process the list of names into a flora. These rules include noting whether species are missing from the dictionary; noting non-specific genera; adding binomial taxa for subordinates without them; substituting accepted synonyms for older entered names; determining the taxonomic rank of species; removing duplicate names; and identifying hybrids.

The flora lists all entered names and synonyms with herbarium collections, however only accepted names are counted as taxa occurring within the flora. When species have more than one synonym, the rules are used to determine which name should be accepted as valid. Processing synonyms involves using the rules to compare each name on the survey list with the lookup dictionary and with other names on the list to determine which of the synonyms should be counted under the given authority (USDA, NRCS 2008+). The output report documents the reason for each decision as it processes the output list. Species with unresolved nomenclatural and taxonomic problems in the dictionary are noted in the report.

### **3. Database structures**

Relational databases, also referred to here as tables, are used to store and organize data. For maintaining a flora, the unit of data is the plant name, organized by the name and date of the earliest collection record for that plant. The data is processed by comparison with a lookup dictionary of plant names.

A database manager, Borland Paradox for DOS, is used to maintain table structures. Paradox has a C-like scripting language that is used to control database input and output. Although Borland no longer exists as a company, Paradox remains unexcelled in speed, power and ease of use.

The creation of the flora is initiated via the script 01VEG, a menu-driven suite of data processing scripts

used for processing taxonomic lists and plant collections. This script has several related modules for processing botany and ecology data.

The Analysis module, AMAINANA, processes floristic surveys, allows input of observed plant species, and generates survey reports. The Analysis module is used to enter or import lists of plants observed within a defined survey area. The Analysis module has an editor for rapidly entering records of plants observed at a survey site, followed by processing that list to remove duplicates and print out a report listing and counting all of plants observed.

The Collections module, COLMAIN, processes herbarium collections and allows data entry and changes. The Collections module can output a report that generates herbarium labels, in addition to other functions related to herbarium management.

The Flora module, AMAINFLO, produces a report listing all collected and observed plant taxa within the area of the flora. The Flora module merges the collections database with the master database of the flora prior to generating the report.

Details about the database structure and function are given in this document. Naming conventions used in this report are: (a) fields are listed within square brackets, e.g., [NUM]; (b) database file name suffixes are \*.DB; (c) script file name suffixes are \*.SC; procedures are indicated by appended parentheses, e.g., cleanalf().

#### **Structure of the flora database, OK4**

The database for the Okanogan County flora, OK4, contains a single unique record for each accepted plant name. Each plant name is associated with a collection record or an observation.

Records in the flora are selected from either of two main sources, a database of plant collections, COLGW, or a list of plants observed during botanical surveys. Examples of surveys include Forest Service rare plant surveys and botany hikes led by the Washington Native Plant Society. Data taken from the collections database is selected with preference for the earliest date with a complete record and a specimen in good condition.

OK4 has three records of header information. Record 1 identifies the table as a flora when field [NOTESOKA] = "COLALF". Record 2 contains the name of the person who processed the data in [NOTESOKA]. Record 3 contains the date when the data was last processed in [NOTESOKA].

Each plant record in OK4 contains a unique full scientific name, sorted alphabetically, in the field [FULLNAME]. This field is used as the basis for linking the names with the authors and synonyms for each taxon. The field [C6] contains a 9-character mnemonic code with a 1:1 correspondence with [FULLNAME], used for linking to related tables. Field [NUM] maintains the sort order of [FULLNAME] and is key field that the data is indexed on, which also improves the speed of data input and output.

The Okanogan County flora contained in table OK4 is backed up in tables OKALF and ALF during operations that change its contents. During preparation of reports from the flora, the data is processed sequentially by scripts that operate on the database contents. During processing, the data is saved in temporary tables. When finished, the scripts output merge the various tables into a text file which is can then be imported into a word document for formatting.

### **Structure of the lookup dictionary, DX**

The lookup dictionary contains a list of plant species names and synonyms (USDA, NRCS 2008+). The names in the lookup dictionary are used to aid rapid data entry, as a nomenclatural reference, and as a taxonomic reference.

Names in the dictionary are dynamically coded with a unique 6- to 9-letter sequence used as a shorthand notation for entering data, and relating records from different data tables. This code is contained in field [C6], and used as the key field in the database to ensure all names are unique, and as a sorted key field to speed up data processing and data entry. The sort order of [C6] is Genus > species > subspecies > variety. The codes contain the first three letters of the genus and then the first three letters of the species, followed by a single letter each for subspecies and variety, followed by the letter “X” for hybrids and lastly, numbers to differentiate duplicate codes.

The script Dynacode is creates the codes in field [C6]. Dynacode is invoked whenever names are added or changed in the dictionary. Dynacode also creates records for hybrids and binomial names of autonyms; counts the number of infraspecific taxa (varieties and subspecies) within each species; and creates a field [LK], which flags unresolved errors in taxonomy or nomenclature, such as ambiguous names or missing authors.

### **Structure of the collections database, COLGW12**

A database of plant collections is used as the primary data source for the Okanogan County flora. It contains collection names and information from the specimen label or collector’s notes, along with additional data on location descriptions. The collection database is named COLGW (or COLGWnn.DB, where nn is the version number)

This database contains data from a number of sources: (1) a partial records of specimens from Okanogan County provided by the Burke Museum herbarium at University of Washington (the “WTU” collection); (2) collections housed at the U.S. Forest Service’s Methow District Herbarium in Winthrop, Washington (3) collections housed by Pam Camp of the Bureau of Land Management in Wenatchee Washington; (4) collections housed by George Wooten of Twisp, Washington, author of this report; and (5) additional specimens cited in botanical literature, but lacking label information or their present whereabouts.

The database of plant collections stored in table COLGW includes two types of records, one for fully

vouchered specimens and another for partially vouchers (“unvouchered”) taxa.

Vouchered specimens can contain any of the data fields shown in table 1 that specify the following data: scientific name of plant, collector name, collection number, collection date, name and date of botanist confirming identification, herbarium name (or physical repository), herbarium acquisition number, and acquisition date, location information, including the county and state where collected, detailed location description (including USGS quad, township, range, section, quarter section / quarter section, latitude and longitude, elevation, aspect, and slope), specimen condition, and notes on habit and habitat. Collections may include undated or partially dated specimens, but these cases are assigned a lower priority for listing in the Okanogan county flora.

Unvouchered records arise when a citation lists a collection, but does not list the herbarium where the collection is housed. Unvouchered records have incomplete or unverified information on plant taxa, but contain at minimum the name of the collector or observer, the plant’s Latin name, and the date (minimum, the year) of the observation.

The collections database, COLGW, is keyed on field COLLID2, which is an 18-character fixed-width string, containing the name of the herbarium, the collector and the collection number. These three string fragments are arranged and coded to determine the sort order of records. Collections can be grouped into three main categories. Field [COLLID2] is formatted so that records are grouped in sets by herbarium. The first group of collections are those contained in institutional or public herbaria, indicated by a 3-letter prefix code for the herbarium. The second group of collections represent cited collections that lack full herbarium documentation, indicated with a 3-letter prefix of “ZZZ”. The third group of collections are those held in a local collection, which in this case is a personal herbarium. Local collections begin with a number. Herbaria are distinguished by the third character in the herbarium code which is an “X” for private herbaria. Records in the local collection begin with a numerical string in [COLLID2] representing the collection ID, as opposed to all other collections, which begin with an alphabetical code representing the herbarium identity. This results in sorting the local collection first as an aid to browsing through the table. Details of how COLLID is interpreted are as follows:

For records in the local (Wooten) collection, the structure of [COLLID2] is formed from three dot-delimited strings representing:

Collection\_no: 7 characters with left-padded zeros. The last character is used to differentiate duplicate specimen sheets, or it is a dot for a placeholder.

Collector\_initials: 3 characters, the last of which can be a dot (see appendix for codes).

Herbarium\_initials: 3 characters; if the last character is an X, the set is housed in a private collection.

*Examples:* 001855B.GW..WTU, 001861.LES.GWX

For records in the collection database that are stored outside the local herbarium, [COLLID2] is formed from three dot-delimited strings, representing:

Herbarium\_initials: 3 characters; if these are “ZZZ” then the record is unvouchered; if the last character is an “X”, the set is housed in a private collection.

Collector\_initials: 3 characters, the last of which can be a dot (see appendix for codes)

Collection\_no: 7 characters, when the last character is used as an optional designator for duplicate specimen sheets, or 6 characters when there are no duplicate specimens. All collection numbers are left-padded with zeroes.

*Examples:* WNP.RDN.002750, PCX.SFC.00012B

When collections are merged with the flora, the information in COLLID2 is transferred to the field [SHOWCOL]. [SHOWCOL] rearranges the strings so that both local and remote herbaria are presented consistently, regardless of how they would sort. SHOWCOL string fragments are separated by the dot character, in the order herbarium.collector initials.collection number, and a trailing letter (A, B, C, ...) to indicate a duplicate collections.

*Examples:* WNP.RDN.002750, ZZZ.WWE.013128, WTU.GW..000123

## **4. Working with the databases**

### **4.A. The database editor**

There are several types of plant lists managed by 01VEG suite, including ecology plots, floras, field surveys (also called field observations) and herbarium collections.

Plant surveys are running lists of plants from a site survey. Survey plant lists include fields for notes and observed habitats and allow redundant observations of the same plant.

In contrast, floras are compiled sets of observations made over many years by many observers, that only allow a single unique name for each species. Floras contain collection information for the earliest known herbarium specimen within the area of interest. Floras are processed by merging observations with a file containing herbarium collection information. Floras require a specialized table structure to manage and sort the collection information.

Edits to both floras and surveys are performed on a temporary table named ALF. Before editing ALF the Editalf routine makes a backup of ALF using the name in record 1 of [NOTES], and appending the character "B" and a sequential number after the table name.

The 01VEG routines identify a file as a flora by whether the field [NOTES] of the first record is labeled "COLALF", which is also the name of the backup file for a flora. The label "COLALF" is generated either from the Collections > ZFLOMRG menu or when a file is imported from the Analysis > Files menu. The "COLALF" flag signals the 01VEG suite that the table is a flora, requiring completion of fields related to collection information, as well as running cross-checking routines and merging changed collections information with the flora edits.

Some files are automatically backed up during collection edits; these begin with the character 'X'. Whenever edits are made outside of the 01VEG suite, it is up to the user to back up files. The most important files to

backup are OK4 and COLGW.

The form for editing Alf surveys, Alfsav, is designed for rapid data input, performed by dittoing the information in field AREA and by accepting shortened mnemonic code names in field NEWCSIX that are then used to automatically fill in the names and synonyms.

Edits use an input form that displays the contents of field LOOKNAME, that lists accepted synonyms of entries. When editing the field FULLNAME in ALF, the Editalf routine beeps whenever names have a different accepted synonym than the one listed in field LOOKNAME. If a plant is not listed in the lookup dictionary, the name should be temporarily coded by entering the code “UNK” in field NEWCSIX. Later, the name can be added to the lookup dictionary DXWA2T, and processed with the script DYNACODE.

### **Importing tables into ALF**

ALF has a routine to import tables under 01VEG > Analysis > File. The Import routine uses the header label both to determine the name of the backup file and in addition, when the value in the header label is “COLALF”, this signals the program that ALF is flora. The import routine can import tables such as the Okanogan flora in table OK4.

The import routine calls the Alfstruc() procedure to allow importing existing tables into ALF. Alfstruc() is designed to be flexible in importing tables in older formats for editing local surveys, allowing the import table to be unnumbered and have extra fields. Fields are restructured in the order used in table ALF and then loaded with the data from the import file.

After importing a table, the Headalf() and Cleanalf() procedures are automatically run to clean up headers and minor data and inconsistencies. Cleanalf() will find words missing from the lookup dictionary and tag them in [NEWCSIX] with “UNCODED”, and in [NOTES] with “Spelled... [*name as entered*]”, as a warning note. Following an import procedure, these misspelled names should be corrected using 01VEG – Analysis – Editalf.

### **Importing ASCII data into Paradox**

ASCII files can be imported into Paradox using the native Paradox commands. Files can be imported as CDF files (comma-delimited files), having text fields delimited within quotes and separated by commas. Fields, field types and field order for table ALF.DB is as follows (A stands for text, followed by the field length; S stands for short integer):

- FULLNAME (A65)
- NOTES (A250)
- COVER (S)
- AREA (A120)
- NEWCSIX (A9)
- NUM (S)

To import into Paradox/DOS, click Tools > Export/Import > Import > ASCII > Delimited. Field headers will have to be manually renamed. The field [FULLNAME] should use a v. instead of var. and an s. instead of ssp.

### Processing the data

Data processing of floras or plant surveys is done in a temporary input table ALF. ALF is prepared for processing by procedures Headalf() and Cleanalf(). The former numbers the records in [NUM], and the latter performs a large number of error checks and corrections, including functions that upgrade old table formats to the most recent. The input fields are then structured to contain the following fields: X-2, X-3, AREA, FULLNAME, C6, DUP, COMMNAME, NEWFAM, FAM, FULLAUTH, LK, LOOKNAME, C6-1, FULLNAME-1, LASTNAME, NUM, NN, NUMU, NUMW, NAREA, SUBAREA, SORTNAME. See the appendix for more details.

Scripts are processed sequentially as sets of numbered routines. Routines are called sequentially by scripts Zrephot1, Zrephot2, Zrephot3 and Zrephot4. This set of scripts processes the list of plant names and counts taxa and synonyms.

### Printing reports

Reports can be output for collections, plant surveys or a flora. Reports of plant surveys are processed by the script AMAINANA, reports of floras are processed by script AMAINFLO. As long as the first record field [NOTES] of table OK4 is not "OKALF" this signals the program to process a vegetation survey and send the output to file VEGLIST.RPT. Reports of collection information is processed by script Prn85 called from within script COLMAIN.

For plant surveys, the output is sent to VEGLIST.RPT including the ability to print either a one- or a two-line list. For floras, the output is sent to VEGOKA.RPT.

After the report has been written to file VEGLIST.RPT or VEGOKA.RPT, for a plant survey or a flora, respectively, additional formatting is done within Microsoft Word, by the macro VEGLIST.

The output reports have codes and key words embedded in them that cue Word where to apply formatting. The Word macro begins by setting page size and margins, and establishing a fixed width font. Family names are boldened by identifying the word fragment "CEAE" and bolding that word. Binomial names are identified when two words are preceded by the characters "|\*", to indicate they should be boldened, or "|~", to indicate they should be italicized. The characters "qq" represent the hyphen character in Veglist.rpt or Vegoka.rpt, that would be misinterpreted by the macro as a space if not hidden. After boldening and italicizing is completed, the characters "qq" get converted back to a hyphen. The codes "v\$", "s\$", "f\$" "c\$" or "X\$" signal that the next word should be boldened and preceded, respectively, by the words "var.", "ssp." "forma" "cv." or x(for hybrid). Similarly italicization of these name fragments is signaled by the characters "|~", "v~", "s~", "f~" or "c~" and "X~". The last part of the macro changes fonts by section.

For plant surveys, script AMAINANA outputs accepted name in bold, followed by entered or added unaccepted synonyms in italics. The fields [AREA] and [NOTES] contain the observation area and notes. These two fields are only processed once per name, even if there are multiple entries under the same name. This differs from the processing of a flora, which has no redundant names. On the other hand, floras have collection information that is contained in the report.

#### 4.B Working with the collections database

The collection database contains the names and associated herbarium label data for plant collections. The following rules apply to plants with voucher specimens (collections). If the name on the label is changed, mis-identified, destroyed, lost or questionable, then those records are edited in the collections database, COLGW, as follows:

- (1) **Annotation.** If the specimen identity was changed by annotating the label, then the name of the plant should be changed in the collection database. The ZFLOMRG routine can then be run to correct the listing of this record within a Flora by clicking 01Veg > Flora > Mrgalf. The ZFLOMRG routine will update the flora with the correct plant name associated with that collection number, and ask the user for confirmation of the change.
- (2) **Misidentification.** If the specimen was mis-identified, but the label is not annotated (or it is unknown whether the label was ever annotated), then the field [CND] should be marked with the code “Z” in the collections database. The ZFLOMRG routine can then be run to correct the listing of this record within a Flora by clicking 01Veg > Flora > Mrgalf. The ZFLOMRG routine will exclude the misidentified record from the flora it was recorded in, allowing other collections of the same taxon to supplant the record in its place, if they exist.
- (3) **Destroyed or lost specimens.** If the specimen was lost or destroyed, then this should be recorded in the collections database by marking field [DEST] with the code “Z9-DESTROYED”. The ZFLOMRG routine can then be run to correct the listing of this record within a Flora by clicking 01Veg > Flora > Mrgalf. The ZFLOMRG routine will exclude the record from the flora it was recorded in, allowing other collections of the same taxon to supplant the record, if they exist.
- (4) **Questionable identification.** If the specimen identification is questionable, then this should be recorded in the collections database by marking field [CND] with the code “Y”. The ZFLOMRG routine can then be run to correct the listing of this record within a Flora by clicking 01Veg > Flora > Mrgalf. If there are no other records for that taxon, the ZFLOMRG routine will list the taxon as questionable, while preventing it from being counted as an accepted taxon.

Ancillary collection information about a collection should be recorded in field [NOTES] and [NOTESTAX] which are not modified when merged with the flora database.

Collections can be edited directly in COLGW or via the editing module by clicking 01Veg > Collections > Editcol. The edit module is only designed for editing collections within the Wooten herbarium. Collections from other herbaria must be made by editing COLGW directly, using native Paradox. Records from other herbaria are generally processed by importing them as blocks of data. Block data processing procedures

are described in separate documents contained in the DB-source folder under the source listing for the data.

Prior to editing COLGW or merging it with the Okanogan flora, procedure Colchek() is called to insure data integrity within table COLGW. If errors are found in COLGW, the program stops so that the data can be corrected.

### **Conventions used when editing collections in COLGW**

Collections indicate the type of herbarium housing the specimens. Collection information for private collections is edited via the routines in Collections > Editcol. Collections in recognized public and academic herbaria can be edited directly within Paradox.

For collections in herbaria, the first three letters of [COLLID2] and [SHOWCOL] must match the value in [DEST], or the scripts will terminate.

Private collections not in herbaria or in unknown herbaria are flagged if the third character in [SHOWCOL] = "X" or the first 3 characters in [SHOWCOL] = "ZZZ". These records must be scored in [DEST] with a code beginning with letter "Z", typically "Z2-RAW". When the herbarium is unknown the code "ZZZ" should be scored in [SHOWCOL] and in [COLLID2].

Collections with unknown collection numbers are preceded by an asterisk in the character positions for collection number.

Collected records in which the collector is unknown (as for example when collection information is concealed for rare plants) can be coded with "UNK" signifying the name of the collector is unknown. In this case, the collection number should be assigned using an asterisk as the first character to signify this. For example, ZZZ.UNK.\*00021 would be a valid value for [COLLID2].

Field [SEL] should be marked "NEW" when adding new records. This occurs automatically during edits via Editcol.

Information that should appear on flora reports, but not on herbarium labels, can be put into brackets in field [NOTES].

Records for rare plants or for plant observations on private property can be concealed by prepending field NOTES with "[Undisclosed ...]", which causes reports to hide information in fields [LOCDESC], [QUAD] and [BASIN], and all information within the brackets of field [NOTES]. The remainder of [NOTES] will be printed in the report. The material in brackets will not be printed on herbarium labels.

Records that are questionable can be marked in OK4 with "Y" in [CND] and in COLGW [NOTES] with the string "Identity unconfirmed." Records that are lost, misidentified, or extirpated can be marked in [CND] in

both COLGW and OK4.

When editing collections, [CND] should be assigned one of the following codes in parentheses:

A – Excellent condition

B – Good condition

C – Fair condition

M – Missing collection no. – given number is assigned

U – Unknown condition

X – Poor condition

Y – this value in OK4 overrides this value in COLGW) specimen ID is questionable; or there is a question mark next to the Latin name on the specimen label.

Z – (this value in OK4 overrides this value in COLGW) specimen is either destroyed (in which case [DEST] = “Z-9-DESTROYED”); or specimen ID is wrong, but the label is not annotated; or the plant is considered extirpated. If it were annotated, the full Latin name must be changed, but the collection no. would not change.

blank – unassigned, assumed to be (U)known.

### **Printing a list from a local collection**

Printouts of lists of specimens are performed by routine Prn85 (called from within script COLMAIN). This script is used to print specimens from the local collection of George Wooten, stored in Twisp Washington, or transferred to other herbaria from that collection. The printouts list each collection on a single line, in order by specimen number. The list prints out the following data to table VEGCOL85.RPT:

Collection no.: This is given in 2 string fragments. The first fragment is a 3-character string containing the codes for the collector’s name, or a 2-character code for collector’s name right-padded with a trailing dot. A dot then follows the first string fragment. The second string fragment contains a 7-character collection number which is left-padded with zeroes. The 7<sup>th</sup> character is an optional letter given to distinguish between duplicate individuals or pieces of the same collection.

Condition of the specimen (field [CND]).

Date of the collection.

USGS quad where the collection was made, truncated to 18 characters.

Name of the taxon, without authors.

Destination of the specimen (field [DEST]).

### **Preparing collections for transfer to herbaria and printing labels**

Changes in file structure and key data in COLGW occurs in the following steps:

Herbarium label preparation is initiated from 01Veg > Collections > PrnLab which calls script ZCOLLBL. Herbarium labels are printed for all selected records. During processing, routine PrnLab modifies the destination codes in COLGW to reflect the new location of the specimen.

#### 4.C Working with the flora database

There are several different procedures needed to edit the flora database, OK4, depending on whether data is being added, deleted or changed, on whether the information represents a collection or an uncollected observation (identified by lacking a collection number in [SHOWCOL]), and on whether the records are being processed as a block of data or individually.

A flora is processed using table ALF as a temporary storage database. ALF is identified as a flora, rather than a survey, when record 1 [NOTES] = "OKALF". A number of procedures, particularly in generating reports, and also in procedure Cleanalf(), treat floras differently from surveys.

An important task for developing a flora is editing records in the flora or related collections database. The 01VEG suite has an internal editor specifically designed for entering and editing scientific names. This editor operates on a temporary table named ALF, which is then copied back over the source data at the end of an edit session. To edit the flora, click 01VEG > Flora > Editflo. This loads the edit form from table Aedoksav.db containing the fields [SHOWCOL], [DATE] and [CND] related to plant collections. These are visible but cannot be edited, thereby preserving herbarium information from accidental modification. Changes to information in any of the OK4 fields should only be made within the editor, in order to preserve data correspondence between the related tables. Similarly, additions to the flora should be made only within the editor in order to preserve data integrity. While it is possible to delete an uncollected observation by editing OK4 directly without disrupting data integrity, deletion within the editor is still preferable.

Whenever changes are made to observations in the flora, they must be followed by ensuring that the information in the collections database and the flora is consistent, and the number of collections hasn't changed. Merging the flora with the collections is done by running the Mrgalf routine by clicking 01Veg > Flora > Mrgalf. The Mrgalf routine is initiated within AMAINFLO, which then calls procedure Zflomrg(). This procedure first merges COLGW with ALF, and then it copies ALF over OK4, after assuring there are no newly added duplicate FULLNAMEs in ALF. See the technical details in that section of this document.

#### Conventions used when editing a flora

The editor uses table ALF.DB as a temporary table for editing the flora. There are a large number of menu-driven editing tools in the editor that are self-explanatory, however the following conventions may also apply.

During edit sessions, it is unnecessary to describe preferred synonyms for taxa, since these will be generated by the output report. However the computer will beep as a reminder whenever an older synonym is entered.

When editing observations within a flora, general notes about a plant's habit, habitat, range, location, and taxonomy should be put into field [NOTES], which will not be overwritten if a subsequent collected record

replaces the uncollected observation for the source of the record.

The [NOTES] fields in ALF are used differently than they are in table COLGW. [NOTES] (A150) holds information on habit and habitat, whereas [NOTESADD] (A255), contains additional details that won't fit into the field [NOTES]. When merging COLGW with OKALF in Colmain case Mrgalf, [NOTES] (A150) is concatenated with NOTESADD (A255) (with an intervening space, and then truncated to A250 before the string is copied into the destination field NOTES (A250) in OKALF.

Records for rare plants or for plant observations on private property should be excluded from reports for public distribution by prepending field NOTES with “[Undisclosed ... ]”, which causes reports to hide information in fields [LOCDESC], [QUAD] and [BASIN], and all information within the brackets of field [NOTES]. The remainder of [NOTES] outside of the brackets will be printed in the report.

Records that are questionable are marked with a ‘Y’ in [CND] and are also marked in [NOTES] with the string “Check identity.”

#### **4.D Working with a plant survey database**

Plant surveys made by botanists and ecologists contain lists of plants observed in a specific area. These lists are often shared with a larger audience, whose needs are simpler than that of the botanist. Typically, this audience is just seeking a list of accepted and common names of all the plants in an area. The 01VEG suite can rapidly enter data from plant surveys and output them as a list of names, sorted either alphabetically or by family.

One of the main objectives for writing this editor was to create a means of rapidly entering data using a 6–to 9–letter alphacode in field [C6]. The alphacode is a mnemonic consisting of the first three letters of the genus followed by the first three letters of the species and any additional single initial letters from the subspecies or variety. The few remaining duplicate alphacodes are appended with a numerical sequence.

To edit a plant survey, Run 01Veg > Analysis > Editalf to prepare a temporary table, ALF, for accepting data. ALF contains three records of header information in field [NOTES]. The first record of the header contains the filename for the database that gets copied over with information from ALF. The second and third records contain the observer name and the date of the survey.

Before the editor is invoked, the scripts check the value listed in line one of the header. If the value in field [NOTES] is “OKALF”, then the script proceeds to editing within the flora module. Otherwise the script proceeds to edit a plant survey. If there is a database with the same name that given in the first record of the header, the script will open that database in edit mode. The user is also given the opportunity to back up data, import data, or start a new survey, with a new date and observer identity.

The editor has a large number of menu–driven editing tools that are self–explanatory with onscreen help cues.

## 5. Generating a flora

### 5.A. Overview of scripts for processing a flora

This section describes the generation of a flora using data processing scripts to generate a report as a text file. The report lists entered names, accepted names, their synonyms, collection information, notes, errors and statistics about the data. The source data for the list is a database containing herbarium records and reliable observations of plants. A lookup dictionary is used to determine the accepted name of the species listed.

The data model is based on the premise that there is only one accepted name for an observed plant species under the given authority. This concept allows a taxon to be symbolized as a data object amenable to data processing.

The full name of a taxon includes its scientific name and its authority, given by the names of authors who have published descriptions of the taxon. A taxon can have several available full names, which are names that meet all mandatory provisions of the rules of the International Code of Botanical Nomenclature (ICBN; McNeill and others 2006).

The valid name, or “correct name”, of a taxon is specified under the ICBN rule of priority as the name given in the earliest publication of an available name for a taxon within a particular circumscription, position or rank, although other rules may specifically override this one. Validly published names other than the correct name are called synonyms.

**BUT** there can be more than one correct name for a taxon if it is treated outside of the circumscription, position or rank of the other names. These names are also called synonyms.

The accepted name determines which correct name to use when there is more than one choice for a taxon listed here. The accepted name is based on the collective opinion of the cited authority, either expressly, as in that of the FNA (2003+), or implicitly, as in the PLANTS (USDA, NRCS 2008+) or Kartesz (1998) databases.

So what does it mean that the definition of an accepted name for a taxon is based on the opinion of the authority?

Both of the names *Mahonia aquifolium* Pursh. and *Berberis aquifolium* (Pursh.) Nutt are validly published names for the same entity. Both are correct names for the same entity; the only difference is rank of the genus. But the former name is the one *accepted* by PLANTS (USDA, NRCS 2008+). Other botanists may choose either authority depending on whether they prefer to split the name into *Mahonia* as a genus or lump *Mahonia* as a subgenus under *Berberis*. Either name is correct, but under the authority of PLANTS, only the former is accepted.

The major tasks of the flora processing scripts are to determine which synonym is accepted under the given authority. There can be more than one validly published name. Three main authorities used here in order of priority are the Flora of North America (1993+), the PLANTS database (USDA, NRCS 2008+), the database from Kartesz (1998+). The latter two databases contain quite a few inconsistencies, ambiguous names and errors. In addition, the observations, based primarily on plant collections, contain misapplied species (misidentifications) and incomplete data that further confound the process.

In order for the rules of nomenclature to be applied within a computer program, the input data must be perfectly consistent with the rules of the ICBN. Hence the data contained in PLANTS and other authorities is rigorously tested for perfect compliance with the rules of the ICBN. Where there is so much as a single character out of place, this becomes a flag that the validity of the authority is suspect. When found, typographical errors and inconsistencies are printed in the appendices for notification to the PLANTS program botanists. Since 1992, thousands of errors have been forwarded to the PLANTS team. Wherever it is possible, the correct name for a taxon is resolved by the flora data processor, but in cases where the name in PLANTS cannot be positively determined, an earlier valid name is listed as the accepted name in the flora instead.

The process begins by compiling a lookup table of plant names, derived primarily from the PLANTS database (USDA, NRCS 2008+) with additions from FNA (2003+), Kartesz (1998+) and the botanical literature.

Next the initial list of plants is developed from data sources listing collections and observations. This list is then joined to a list of potential synonyms for the initial list of names. Potential synonyms include ordinal names that can be treated *sensu lato* (names with higher rank inclusive of all subordinates); *sensu stricto* names (names in the narrow sense, excluding similar taxa and infraspecific taxa that otherwise would be considered together); autonyms (subordinates with the same epithet as the specific epithet); taxa with mixed rank subordinates; orthographic variants (names with different spellings); unpublished taxa; provisional names; *pro parte* synonyms (entities split into two or more taxa); hybrids; *pro specie* hybrids (names originally describing distinct species but currently considered as hybrids). The complete list of plants maintains both the target and the pointer synonym in each record through each step of the process. When all the records have been processed the list is printed alphabetically in order of the highest rank, with subspecific entities indented below.

Because species can have more than one name, but only one accepted name under the given authority, the data model segregates the names into sets of accepted and unaccepted names. Hence the data model uses set counts as the equivalent of accepted names. This is an exhaustive task ideally suited to a relational database.

Determining which names are accepted or not involves successively iterating through the list of names with algorithms that test for taxonomic rules that have been established by the ICBN. Each record is flagged with the results of the taxonomic tests.

An important test is determination of the authority under which a name is published. When two different authorities do not agree, the record is annotated with a reason for choosing one over the other. The final report contains numerous appendices that list plants with incomplete data.

**Sidebar: A word to the wise**

For those who simply want a list of plants and don't want to be bothered with how it was arrived at, at least consider the following.

It is important to understand the difference between an object (the taxon) and its symbolic representation (its name). A taxon is a continuum of self-replicating living matter distributed in time and space. The name of a taxon (its nomenclature) is a collection of observations (a classification) that taken together describe the taxon by an accepted name.

A flora is a changing, virtual concept and any or all of its members may be interpreted with different concepts for what constitutes a species. Without historical and social context, a list of plant taxa is little more than a meaningless counting of virtual bits of the universe. What we call a taxon is tinged and shaded with the colors of perception, experience and unseen cominglings of DNA. It is true that the goal of this flora project is to list and count the accepted names of plants in a given area. But this flora also lists as many synonyms as possible for these same entities, each of which offers a rich alternative narrative about that taxon.

The task of determining which name is to be counted as accepted is complicated for many taxa. Walter Berendsohn (1997) warns,

“As outlined above, the circumscription of a taxon may vary from one author to another, the system the authors adhere to may be different, and a huge amount of extant information about plants is linked to nomenclaturally flawed names, synonyms, or misapplied names.”

Berendsohn's warnings cannot be overemphasized. Botany and the concept of what constitutes a taxon will always be subject to reinterpretation, and indeed that is a desirable feature of botany and science in general.

The opinions expressed by any particular authority are always being challenged with the result that species' names are constantly changing. The use of PLANTS as an authority is a tool. The taxonomic opinions implicit in PLANTS are not interpreted to contradict the validity of other correct names with a different circumscription, position or rank. Hence it is desirable to know what these synonyms are.

For an authority to be the ultimate arbiter of a taxon would require that its taxonomy is expressly justified with literature citations and a measure of consensus by experts of that group, along with dissenting opinions. Our current inventories of plant species lack this justification, and arguing on their behalf is a pitfall to be avoided.

Ultimately there is no right name or wrong name for a plant, only successive approximations of the truth. For many entities, there may never be consensus of opinion on its name and phylogeny. The best that can be hoped for in accepting a taxonomy is that the taxon was published by a respected authority based on abundant research, with only a few dissenting opinions. Because of this, the fifth rule of thermodynamics should probably be stated as: “the nomenclature of a taxon always increases”.

Creative thinking is stimulated by considering the history and context of what we consider to be truth. A casual observation reveals that science often leaps forward when it is unsettled and punctuated with abundant dissent or when major discoveries lie hidden in obscure crevices. There is little value in the representation of a flora by its species number alone. Only by considering alternative narratives for a taxonomic concept can one grasp the context for understanding evolution, life and perhaps even the universe.

To generate a flora requires several sequential procedures. First the module Flora > Mrgalf should be run to merge records from the collections database. Mrgalf calls script ZFLMRG to process the set of collections into a set of records limited to the county of interest, and containing a single unique name for each collected plant, prioritized by date of collection, condition of the collection, and authority of the names. If there are changes in the data from the previous flora data set, the user will be requested to verify them.

The next step is to run Flora > Report to generate the flora. The report gives taxonomic and nomenclatural notes for each species; collection information and location descriptions; counts of taxa; names and authors of synonyms; processing steps used; and appendices allowing identification of data gaps in the floristic record.

The report lists each unique plant name, along with collection information for specimens with vouchers. The flora report gives a list and count of each species occurring within the area, brief habitat information and field notes, and a citation for the earliest collection for each species in the list, under the original synonym for that species when it was collected.

The report counts the number of taxa two ways. One count is based on substituting all names with the names used in the lookup dictionary (USDA, NRCS 2008+). The other count of taxa simply enumerates the list of unique taxa as given on the specimen labels or on botanical surveys.

This process for creating a list of plants occurring within a flora is based on determining the accepted names of all taxa within the geographic limits of the flora. The process starts by enumerating a list of plant observations within area using whatever synonyms were reported. These synonyms are then expanded with a recent list of accepted names. Redundant names are eliminated, with preference for retaining records that have validated collections. The process then successively “un-counts” the unaccepted names, while marking the corresponding accepted synonyms to be counted. Many steps iterate over previous tests, sometimes requiring changes to prior determinations. Some of the operations confer stronger confidence in the determination of an accepted or unaccepted name, in which case the rules provide for resolution based on

the relative strength of the determination.

The tests provide for processing ambiguous names in special ways. *Pro parte* names with ambiguous pointers are flagged and uncounted. Indeterminate *s.s.* names that point to other synonyms are counted in the flora for lack of the known name, but are not considered as accepted.

### **Scripts for processing a flora**

The flora is generated by running the scripts within Paradox in a DOS window. Before generating the report, set default run parameters and breakpoints in AMAINFLO.SC, as described in the appendix, then run the script 01Veg > Flora > Repflo.

The presence of the value “OKALF” in the first record field [NOTES] of table OK4 signals the program to process a flora. Prior to processing, the input table ALF is prepared by procedures Headalf() and Cleanalf(), which checks for input errors. The input fields are then structured in a standardized form and the field CND is added specifically for processing floras. See the appendix for more details.

Scripts are processed sequentially as sets of numbered routines. Routines are called sequentially by scripts Zrephot1, Zrephot2, Zrephot3 and Zrephot4. This set of scripts processes the list of plant names and counts taxa and synonyms. The report is output to VEGOKA.RPT at the end of Zrephot4 with accepted names in a bold font. At the end of Zrephot4, the scripts ZREPAPP and ZREPSEC are called to output the appendices.

The parameters to run Paradox within a Microsoft Windows command window are as follows. The command line is C:\PDOX40\PARADOX.EXE -extk 12000. Memory defaults are Total=Auto; Initial environment=Auto; Expanded memory=Auto; Extended memory=16384 (using High Memory Area, HMA); MS-DOS protected-mode memory (DPMI)=Auto.

The scripts and flags used during generation of a flora are listed in Table 1, in the sequence that they are invoked. In the table, the term “counted” is equivalent to “accepted” unless it specifically states otherwise, (as when referring to a count of names in column A).

Appendix 3 Describes details of the scripts and flags used to generate a flora.

### 5.B. Results of the flora generation process

The output report lists names and statistics of the species determined within the flora. Important outputs include the following:

- The number of accepted taxa, where [X-2] = “CB..” or “C2..”) and of entries (where [LK] “-..”).
- The following broad categories of names:
  - Unswitchable names counted both as entries and as accepted names
  - Switchable names counted both as entries and as accepted names
  - Switchable names counted only as entries
  - Accepted names counted only as switched synonyms
- A list of the before and after results of each operation performed by the scripts.
- Problematic taxa including the following:
  - A list of taxa with nomenclatural or taxonomic problems.
  - A list of taxa without any collections under any name.
  - A list of collections with questionable identifications or with a ? on the label.
  - A list of collections with questionable synonyms.
  - A list of collections with incomplete collection information.
- A correspondence table listing omissions and commissions between the PLANTS database (USDA, NRCS 2008+) and the flora.

The report is not considered until it is free of processing error flags. Error checking is performed throughout the scripts and in the output. Many error checks are internal to the scripts. Many of error checks function by summing set membership before and after operations. When the subset totals do not match, program flow is paused or stopped with an error message printed to the screen. Additional error checks are output in the report with a bold error message. There are still processing errors in the output that the staff has not had time to find and fix yet. If you find a processing error in the output, please call the data department at 509-997-6010.

The output report also identifies data gaps in the input data, particularly where there is a lack of collection information or where the nomenclature is inconsistent with the rules of the ICBN.

A third set of errors are inconsistencies in the use of accepted conventions for naming species. These are relatively minor inconsistencies that nonetheless create havoc when used in a database with a 1:1 correspondence to taxa in a flora. Examples include the following:

- Names that are collected or observed once as a variety and another time as a subspecies, but which lack a matching record in the lookup dictionary.
- Names that are collected or observed under a binomial name without listing an available subordinate name or autonym known to occur within the flora.
- Names that are collected or observed as an autonym that is not listed in the data dictionary.
- Names that were collected under a pro parte synonym that results in an ambiguous assignment to more than one accepted name.
- Names of interspecific hybrids that are also treated as non-hybrid species.

- Names of apomictic hybrids that inconsistently accepted or rejected.

Ideally, these latter types of errors will come to the attention of the data stewards for those herbaria or for the PLANTS botany team.

## 6. Merging collections into the flora

There is a need to merge collection data into the flora database whenever records are changed in these tables. The routine Mrgalf is run to merge the collections in COLGW.DB with the county flora database OK4.DB, whenever the contents of either is changed independently of the other. The Mrgalf routine involves processing the list of plant collections so that each taxon in the county flora has only one record.

Mrgalf is run after editing either the collections database or the flora by clicking 01Veg > Flora > Mrgalf. Mrgalf updates the flora in OK4 with new, changed or deleted records, calling script Zflomrg(), contained in AMAINFLO.SC. to complete the majority of the procedures. The merge routine is memory- and processing-intensive, and makes several backup copies of the databases as it runs, in addition to checking the integrity of the collections database. If the merge routine encounters any errors, the user is requested to correct the error and the scripts terminate.

As Zflomrg() runs, the user is informed of changes to the data that will affect the number of taxa in the flora. Minor changes to the flora such as changes in the field [NOTES] are not reported. The merge routine finishes when Zflomrg() returns control to the calling scripts, and asks the user whether to accept the changes and overwrite the flora.

The sequence of operations in Mrgalf is as follows:

a. The Mrgalf routine to Colcheck() in script Zcoloka to insure data integrity in table COLGW. Procedure Colchek() fills in field [COLAREA] with data from [LOCATION] and [QUAD]. If those fields are blank, then it fills [COLAREA] with data from [LOCDESC], and if that field is blank, the procedure tries to fill [COLAREA] with [TRS] data containing public lands survey sections or latitude and longitude.

Data integrity is ensured in the flora database by excluding certain records from it during the procedure call to Colcheck(). The following types of records are excluded from the flora database: (1) collections made outside of Okanogan County (records exactly on the boundary are listed under Okanogan County to assure inclusion); (2) non-vascular plants; (3) collections that are only identified to the level of genus or family; (4) misidentified collections not annotated on the label (signified by [CND] = "Z"); (5) destroyed specimens (signified by [DEST] = "Z9-destroyed" and [CND] = "Z"). Colcheck() also prepares the field [COLAREA] with location data, for use by subsequent scripts that generate the flora report.

b. Procedure Okstruc(), in script Zcoloka, is called to renumber and backup OK4.

c. Procedure Okhead(), in script Zcoloka, is called to compare the number of records in OK4 with the

recorded number in the header line for the file, and these numbers are passed to the script Zflomrg().

d. The merge routine Zflomrg() is then called. Zflomrg() begins after the user to reply “yes” to delete back-up file XOKB, which is generated each time ZFLOMRG is run. As the merge routine proceeds, changes to the databases are recorded in temporary tables beginning with the letter “X” to make them easily visible. If there are no changes to the flora, there will be no temporary tables beginning with the letter “X” following completion of the routine.

e.1. (Print screen message @2,1) Zflomrg() tests whether the flora database, OK4, has collection numbers not found in the collections database, based on the collection numbers in the field [SHOWCOL]. If found, the routine asks the user to make necessary additions, subtractions and changes. To assist the user Zflomrg() searches OK4 for records with changed names in COLGW [FULLNAME], and moves these records into table XOKFN. If there are records that need to be subtraced from OK4, the script reports the results in table XOKMIS and quits so that the records can be subtracted. Otherwise Zflomrg() continues.

e.2. (Print screen message @3,1) Zflomrg() checks for changed OK4 FULLNAMEs and updates these with information from the lookup database, DX.

e.3. Zflomrg() prepares to update the flora with collections data by prioritizing records in the collections database so that each taxon is represented by a single record that is the oldest record with a minimum threshold of quality.

e.4. (Print screen message @4,1). Zflomrg creates a copy of the COLGW database containing only a single record for each taxon that has the highest priority for merging with the county flora in table OK4. The priority is determined by the following sort order: [FULLNAME] > [SEL] > [DATE] > [CND] > [DEST].

This sort order is determined as follows:

The Convcol() routine marks field [SEL] as a temporary sort field with the following codes:

1 = dated herbarium specimens; herbarium ([DEST] char1 <>Z) & [DATE]<>BLANK).

2 = partially dated herbarium specimens ([DEST] char1 <>Z) & len([DATE]<10)

3 = undated herbarium specimens ([DEST] char1 <>Z) & [DATE]=BLANK)

4 = unvouchered specimens not in a herbarium ([DEST] char1 =Z)

5 = dated or undated specimens with [CND]="Y"

6 = dated or undated specimens with [CND]="Z" (in which case the record will be blocked or eliminated from the county flora)

[DATE] sorts earliest 1<sup>st</sup> for fully dated specimens

[CND] sorts in alphanumeric order: from A (excellent condition) > B (good condition) > C (fair condition) > M (missing collection no.) > U (unknown cond.) > X (poor condition) > Y (identity uncertain) > Z (identity wrong, but label not annotated, in which case the record will be blocked or eliminated from the county flora).

[DEST] sorts in the following order: herbarium name > Z0-PENDING > Z1-HOLD > Z2-RAW > Z3-POOR > Z6-UNKNOWN > Z9-DESTROYED. In the latter case, the record will be excluded from the county flora.

The procedure then resorts the data using SEL as a sort field and then flags [SEL] with “1” to delete those records as lower priority duplicates. Any records with a non-blank value in [SEL] are eliminated, allowing manual override of the program.

e.5. Next Mrgalf() performs the actual merging of COLALF with OK4 in two steps. The first step updates records in OK4 by matching field [FULLNAME] with the highest priority FULLNAME given in COLALF and substituting the COLALF data for the record with that [FULLNAME].

Zflomrg() updates OK4 with changed records from the collections database for the following fields: SHOWCOL, DATE, CND, COLAREA, LOCDESC. However, if [NOTES] is not blank, Zflomrg() will not overwrite that field with COLGW data.

e.6. Zflomrg() checks for new records in COLGW that will be added to OK4, and reports how many there are. The number of potential changes are displayed to the user. If the user accepts these changes, the merge is completed by replacing the old version of OK4 with the temporary working table OKTMP containing the updated and new data. The overwrite procedure also creates a version of the county flora restructured as table ALF.DB with survey name “COLALF” in the [NOTES] field.

f. Zflomrg() returns control to the calling script and the header information in the flora, record 1, field [NOTESTAX] is recalculated.

g. Cleanalf() is called to do clean up the data, fill in missing information, and find misapplied names, identified by having non-blank values in field [DUP]. Misapplied names are flagged by coding [NEWCSIX] as ‘UNCODED’ and appending “Ambiguous p.p. name.” to field [NOTES].

## 7. Glossary

Accepted name. The unique full name assigned for a taxon by a given authority, specified here as FNA (1993+), PLANTS (USDA NRCS 2003+) or Kartesz (1998), unless otherwise noted.

Autonym. A subordinate name with the same epithet as the binomial species.

Available names. Names of taxa that meet all mandatory provisions of the rules of the International Code of Botanical Nomenclature (ICBN; McNeill and others 2006).

Binomial name. The genus and species of a taxon.

Combinations. The set of all unique names in the plant list, valid or not.

Correct name. See valid name.

Counted names. The number of taxa within a flora, counted either as entered names, or as accepted synonyms.

Database; data table; table. The source of input data that is processed using scripts.

Deference. A duplicated record within a set of records with the same name or equivalent synonym that gets listed in the flora because it has an earlier collection date.

Dictionary (lookup dictionary). A database used to look up accepted names and synonyms.

Doublet. A listed name that is counted both as an entry and as a synonym.

Duplicate names. Records with identical full names, but different synonyms.

Enforced name. A names that is switched to its given synonym or not based on a predetermined setting in the database.

Entry; entered name. A plant name that is listed in a survey or a collection within an area.

Equivalentents. Alternate, valid full names for a taxon, accepted or not.

Flora. A complete list of plants within an area. An alternate definition is a key to the plants of an area.

Full name; Latin name; scientific name. A taxonomic name with its author(s). This definition should not be confused with the variable FULLNAME used here to represent the taxonomic name without authors.

Homonyms; isonyms. Names with identically spelled scientific names with different authors.

Infraspecies; infraspecific taxa. A subspecies, variety, form or cultivar.

Listed name. A plant name listed within a flora, valid or not. These procedures output two sets of lists, one containing the entered names, the other containing synonyms of names in the flora.

Name. The name of a taxon used as symbolic variable to process a flora.

Non-counted name. An uncounted name that was uncounted two times.

Ordinal. A taxon with a higher rank than its subordinates.

Orthographic variant. An orthographic variant is an incorrect alternate spelling of a name.

Pointee. A synonym for another name that is a pointer (same as target).

Pointer. A name that points to a synonym.

Preferred p.p. synonym. The most likely correct pro parte synonym within a flora. Nonpreferred p.p. synonyms refer to unlikely, but nonetheless valid, taxa.

Pro parte synonym (p.p.). A taxon that has been split into two or more new taxa.

Rank (status). The taxonomic rank of a species' given by its final epithet. Rank order is heirarchical from higher to lower in the order species, subspecies, variety. Higher-ranked taxa may include ambiguous names, e.g., they may refer to an autonym in the narrow sense (*sensu strictu; s.s*), or to all subordinates in the broad sense (*sensu lato*).

Record. The data associated with each unique plant name. Records are subdivided into fields.

Report. The printed output of the program 01VEG that lists plants found in surveys of an area.

Retained names. A single name counted as the accepted taxon from a group of synonyms.

Selfer. Names that are not pointers to synonyms, but which may be targets (same as "uninym").

Sensu lato ("*in the broad sense*"). A qualifier for a taxon that includes all subordinate taxa.

Sensu strictu ("*in the narrow sense*"). A qualifier for a taxon that only refers to its autonym subordinate.

Singlet. A listed name counted either as an entry or as a switched synonym, but not both ways.

Subordinate. A names of an infraspecific taxon.

Survey. This refers to a list of plants found in a botanical field survey and used as input for developing a flora.

Switched name. A name for a plant assigned by substituting a synonym for the entered name.

Synonym. An alternate name for a taxon listed here in the database (USDA, 2004).

Target. A synonym for another name that is a pointer (same as pointee).

Taxon (pl. taxa). A member of a set of biologically related individuals. Each taxon is designated by a formal scientific name (full name). Taxa are hierarchically divided into subordinate ranks, of which the rank of species is the basic unit. A species is the highest rank typified by a specimen and bearing a binomial

- name. A species is also the lowest of the principal ranks of the tree of life given by the kingdom, division (phylum), class, order, family, genus and species. The definition of a species varies depending on the treatment; species may also be morphological, phylogenetic, ecological, consensual, etc.
- Tentative name. A name with a synonym given in the input data that will be tested for listing as the accepted name.
- Unaccepted name. A name that is not accepted. Used here in the logical sense, i.e., any name that is not specifically accepted. This definition is similar to, but not identical to, the definition for a “rejected name”. The ICBN provides for rejected names that are specifically rejected, but there are many other names that are not specifically rejected, that are nonetheless not accepted.
- Uncounted name. A names that is listed in this flora but not counted as part of the flora.
- Uninym. A self-synonymous name that may also be a target synonym of another entity (same as “selfer”).
- Unswitchable name. This is a non-target uninym without a synonym in the dictionary.
- Unswitched name. This is a name that was listed as an entry, rather than one of its synonyms.
- Valid name. The correct name for a given taxon which may have several available names, only one of which is the valid name. Under the ICBN rule of priority the valid name is frequently the earliest published name, although other rules may override this rule.

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## Appendix 1. Flowchart of key algorithmic steps in the 01VEG program suite

The following flowchart describes important algorithms in the 01VEG program suite, along with called procedures.

### AMAINANA.SC (Analysis)

Case File (Procs: ZALFPROC, Zshared). Save/Backup/Administer ALF databases.

Case EditAlf (Procs: ZALFPROC, Zanaed). Edit ALF records.

Case Report (Procs: ZALFPROC, Zanarep, Zshared). Create a report from the database information.

IF SURV="COLALF" THEN ask, DO YOU WANT AN HERBARIUM LIST MERGED WITH OKALF3?

If No then:

DOMRG="N"; FF=VEGLIST.RPT

@ DESPREP1, DESPREP2, Sort "Tmptax" on "FULLNAME", "X-3"

If Yes then:

DOMRG="Y"; FF=VEGCOL.RPT

In Cleanalf() Checkplus to add [COLDEST], [COLAREA]

@ DESPREP1, DESPREP2, Sort "Tmptax" on "NEWFAM", "FULLNAME", "X-3"

### COLMAIN.SC (Maintain collections)

Case EditCol (Procs: Zcol). Modify/Add collection records.

Case LocEdit (Procs: Zcol). Edit location database.

Case Selrecs (No procedures called, formerly called Zcol, Zshared). Select or unselect records.

Case Prn85 (Procs: Zcol, Zshared). Print 8.5" wide list of selected.

FF=VEGCOL85.RPT

Case PrnLab (Procs: Zcol, Zshared, Zcollbl). Print herbarium labels for selected.

FF=HRBLABEL.RPT

Case ZFLOMRG (Procs: Zcol, ZALFPROC). Convert collections DB to ALF format.

COLGW.DB is copied as TMPALF.DB

Call Colchek() on Tmpalf to get fields in correct ALF order.

Call Convcol() to load data into COLALF.DB and process as follows:

Select only records with at least 2 names in FULLNAME (no genera or families), [CO]="Okanogan" and DEST<>"Z9.."

Create [COLAREA] from [CONFNAMEPLACE] (A43)

Scan to edit SEL to allow sorting by FULLNAME, SEL, DATE, CND, DEST

[SEL] sorts as follows:

- 1 = dated specimens deposited in a herbarium ([DEST] char1 <>Z) & [DATE]<>BLANK).
- 2 = partially dated specimens deposited in a herbarium ([DEST] char1 <>Z) & len([DATE]<10)
- 3 = undated specimens deposited in a herbarium ([DEST] char1 <>Z) & [DATE]=BLANK)
- 4 = specimens not deposited in a herbarium ([DEST] char1 =Z)
- 5 = dated or undated specimens with [CND]="Y"
- 6 = dated or undated specimens with [CND]="Z"

[DATE] will sort earliest first for fully dated specimens.

[CND] will sort first as BLANK (fair to excellent condition), U (unknown condition) or X (poor condition).

[DEST] will sort in the order: Z0–PENDING (prepared to send to herbarium) > Z1–HOLD (do not send to herbarium) > Z2–RAW (unprepared) > Z3–POOR (specimen in such poor condition as to avoid use) > Z6–UNKNOWN (location unknown or misplaced) > Z9–DESTROYED (destroyed specimen, in which case CND must="Z).

The scan continues by updating the records as follows:

    annotate [COLAREA] with [LOCNUM] @[QUAD] + LOCATION description and if COLAREA is still blank, TRS data

During the edit–scan, Convcol() edits [COLAREA] to annotate the collection with LOCATION and QUAD in the format [LOCNUM].[QUAD]. If those fields are blank, then it annotates COLAREA with LOCDESC, and if that is also blank, the procedure tries to annotate COLAREA with TRS data.

Convcol()resorts the data using SEL as a sort field and then scan–edits the file to mark [SEL] with "1" to delete those records as lower priority duplicates.

Convcol() then queries the table to eliminate records with non–blank [SEL] and include only fields [SHOWCOL], [FULLNAME], [DATE], [CND], [COLAREA], [LOCDESC], before returning to the ZFLOMRG routine.

OKALF3.DB is copied as OKALFTMP.DB. OKALFTMP.DB records are updated with [COLDEST] and [COLAREA] from COLALF.DB.

A query is used to get records in COLALF.DB missing from OKALF3.DB into table COLNEW.DB. If there are new records, these are added to OKALFTMP.DB, and COLNEW.DB is deleted.

OKALFTMP.DB is then sorted. OKALF3.DB is backed up as OKALF3B.DB and OKALFTMP.DB is used to overwrite OKALF3.DB.

ALF is then backed up and OKALFTMP.DB is renamed as ALF.DB with SURV="COLALF".

OKALFUPD.DB is renamed as XOKALFUPD.DB.

## Appendix 2. Procedure calls in the 01VEG program suite

This appendix lists procedure calls in scripts used in the 01VEG program suite.

### ZALFPROC.SC procedures:

AlfStruc() restructures Tmpalf to place fields in the same order as table ALF.

Bkp() makes a backup of ALF.DB

Cleanalf() cleans and renumbers the ALF table.

Unkeyalf() from Cleanalf() unkeys [NUM].

ReKeyAlf() called from Cleanalf() re-keys unkeyed table.

HeadAlf() called from Cleanalf() cleans ALF headers.

### Zanaed.SC procedures

wrahead() performs a write-ahead for the next record down, and fills in blank fields with "LAST=".

minied(edtable) edits ALF.DB.

### Zshared.SC procedures

Proc Specchar() converts output to ANSI special characters.

Proc Repvs() flags strings to bolden or italicize reports using symbols \$ and @ .

Proc AlfStruc() restructures ALF if it has structural errors.

### Zanarep.SC procedures

These procedures are used to save stack space during report generation by the script AMAINANA.SC: stacksav(), Stacksav2(), Stacksavdef(), Stacksav3(), and Vartbl().

### Zcol.SC procedures

Convcol() edits COLALF.DB.

Edcol() edits COLGW.DB

Fresh() called from Edcol() updates [FULLNAME] in COLGW.DB

### Zcollbl.SC procedures

RTRM() right-trims the current string in HRBLABEL.RPT.

ADDPER() adds a period to the current string in HRBLABEL.RPT.

WWRAP() word-wraps the current string in HRBLABEL.RPT.

DEJUST() called from wwrap() deletes leading spaces from STRINGSUB in HRBLABEL.RPT.

### Appendix 3. Script program flow during flora generation

#### Processing flags

The data and scripts are flagged during processing. These flags define the data categories that are output in the final report. They also help track data and processing errors.

**Default processing flags.** Before running the script to create a flora, set the default output parameters at the beginning of AMAINFLO.SC. The default settings for processing a flora are as follows:

DOLIN="2" – "2" to print a 2-line vsn of Section 3, sorted by Family > Fullname ; 0 skips this section.

DOHAB="N" – "Y" to sort and list App G – Taxa by habitat.

DOFAM="Y" – "Y" to write Section 4 – List of taxa by family

DOAPD="Y" – "Y" to write Appendix E.6 – Binomials w/un-identified infraspecies. Only use with surveys; don't use with a flora as the results are too numerous).

DOCOL="Y" – "Y" to write Appendix E – Reported, but uncollected taxa.

**Breakpoints.** There are several breakpoints in the scripts that can be set to stop processing. These options will allow inspection of all of the Temporary files. The most important breakpoints are:

(a) after printing the Checklist, Section 3

(b) after printing the detailed listing in Section 4.

**Processing flags.** Important routines within the scripts are flagged with the following codes:

K2MOD – These are routines that modify variable K2, which is coded in the first two characters of [LK] in the data dictionary. K2 sets rules for processing names that based on whether or not the USDA NRCS taxonomy is accepted as follows:

K2= I – uninum; USDA taxonomy accepted.

K2= W – USDA taxonomy accepted; switched to its synonym.

K2= U – USDA taxonomy accepted; leave unswitched

K2= 0 – misapplied p.p. name; maintain name as an ambiguous uninum.

K2= 1 – taxonomy not accepted; override USDA NRCS taxonomy; leave unswitched.

K2= 2 – taxonomy not accepted; enforce the switch to the synonym.

K2= 4 – taxonomy accepted; enforce the switch, but also count the entry. If this is a hybrid couplet, then the pointed-to hybrid will be noncounted.

DUPMOD – These are routines that modify [DUP], the field that uses a letter code to track how the taxonomy was treated).

DESPREP – These are routines that prepare the report format to output designator codes that track the applied taxonomy for each record.

SORT@ – These are routines that sort data.

Restructure – this is the Paradox command to modify the structure of a database.

**[DUP]** – This field organizes the data in broad categories, and tracks whether the data has been processed or not as follows.

E – Unswitchable names counted both ways contained in Tmpself.db

L – Name is uncounted. This includes uncounted s.l. binomials added for context [X-2]="+".

T – Name tentatively counted as an unswitched entry. This code gets revised by the scripts.

U – Name tentatively counted as its switched synonym. This code gets revised by the scripts.

V – Name assigned as an unswitched entry.

W – Name assigned to its switched synonym

[X-2] flags how the pointer/target pair is counted in [SETNO] as follows:

- != CB or CBS in [SETNO]; counted in column B (variable NCOLB=NTB1 in Tmpcolb1.db)
  - !S ([SETNO]=CBS) is the single counted accepted target of otherwise multiple debatable FNA assignments e.g., *Poa secunda* is counted once as a synonym when it is indicated as the accepted synonym of multiple names (*Poa scabrella*, *P. nevadensis*, ...).
  - !!P indicates counted uncollected targets of collected synonyms (X-2=/E, /F or /N) counted only as entries.
- & = C2 in [SETNO]; names counted in both columns (variable NTBO in Tmpboth)
- / = CA in [SETNO]; pointers entered; counted in column A only (variable NCOLA)
  - /DH, /DR = redirected pointers; CA names counted in column A only
- C.. = UC in [SETNO]; uncounted names (variable UCL)
- + = UC in [SETNO]; uncounted s.l. binomials added for context (variable BIADD)

[SETNO] is a classification of the synonymy containing a reference to the routine number. [SETNO] is flagged CA., CAB., CB., C2., C2s1f, CBS., or UC.. to determine how records will be counted.

[FLAG1] is a temporary flag used to flag and count sequential duplicates and to determine the sort order.

[FLAG2] is used to flag s.s. species; [FLAG2] is used in routine 13 to tabulate CA counts.

[FONT] (Initially, A30) Is a multipurpose field, holding different string variables at during times in the scripts. Initially it is used to count records, then later it counts subordinates. In routine no. 15 through 19, [FONT] flags binomial names with "BINO1". In routine no. 16, [FONT] is restructured to A5. In routine no. 19, [BIFLAG] = substr([FONT],1,2). From this point on, [FONT] is used to indicate whether a record is accepted. To indicate whether a record is accepted, [FONT] is flagged with a # for the 1st name in a SORTNAME set of duplicate names. Unaccepted names have an underscore in character 1. The second part of routine 19 modifies [FONT] when it finds a first SORTNAME that isn't flagged as being accepted. It does this by changing [FONT] in that name to a "#" and changing [FONT] in the subsequent full names to the character "S" instead of the character "#". This allows the report to show the first name as accepted by bolding it, while italicizing the latter name, that is otherwise unchanged in the database.

[F2] This field is used to indicate and whether a record is a reported entry. [F2] indicates a reported entry with the @ character, otherwise this character is an underscore.

[BIFLAG] is used to identify binomial names. In routine 20, the flag is transferred from [FONT], where "BINO1" flags binomial names. Values for BIFLAG are:

[BIFLAG]="BI" for binomial names

[BIFLAG]="BUNC" for uncounted binomials without subordinates or binomials that only have uncounted subordinates.

[NDX] [NDX] flags ROOT sets and SORTNAME sets in routine 20. SORTNAME sets are sets of records with the same FULLNAME. The values of [NDX] are as follows:

[NDX] = ..1 for the first name in a SORTNAME set.

[NDX] = R\_S\_ or R\_H\_ for duplicate FULLNAMEs

[NDX] = R1S1 or R1H1 for a new ROOT set. A ROOT set is a sequential set of names that begins with the binomial name and then includes all the subordinates of that name in one or more

**SORTNAME** sets.

[**NDX**] = R\_S1 or R\_H1 for a new **SORTNAME** set with the same binomial but a different **FULLNAME**

[**ORD**] is used to modify the sort order.

[**SYN**] contains the output text string for the synonym of a species. [**SYN**] is also used as a temporary flag to indicate pointers and whether a name is a binomial.

[**COLMSG**] is used in routines 6 through 15 as a temporary flag to indicate the rank and synonymy of names; after routine 17 [**COLMSG**] is overwritten in routine 17 with collection status that is output to the final report (see table 1 for these values). The temporary status flags used by **COLMSG** are as follows:

anym=autonym

anym of binomial

anym strict

anym strict of binomial

bino = binomial name w/o ssps

bino autonym root pointee strict

bino autonym root pointee subord root

bino autonym root pointee subord root pointee

bino autonym root strict=autonym roots of ssps, strict autonym

bino autonym root subord root=non-strict autonym (2 are from bino-DUP1)

bino autonym root subord root pointee

bino subord root=bino ROOT of ssps (2 are from bino-DUP1)

bino subord root pointee

bino-DUP autonym root subord root (bino-DUP= bino w/ROOT having DUP<>blank in DX)

bino-DUP subord root (bino-DUP= bino w/ROOT having DUP<>blank in DX)

bino-DUP1=binomial with ROOT having DUP=1 in DX

bino-DUP1 autonym root subord root

bino-DUP1 subord root

hybrid=interspecific hybrid excluded from further subcategorization

s-subord=non autonym subordinate

s-v-subord

subord

v-subord

The scripts and flags used during generation of a flora are listed in Table 1, in the sequence that they are invoked. In the table, the term “counted” is equivalent to “accepted” unless it specifically states otherwise, (as when referring to a count of names in column A).

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Table 1. Scripts and flags used during flora generation, given in the sequence they are invoked.

#	Script	Flags	Procedures
	01VEG.SC		Call AMAINFLO.SC
	AMAINFLO.SC		<p>Import the list of plants to process from table ALF.DB. Standardize the structure &amp; remove the 3 header lines and unnecessary fields s that may be added back during subsequent procedures.</p> <p>Dependencies are in Zalfproc.sc.</p> <p>Bkp() called from Amainana – makes backup of ALF</p> <p>Unkeyalf() called from Cleanalf() – unKeys [NUM]</p> <p>ReKeyAlf() called from Cleanalf() – re-keys unkeyed table</p> <p>HeadAlf() called from Amainana – cleans ALF headers</p> <p>Cleanalf() called from Amainana – cleans, renumbers</p> <p>The I/O data table is named Tmp.db. Data fields are:</p> <p>NUM (S)</p> <p>NEWCSIX (A9)</p> <p>AREA (A120)</p> <p>COVER (S)</p> <p>NOTES (A250)</p> <p>FULLNAME (A65)</p> <p>Call Zrephot1.sc – step 1 of report generation</p> <p>Call Zrephot2.sc – steps 2 through 10 of report generation</p> <p>Call Zrephot3.sc – steps 11 through 15 of report generation</p> <p>Call Zrephot4.sc – final steps of report generation</p>
			<p>Routines 1 to 4 set up the initial list of plants and synonyms prior to routine 5, which creates new ordinal names that are missing from the list. The basic structure is set up to flag different types of synonyms and duplicate names and then apply rules that choose whether or not to count a given record. Routines 1 to 4 also flag the most problematic names, i.e., pro parte names and hybrid entities, to prevent these from further processing and also to prevent misapplied subordinates of these names from being used to create new binomials.</p>
#1	Zrephot1	<p>Process tables Tmprecs.db -&gt; Tmpnames.db</p> <p>[SETNO] has 4 classes based on the 1<sup>st</sup> 2 or 3 characters and a number indicating the routine it was flagged in.</p> <p>CA.. (uncounted entries; DUP=U)</p> <p>CB.. (switched synonyms; DUP=W)</p> <p>C2.. (names counted in both columns; ambiguous names; DUP=W)</p> <p>UC.. (uncounted names; DUP=L)</p>	<p>Use restructure twice. Add the synonyms to the list of names. Generate synonyms by switching the names in ALF.DB with their synonyms. Put these records into table Tmpsw.db and then merge this table with Tmprecs.db. Records are marked as switched or unswitched names by whether field [LK] = + or -. Process initial sets of enforced switches or retentions. Eliminate ambiguous names and unknowns. Flag non-hybrid enforced pointers; uncount duplicates.</p>

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		<p>[SETNO]=CA01a ([X-2]="/PP") p.p. name w/o synonym                  [SETNO]=CA01b ([X-2]="/P2") p.p. name w/counted synonym                  [SETNO]=CA01c ([X-2]="/G") retained non-FNA name w/                  lumped synonym                  [SETNO]=CA01e ([X-2]="/J") pointers to enforced switches that                  can change to uncounted                  [SETNO]=CA01f ([X-2]="/X") col A non-hybrid synonym                  [SETNO]=CA01g ([X-2]="/Q") indeterminate synonyms counted                  in column A, but if not counted later, then counted both ways.                  [SETNO]=CB01b ([X-2]="!T") enforced switches                  [SETNO]=CBS01 ([X-2]="!S") enforced unswitched non-FNA                  targets                  [SETNO]=C201a ([X-2]="&amp;Q"); indeterminate synonyms counted                  both ways                  [SETNO]=C201b ([X-2]="&amp;4Q" ) non-hybrid synonyms of                  hybrids (non-FNA) counted in both columns (NOCASE)                  [SETNO]=UC01a (ambiguous name; [X-2]="C0"                  [SETNO]=UC01b ([X-2]="CJ") uncounted target (non-FNA)                  [SETNO]=UC01c ([X-2]="C1") uncounted sequential duplicate of                  enforced target</p>	
#2	Zrephot2	<p>Process table Tmpnames through step 10.                  [SETNO]=CB02c [X-2]="!B" [DUP]="W"                  [SETNO]=CB02b [X-2]="!B"                  [SETNO]=UC02b [X-2]="C2" [DUP]="L"                  [SETNO]=UC02c [X-2]="C2" [DUP]="L"</p>	<p>Finish processing p.p. synonyms and indeterminate synonyms. Sort on "FULLNAME",                  "FULLNAME-1".</p>
#3	Zrephot2	<p>[SETNO]="CA03a" [X-2]="/K" [DUP]="U"                  [SETNO]="CB03a"+XSET [X-2]="!J"                  [SETNO]="CB03b"+XSET [X-2]="!J" (NOCASE)                  [SETNO]="UC03a" [X-2]="CK" [DUP]="L"                  [SETNO]="UC03b" [X-2]="C3" [DUP]="L"                  [SETNO]="UC03c" [X-2]="C3" [DUP]="L" (NOCASE)                  [SETNO]="UC03d" [X-2]="C3" [DUP]="L"                  [SETNO]="UC03e"+XSET [X-2]="C3" (NOCASE)</p>	<p>Process and retain enforced switches.                  (3.a.) Flag duplicate targets of debatable FNA assignments (e.g., <i>Poa secunda</i>) to                  prevent them from being duplicated in the report.                  (3.c.) Flag non-hybrid enforced pointers; exclude pointers to pointers.                  (3.d.) Sort records on "FULLNAME", "SETNO", "FULLNAME-1" . Uncount duplicates of                  enforced switches. (3.e.) Sequentially count sets of duplicate names, counting names                  that are the first in the sequence and uncounting sequential duplicates.</p>
#4	Zrephot2	<p>Restructure Tmpnames.db. Add [NN] [NUMU] [NUMW] [X-3]                  [SORTNAME] [FLAG2] [TEST].                  [SETNO]="CA04a" [X-2]="/K" [DUP]="U"                  [SETNO]="UC04a" [X-2]="CN" [DUP]="L"                  [SETNO]="UC04b" [X-2]="CN" [DUP]="L"                  [SETNO]="UC04c" [DUP]="L" [X-2]="CX" [SYN]="(hybrid                  uncounted)."</p>	<p>Process debatable assignments and questionable names; uncount interspecific hybrids.                  (4.b) Uncount duplicate unswitched [FULLNAME]s of enforced switched assignments.                  (4.c.) Restructure Tmpnames.db. Flag interspecific hybrids in [COLMSG] and uncount                  them.</p>

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		[SETNO]="UC04d" [DUP]="L" [X-2]="C4" [SYN]="(hybrid syn of non-hybrid; <  ~" +XFN1 +")."	
			Routines 5 to 10 complete most of the remaining tasks of identifying synonyms and determining which ones to count as part of the flora.
#5	Zrephot2	[SETNO]="UC05a" [X-2]="+" [SYN]="(ordinal added..	Add new binomials for context by stripping the subspecific ranks and comparing the result with the current contents of the database.
#6	Zrephot2	[FLAG2]="ss"	Flag COLMSG autonyms, subordinates, and strict binomials of autonyms (having only autonym subspecies); flag [ROOT] with the binomial names of all subspecific entities that will be used for heircharchical organization in the report and will provide alternate synonyms for autonyms. Flag pointers to pointers to prevent incorrect synonymies.
#7	Zrephot2	[SETNO]="CA07a" [X-2]="/DH" [DUP]="U" [SETNO]="CA07b"+[SETNO] [X-2]="/DH" [DUP]="U" [SETNO]="CA07c" [X-2]="/A" [DUP]="U" [SETNO]="CA07d"+[SETNO] [X-2]="/A" [DUP]="U" [SETNO]="CA07e" [X-2]="/DH" [DUP]="U" [SETNO]="CA07f" [X-2]="/A" [SETNO]="CA07g" [X-2]="/A" [SETNO]="CA07h"+XSET [X-2]="/A" [DUP]="U" [SETNO]="CA07i"+XSET [X-2]="/A" [DUP]="U" [SETNO]="CA07k"+XSET [X-2]="/A" [DUP]="U" [SETNO]="CA07l" [X-2]="/A" [DUP]="U" [SETNO]="CA07n" [X-2]="/A" [DUP]="U" [SETNO]="CA07o"+[SETNO] [X-2]="/A" [SETNO]="CA07q" [X-2]="/A" [DUP]="U" [SETNO]="CB07a" [X-2]="!N" [SETNO]="CB07b" [X-2]="!F" [SETNO]="CB07c" [X-2]="!F" [SETNO]="CB07d" [X-2]="!N" [SETNO]="CB07e" [X-2]="!N" [DUP]="W" [SETNO]="C207a" [X-2]="&P" [SETNO]="C207b" [X-2]="&P" [DUP]="U" [SETNO]="UC07a" [X-2]="C7" [DUP]="L" [SETNO]="UC07b" [X-2]="CF" [DUP]="L" [SETNO]="UC07c" [X-2]="C7" [DUP]="L" [SETNO]="UC07d" [X-2]="C7" [DUP]="L" [SETNO]="UC07e" [X-2]="C7" [DUP]="L" (NOCASE) [SETNO]="UC07f" [X-2]="C7" [DUP]="L" [SETNO]="UC07g" [X-2]="C7" [DUP]="L" [SETNO]="UC07h"+[SETNO] [X-2]="CV" [DUP]="L"	Identify and count rank synonyms and their binomials. Flag records in [FLAG1] [SYN] and [FONT]. (7.c.) Redirect pointers of equivalent rank synonyms to both point to the same target and uncount targets of redirected entries. (7.e.) Flag binomials that have counted non-autonym subspecies. (7.f.) Flag the highest rank in [SORTNAME] and use this to determine the synonymy of non-autonym subordinates. (7.i.) Ensure that subordinates do not point to counted names with mixed ranks and flag the entities that have become counted targets.

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		<p>[SETNO]="UC07i"+[SETNO] [X-2]="CV" [DUP]="L"          [SETNO]="UC07j"+[SETNO] [X-2]="CV" [DUP]="L"</p>	
#8	Zrephot2	<p>[SETNO]="CA08a" [DUP]="U" NCAM=NCAM+1 [X-2]="/M"          [SETNO]="CA08b" [X-2]="/R" [SYN]="pointer to binomial"          [SETNO]="CA08c" [X-2]="/R" [DUP]="U" [SYN]="pointer to binomial"          [SETNO]="CA08d" [X-2]="/N" [DUP]="U" [SYN]="pointer to syn"          [SETNO]="CA08e" [DUP]="U" [SYN]="pointer to binomial" (NOCASE)          [SETNO]="CA08f" [X-2]="/N" [DUP]="U"          [SETNO]="CA08h" (overwrite CA08b) [X-2]="/N" [DUP]="U" [SYN]="pointer to syn not binomial"          [SETNO]="CB08a" [X-2]="!M"          [SETNO]="CB08b" [X-2]="!R" [DUP]="W"          [SETNO]="CB08c" [X-2]="!MW" [DUP]="W" [SYN]="(rank autonym and selfer; =l)."          [SETNO]="CB08d" [X-2]="!MS" [DUP]="W" explicit binomial target of subordinate          [SETNO]="CB08e" [X-2]="!MR" [DUP]="W" [SYN]="(binomial target of redir autonym)."          [SETNO]="C208b"+XSET [X-2]="&amp;M" [DUP]="U"          [SETNO]="C208c"+XSET [X-2]="&amp;D" [DUP]="U"          [SETNO]="C208d"+XSET [X-2]="&amp;M" [DUP]="U"          [SETNO]="C208e"+XSET [X-2]="&amp;M" [DUP]="U" [SYN]="(=l)."          [SETNO]="C208f"+XSET [X-2]="&amp;M" [DUP]="U" (NOCASE)          [SETNO]="C208h" [X-2]="&amp;D" [SYN]="(redir to self not ordinal; =l)."          [SETNO]="C208i" [X-2]="&amp;IM" [DUP]="U" [SYN]="(binomial target of redir autonym; =l)."          [SETNO]="UC08a" (NOCASE)          [SETNO]="UC08b" [X-2]="C8" [DUP]="L" (NOCASE)          [SETNO]="UC08c" [X-2]="C8" [DUP]="L"          [SETNO]="UC08d"[X-2]="CR" [DUP]="L"          [SETNO]="UC08e" [X-2]="C8" [DUP]="L"          [SETNO]="UC08f" [X-2]="CR" [DUP]="L"          [SETNO]="UC08g" [X-2]="CR" [DUP]="L" (NOCASE)          [SETNO]="UC08i" [X-2]="CS" [DUP]="L" [SYN]="(ordinal of redir pointer; =l)."          [SETNO]="UC08j" [X-2]="CS" [DUP]="L" [SYN]="(ordinal of redir pointer; &lt;  ~" +XFN1 +)."</p>	<p>Process autonyms unless they are uncounted duplicates or uncounted binomials.          (8.b.) Flag autonyms pointed to by non-autonyms and redirect. Flag all autonyms to indicate their rank with regard to other records. Flag autonyms to point to their binomial names when both ranks occur in the flora unless a specific alternate synonymy is already indicated.          (8.f.) Identify strict autonyms (with the binomial having no subordinates other than the autonym). These flags will be used to partially determine the sort order in the report and whether to bolden the font of names that are accepted or are the first instance of a binomial. The synonymy produced in this set of routines will be output as pointers and targets in the report.</p>

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#9	Zrephot2	<p>[SETNO]="CA09c" [X-2]="/B" [DUP]="U"                  [SETNO]="CB09a" [X-2]="!D" [DUP]="W"                  [SETNO]="CB09b" [X-2]="!D"                  [SETNO]="CB09c" [X-2]="!D"                  [SETNO]="UC09a" [X-2]="C9a" [DUP]="L"                  [SETNO]="UC09b" [X-2]="C9a"                  [SETNO]="UC09c" [X-2]="C9a" [DUP]="L"                  [SETNO]="UC09d" [X-2]="C9b" [DUP]="L"                  [SETNO]="UC09e" [X-2]="C9a" [DUP]="L"</p>	<p>Finish processing binomials.                  (9.b.) Subtract and uncount corresponding subordinates of binomials in order to eliminate validly collapsed subordinates of retained names, e.g., <i>Salix planifolia</i>.                  (9.e.) Ensure there are no duplicate counted names; prevent binomials of counted subordinates from being counted.</p>
#10	Zrephot2	<p>[SETNO]="CA10b" [X-2]="/E" [DUP]="U"                  [SETNO]="CA10c" [X-2]="/F" [DUP]="U"                  [SETNO]="CB10a" [X-2]="!P"                  [SETNO]="CB10b" [DUP]="W" [X-2]="!E"                  [SETNO]="CB10c" [X-2]="!E" [DUP]="W"                  [SETNO]="CB10d" [X-2]="!E" [DUP]="W"                  [SETNO]="UC10a" [X-2]="CG" [DUP]="L"                  [SETNO]="UC10b" [X-2]="CH" [DUP]="L"                  [SETNO]="UC10c" [X-2]="CU" [DUP]="L"                  [SETNO]="UC10d" [X-2]="CU" [DUP]="L"                  [SETNO]="UC10e" [X-2]="CC" [DUP]="L" [SYN]="(&gt;  ~" +XFN1 +")."                  [SETNO]="UC10f" [DUP]="L" [X-2]="CD"                  [SETNO]="UC10g" [X-2]="CM" [DUP]="L"                  [SETNO]="C215fCA01g" [X-2] = "&amp;QM"; indeterminate synonyms</p>	<p>Uncount duplicates of counted names. Identify sequential duplicates after sorting on "FULLNAME", "FULLNAME-1". Sort the file to prioritize ordinals and first sequential duplicates.                  (10.d.) Uncount pointers with counted subordinates; uncount pointers without subordinates; uncount records with no counted targets.                  (10.e.) Assure all sets of target duplicates are in the right order and counted or uncounted                  (10.f.) Count s.s. names or autonyms with indeterminate targets where no other choice exists for counting the entity.</p>
			<p>Routines 11 to 15 use table Tmptax.db, which reflects that the data is now a essentially flora, and isn't just a collection of records. These routines perform tasks requiring the list to be sorted differently in order to find sequential duplicates and also to uncount binomials with counted infraspecies.</p>
#11	Zrephot3	<p>Records with blank XFN1 are retained ([FLAG1]=X..). Records with [FLAG1]=X2.. are switched into [FLAG1]=X1.. which sorts differently for duplicates of retained autonyms. Duplicates with [FLAG1]=X2 get uncounted here with DUP=L, but will be flagged later, e.g., with } in routine 15.                  Sequential duplicates with [FLAG1]=blank (!) are uncounted ([FLAG1]=Z..). The sort order of FLAG1=Z is modified whenever a 2nd, identical FULLNAME occurs with the same 1st char in [X-2]. If so, then the 2nd character (a number) is scored to determine the sort order.                  X1 = counted retained names; first in set; [DUP]=U,W.</p>	<p>Sort "Tmptax" on "SORTNAME", "FULLNAME-1", "ORD".                  (11.a) Sort hybrids last.                  (11.b.) Renumber duplicates in [FLAG1] and uncount out-of-order duplicates of counted names. subsort within [SORTNAME], [ORD]; ID sequential duplicates in [FLAG1].                  (11.c.) Fix incorrectly flagged [FLAG1] duplicates and uncount incorrectly counted names. Re-sort "Tmptax" on "SORTNAME", "FULLNAME-1", "ORD" and ensure that [ORD]+z has not changed the sort order. Re-sort "Tmp1" on "FULLNAME", "FLAG1", "FULLNAME-1" to fix records misclassified in [FLAG1] . Restore original sort order by sorting "Tmptax" on "SORTNAME", "FULLNAME-1", "ORD".                  Use [TEST] to ensure correct sort order.</p>

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		<p>X2 = un-counted duplicates of retained taxa with &gt;1 synonyms; [DUP]=U,W.  Y1 = counted unprocessed FULLNAMEs; DUP=T,V.  Y2,Y3 = duplicates of unretained FULLNAMEs with &gt;1 synonyms; [DUP]=T,V.  Z0 = uncounted added binomials or uncounted binomials of counted autonyms [X-2]=M  Z00, Z01.. = uncounted duplicates of records with [FLAG1]=Z0; also a signal to append another sort number to [ORD].  Z1,Z2 = uncounted duplicates of FULLNAMEs with &gt;1 synonyms  Z4 = uncounted duplicate of a hybrid with &gt;1 synonyms (NOCASEs).  [SORTNAME] = .. 8X – sorts switched non-hybrid after ordinal, but before 9X true hybrid  [SORTNAME] = .. 9X sorts hybrids last  [TEST]= "" – ensures correct sort order</p>	
#12	Zrephot3	<p>[SETNO]="UC13"+XSET [X-2]="CE" [DUP]="L" (sequential duplicates)  [FLAG1]=X01+strval(R) sorts first; add a leading space to [ORD] to make it sort first  [FLAG1]=X02.. sorts secondly  [TEST]= "" – ensures correct sort order</p>	<p>(12.a.) Identify all sets of names with duplicates and flag sequential duplicates in [X-2]=2.  (12.b.) Sort "Tmp3" on "FULLNAME", "FULLNAME-1", "ORD". sorted by binomial stored in SORTNAME w/hybrids subsorted. Set [FLAG1]=X01+strval(R) to sort first and set subsequent records [FLAG1]=X02.. to sort secondly.  (12.c.) Change [ORD] sort order when [FLAG1]=X01 and uncount sequential duplicates. Sort "Tmptax" on "SORTNAME", "FULLNAME-1", "ORD".  Use [TEST] to ensure correct sort order.</p>
#13	Zrephot3	<p>Tmpself: [SETNO]="C2s1f"+XSET [X-2]="I" [DUP]="E"  [SETNO]="UC13"+XSET [X-2]="CE" [DUP]="L"  [TEST]= "" – ensures correct sort order  Tmpcasu2: [X2CNT] is the original sum of this category  Tmpcasu2: [SETSUM] is the sum of this SETNO only  Tmpcasu2: [SUMSETSUM] is the final sum of this category  Tmpcasu2: [SUMCHNG] is the sum of changes within this changed category  Tmpcasu2: [SUMCHSET] is the final sum of the category changes</p>	<p>(13.a., 13.b.) Segregate names into separate tables based on synonymy of whether the names are counted as entries or accepted taxa. The tables are Tmpcola, Tmpcolb1, Tmpboth and Tmpself.  (13.c.) Run error checks on the numbers of names in each set.  (13.d.) Tabulate all the types of synonyms for names counted in column A ((SETNO)=CA..) that will identify if any of the names changed categories during the scripts. Use [TEST] to ensure correct sort order.  (13.d.) Count and flag Tmpcola as CA.  (13.e) Determine CA category changes using Tmpcola.DB. Tmpcola.db -&gt;Tmp -&gt;Tmp1 -&gt;Tmpcasum -&gt;Tmp3 -&gt; Tmp4 -&gt;Tmpcasu2. Flag * for CA categories where [X2CNT]&lt;&gt;[SUMSETSUM]+[SUMCHSET].  Ex. Final pntrs to cntd switches (*208/264) /E CA10a 208 NCAE  (where the error flags are *SUMSETSUM/X2CNT)</p>
#14	Zrephot3	Count number of records in synonym categories based on the	(14.a.) Sort "Tmptax" on "NEWFAM", "SORTNAME", "FULLNAME-1", "ORD" . This sorts

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		<p>value of the string in a "Designator code" given by the first or first and second characters in [X-2].</p> <p>If Designator = "E" then increment [NUMU] and [NUMW].</p> <p>If Designator = "CS" then increment [NUMW].</p> <p>If Designator = "L" then do not count this record.</p> <p>If Designator = "C2" then increment [NUMU] and [NUMW].</p> <p>If Designator = "U" then increment [NUMU].</p> <p>If Designator = "W" then increment [NUMW].</p>	<p>records with [ORD] before records with [ORD] + a space + a name, unless [FULLNAME-1] is blank.</p> <p>(14.b.) Number and count records in Tmptax; count categories of synonyms given in by a "Designator code" given in [X-2].</p>
#15	Zrephot3	<p>[SETNO]="UC15a" [X-2]="CT" [DUP]="L"</p> <p>[SETNO]="UC15b" (NOCASE)</p> <p>[FONT]="BINO1" for all binomials</p>	<p>(15.b.) Count unique binomials and flag them in [FONT]="BINO1".</p> <p>(15.c.) Identify entered counted binomials with unidentified valid non-autonym subordinates.</p> <p>(15.d.) Error check to make sure all subordinates have binomials and all binomials with subordinates have been identified.</p>
			<p>Routines 16 to 19 calculate summary statistics and prepare the database for report output.</p>
#16	Zrephot4	<p>Restructure Tmptax.db – add [SHOWCOL] [BIFLAG]</p> <p>[SYN] = "..\"&gt;?\"..\" – Questionable name.</p> <p>[SYN] = "..\"&gt;\"..\" – Pointer already flagged in [SYN].</p> <p>[SYN] = "..\"=I\"..\" – Selfer already flagged in [SYN]</p> <p>[SYN]="(p.p. name without a synonym here; =I)." OR [SYN] = [SYN]="(p.p. name; &gt;  ~" +XLOOK +)"." – P.p. name</p> <p>[SYN]="(pointer to hybrid; &gt;  ~" +XFN1 +)"." – Pointer to a hybrid.</p> <p>[SYN]="(&gt;  ~" +XFN1 +)"." – Remaining pointers not already flagged in [SYN].</p> <p>Tmpto.DB: [SYNSTRIIP], [SYN] = "..\"&gt;  \"..\".</p> <p>Tmpfrom.DB: [SYNSTRIIP], [SYN] = "..\"&lt;  \"..\".</p>	<p>(16.a.) Flag [SYN]. These include questionable names, pointers already flagged in [SYN], selfers already flagged in [SYN], p.p. names, pointers to hybrids, and remaining pointers not already flagged in [SYN]. [SYN] can have only one semicolon which must be followed by &lt; &gt; or =.</p> <p>(16.b.) assure there are no pointers to records that are only uncounted.</p> <p>(16.c.2.) Flag [SYN] with a period to indicate records that have a completed [SYN] field.</p> <p>(16.d.) Sort "Tmptax" on "NEWFAM", "SORTNAME", "FULLNAME-1", "ORD". this sort order puts names with ORD(-) before ORD(+) unless [FULLNAME-1] is blank.</p> <p>(16.e.) Restructure Tmptax.db; join new fields from ALF.DB.</p> <p>(16.g.) List problematic taxa &amp; synonyms in Tmpdot, resolved or not.</p> <p>(16.h.) Created Tmpto.DB containing all pointers; flag [SYNSTRIIP]; flag [POINT] with pointers for collections or rare species.</p> <p>(16.h.2.) Create Tmpfrom.DB containing all targets. Flag [SYNSTRIIP]; flag [POINT] for collections or rare species.</p>
#17	Zrephot4	<p>[COLMSG] values can be as follows:</p> <p>[COLMSG]="(collected as synonym)"</p> <p>[COLMSG]="(no collections under any synonym)"</p> <p>[COLMSG]="(partial; collected as synonym)"</p> <p>[COLMSG]="(partial; no collected synonyms)"</p> <p>[COLMSG]="(partial; see source)"</p> <p>[COLMSG]="(uncollected autonym)"</p> <p>[COLMSG]="(uncollected under this name)"</p> <p>[COLMSG]="(uncollected; see rank syn)"</p> <p>[COLMSG]="(uncollected; see subordinates)"</p>	<p>Process collection information. Prepares a text string in [SHOWCOL] to output collection information for accepted records where [X-2] = "CB.." or "C2.." Records with partial collection information have the text "(partial.." prepended to [SHOWCOL]. If no collection information is available for a record, attempt to find collection information from another record that is either pointed to or pointed from this taxon. In this case, the record will be flagged with [COLMSG]= "(uncollected.." and the collection information will be transferred to the record being pointed-to or pointed-from by flagging [COLMSG] = "..collected as syn.." to that record.</p> <p>This routine also hides locations for pointers-to or pointers-from rare plants. Records of rare plants or pointers to or from rare plants have the location information stripped out of [COLAREA] and are flagged with [NOTES] "..[Undisclosed..\".</p>

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		<p>[WA]="&gt;" +[WA-1]                  [WA]="&lt;" +[WA-1]                  [NOTES] "..[Undisclosed..". and [COLAREA] = stripped location information for K2="E" or K2="T" or K2="S" or K2="X" (rare spp).</p>	<p>Sort the taxa in the final order of Section 4 by [NEWFAM] &gt; [SORTNAME] &gt; [FULLNAME-1] &gt; [ORD] and preserve this order in [NN].</p>
#18	Zrephot4	<p>See final report for documentation of concordance categories.</p>	<p>(18.a.) Count the number of accepted taxa (where [X-2] = "CB.." or "C2..") and entries (where [LK] "-..").                  (18.b.) Generate Appendix B.1.b – a correspondence with the PLANTS synonymy. Tmpscs is input; Tmpscs2 is answer summary table                  (18.b.4) Determine correspondence between [PLANTS] &amp; [FLORA] in categories of accepted, unaccepted, or uncounted; use [SYN] to determine subcategories.                  (18.b.5) Run error checks on the data.                  (18.c.) Create some appendices and reported calculations.</p>
#19	Zrephot4	<p>Restructure Tmptax.db – add [NDX]                  Flag [NDX] with ROOT sets and SORTNAME sets. SORTNAME sets are sets of records with the same FULLNAME.                  [NDX] = ..1 for the first name in a SORTNAME set.                  [NDX] = R_S_ or R_H_ for duplicate FULLNAMEs.                  [NDX] = R1S1 or R1H1 for a new ROOT set. A ROOT set is a sequential set of names that begins with the binomial name and then includes all the subordinates of that name in one or more SORTNAME sets.                  [NDX] = R_S1 or R_H1 for a new SORTNAME set with the same binomial but a different FULLNAME.                  [BIFLAG]="BI" for binomial names indicated by whether [FONT] from routine 15, = "BINO1". [FONT] is used for a different flag later in this routine.                  Set [BIFLAG]="BUNC" for uncounted binomials without subordinates or binomials that only have uncounted subordinates.                  [FONT] is set to #.. for counted recs; otherwise this character is an underscore.                  [FONT] is flagged "#" for additional names changed to accepted from unaccepted by switching with duplicate names.                  [FONT] is flagged "S" to flag names changed to unaccepted from accepted by switching with duplicate names.                  [F2] is set to @ for reported entries; otherwise this character is an underscore.</p>	<p>(19.a) Restructure Tmptax.DB to flag [NDX] and [FONT] with the output font, bolding, italicization and and indentation. The accepted names are sorted by family, genus species and then subordinates. A group of accepted names and its duplicates is referred to as a ROOT set, which is coded in [ROOT] as the binomial name. [ROOT] is the same for all subordinates. Duplicate accepted names are allowed within ROOT sets without counting to show alternate synonymies. Within each ROOT set there can subordinates with the same binomial name but different full names. This group of names is referred to as a SORTNAME set, which is coded in [SORTNAME].                  [NDX] is flagged "R1.." in characters 1 and 2 for each new binomial name in (in [ROOT]).                  [NDX] is flagged in characters 3 and 4 as "S1.." (or "H1.." for hybrids) for each new name in a SORTNAME set, which is essentially each occurrence of a new subordinate.                  [NDX] is flagged with an underscore in character 2 for duplicate names in a ROOT set and with an underscore in character 4 for duplicate names in a SORTNAME set.                  Ex. Arabis divaricarpa has 3 synonyms: Arabis divaricarpa (s.s.), Arabis xdivaricarpa and Arabis divaricarpa var. divaricarpa. The first name is counted as the accepted name. [NDX] is flagged for the above synonyms, respectively as: R1S1, R_H1, and R_S_                  Example: 1.ARADIV=R1S1 2.ARADIV(dup)=R_S_ 3.ARADIVX=R_H1                  [FONT] is flagged with a # for the 1st name in a SORTNAME set of duplicate names, otherwise unaccepted names have an underscore. The second part of routine 19 modifies [FONT] when it finds a first SORTNAME that isn't flagged as being accepted. It does this by changing [FONT] in that name to a "#" and changing [FONT] in the subsequent full names to the character "S" instead of the character "#". This allows the report to show the first name as accepted by bolding it, while italicizing the latter name, that is otherwise unchanged in the database.                  (19.b.) Flag [BIFLAG].                  (19.c.) Run error checks for output in Section 4 dependent on [COLMSG] or [SYN].</p>

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			Routines 20 through 22 output the report to a text file. They use and modify table Tmptax.db (backed up as Tmptaxb.db).
#20	Zrephot4	<p>XLAST holds ROOT: If XRT&lt;&gt;XLAST then K3="R1" XLAST=XRT Else K3="R_"</p> <p>Bolden names that have ([BIFLAG]="BI" AND K3="R1")OR NW&gt;0 Bolden names that have [FONT]1,1=#.</p> <p>Bolding and character substitution is set in Zrepsc: Repsvauth() and Specchar(). To bolden a name, Q is set to "\$"; for italicizing a name Q is set to "~". Output for boldened names is preceded with " *", output for italicized names is preceded with " ~"</p> <p>Specchar() variables are B C Z Z1 Z2</p>	<p>Print Section 1 – Introduction, from prnsec1()</p> <p>Print Section 2 – Summary Statistics from prnsec2()</p> <p>Print Section 3 – background statement from prn3hed()</p> <p>Print Section 3 – Counts of taxa listed alphabetically by Latin name</p> <p>Section 3 output is formatted as follows: line1:C6 NU NW  *FULLNAME (SYNONYM) [NOTES] (XC6 X2 X3 K3 XNO) line2 (X4):DES SHOWCOL (DATE &amp; CND) WNHP rarity {AREA=BASIN} [COLAREA=LOCNUM-BASIN/QUAD] [LOCDESC] (XSCOL +D +XCOLAR +XAR)</p> <p>Specchar() is called to convert characters in string X to ANSI special characters &amp; convert dash character to "qq". Variable C counts each char of the string in X.</p> <p>Repsv() is called to replace substrings in full name variable X with special codes for processing by a Word macro. The search strings are " s. ", " v. ", " X ", " f. " and " cv. ". These are converted to s\$, v\$, X\$, f\$, or c\$ for bolded names or s~, v~, X~, f~, or c~ for italicized names. Variable Q determines whether to use character "\$" for bolded names or character "~" for italicized names. It is also used to prefixed the entire name with a bar " " followed by a \$ or a ~ that flags a line as containing a Latin name.</p>
#21	Zrephot4	<p>See Zrepsc.sc prnbyfam(), wrapxin, and getfields()</p> <p>XSET="Hybrid" or XSET="Species" SETR=substr(XSET,2,1) SETS=substr(XSET,4,1) XSET=substr(XSET,3,1) is the output name category.</p> <p>Getfields() variables are XLOC X X2 XWA NSYNR INDX XIN TF XSCOL D XCND XCOLAR XMSG L XAR XNO Wrapxin() variables are L LF LX F1 F2 INDX TF X3</p> <p>INDX=spaces(IND). This is the number of spaces of indentation to add along the left margin. IND=0 for a new ROOTSET; otherwise IND=3. Subordinates are indented 3 more spaces. Variable INDX needs to be recalculated just before printing because it gets reset when forming [SYN] output using getfields().</p>	<p>Print Section 4 – List of Names by Family from Zrepsc: prnbyfam(). The output is formatted using up to four sets of lines, referred to as linesets. Linesets contain the following data</p> <p>Lineset 1 = [X4] = Species name (or Subordinate) (XG=reported) (XG=#): FULLAUTH; COMMON</p> <p>Lineset 2 = [XSYN] = Synonymy.</p> <p>Lineset 3 = [XSCOL] = SHOWCOL(DATE,CND) (COLMSG) [COLAREA=-WATERSHED/quad] {AREA=-BASINS;surveys}. [LOCDESC]. OR = XSCOL = [COLMSG].</p> <p>Lineset 4 = [XNO] = WNHP rarity. NOTES.</p> <p>Lineset1 is triggered when SETS=1 (substr(XSET,4,1)). This causes the routine to process all subsequent identical SORTNAMEs until a new SORTNAME is detected. The first operation outputs the family name if it is new. Then the line is bolded or not; "..reported.." is added if the name is an entry; "s.s." is added if the name is sensu strictu; and the common name is added. The indent is set by IND to be 0 for the first ROOTSET name, otherwise it is 3 spaces. Lineset1 is finished by prepending "Species", or "Hybrid" to name and printing it.</p> <p>Linesets 2-4 are processed next. After printing lineset1, getfields() is called to get variables for linesets 2-4. This procedure is called iteratively for each duplicate [FULLNAME], determined by [SETS]&lt;&gt;1. Getfields variables are all initially blank; once</p>

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			<p>set they remain unchanged, except for [SYN] which prints a line every time it finds a new synonym. Upon return from getfields(), the remaining non-blank fields are printed.</p> <p>Before printing linesets 2–4, the routine tests the subsequent record. If this record is a duplicate FULLNAME, determined if substr([INDX],2,1)&lt;&gt;"1" AND substr([INDX],4,1)&lt;&gt;"1", then getfields is called again for that line, overwriting the previous variables. This call to getfields is contained in a loop that is repeated for each duplicate FULLNAME. As soon as a new FULLNAME is encountered, the loop is exited and linesets 2–4 are processed. For report output, the indent is set by variable IND, which is 0 for a new ROOTSET and 3 for all other records. Subordinates are indented 3 more spaces.</p> <p>Proc wrapxin() inputs [XIN], [INDX]; outputs X3 wrapped when the line length exceeds 95 characters.</p> <p>Specchar() and Repvsauth() are called when necessary. The latter behaves similarly to repvs() but operates on names with authors and slightly different abbreviations: ssp. var. forma, cv. and X (for hybrids).</p>
#22	Zrephot4		<p>Print Section 5 – Glossary from a call to Zrepsec.sc: prn7appdef().</p> <p>Print Section 6 – References from a call to Zrepsec.sc: prn7appref().</p> <p>Print Appendices from Zrepapp.sc.</p>

#### Appendix 4. Names of collectors in the collections database

Collector identities are stored in relational tables ACOLINI.DB and INICOL.DB. The table ACOLINI is used as a lookup table for plant collector names when entering data. The field [COLINI] contains initials of plant collectors that are linked to the table ACOLINI which is used to fill in the field [COLLNAME]. A more comprehensive table of plant collector names is contained in INICOL, which also contains a field listing the herbarium or collection where the collection is deposited and the name of the collector as used on the specimen label. INICOL contains duplicates of collector names with different spellings, e.g., C.L. Hitchcock and C. Leo Hitchcock. Therefore it does not have a key field that can be used to look up name abbreviations.

In order to merge new collector names into ACOLINI, table INICOL is used as a correspondence table containing different versions of the collector names. INICOL is used to generate new records to add to ACOLINI, after first determining that there would be no key violations or collector aliases. The structure of INICOL.DB is as follows:

COLINI (A8)	Keyed lookup value in table ACOLINI.
COLLNAME (A28)	field used to field in COLGW during data entry
LASTNAME (A28)	last name of collector, used for sorting this table when unkeyed
COLORG (A37)	name of collector given on herbarium label
SOURCE (A8)	database of names from the following herbaria or collections: COLGW = Collector names entered into the COLGW database prior to April 2005 INIPC05 = names from Pam Camp collections imported in April, 2005 INIWTU05 = names added from WTU collections imported in April, 2005

A list of collector names and codes for their names used in COLGW is as follows:

ABA – A.B. Adams	CRB – Curtis R. Bjork	FLP – F.L. Pickett	JBP – J.B. Phipps
ACY – Alan C. Yen	CSE – Carl S. English	FS – Fayla Schwartz	JCM – J.C. Moomaw
ADE – A.D.E. Elmer	CVP – C.V. Piper	GG – G. Garrison	JES – J.E. Schwartz
AH – Al Hanners	DC – D. Costello	GGH – George G. Hedgcock	JGH – Juanita Gurung, Noelle Husen
ANS – Albert N. Steward	DG – D. Gunderson	GH – G. Horn	JGS – J.G. Smith
ARK – A.R. Kruckeberg	DH – Douglass Henderson	GLW – George Wooten & L. Smith	JJ – John Jakubowski
BC – Bill Carleton	DH2 – David Hill	GM – Grace Meikle	JP – J. Parsons
BCH – Bill Carleton & N. Hedges	DK – Don Knoke	GP – G. Patrick	JW – Jean Wood
BJL – Betty J. Lowrey	DN – Dorothy Naas	GW – George Wooten	JWT – J. William Thompson
BOM – B.O. Mulligan	DV – Dana Visalli	GW2 – George Wright	KD – Ken Davis
BRM – Burt R. McConnell	EA – Ed Alverson	GWD – G.W. Douglas	KK – Kevin Kane
CBF – Charles B. Fiker	EB – Elroy Burnett	HKS – H.K. Svenson	KM – Katie Mitchell
CFY – C.F. Yocom	EB2 – Edmund Broch	HSJ – Harold St. John	KMJ – Kevin M. James
CHR – Christina Hanson & S. Roys	EH – Eliza Habegger	ICO – I.C. Otis	LAD – Louis A. Dillon
CHT – Chris H. Troth	EH2 – Eugene Hunn	JA – Jonna Ahl	LAS – Lisa A. Standley
CLH – C. Leo Hitchcock	EJ – E. Joyal	JB – Jim Barrett	LES – Lanette E. Smith
	EM – Edith MacFarlane		LH – Lisa Healy
	FJH – Hermann		

LL – Larry Loftis  
LLH – L.L. Houglan  
LLP – L.L. Phillips  
MA – Mildred Arnot  
MAS – Mark A. Schlessman  
MB – Mary Barkworth  
ME – Mark Egger  
MFD – Melinda F. Denton  
MO – Marion Ownbey  
NG – Nicole Galland  
NH – Neal Hedges  
OTE – O.T. Edwards  
PC – Pam Camp  
PE – P. Elvander  
PFZ – P.F. Zika  
PM – Peter Morrison  
PW – Peter Wimberger  
PWD – Peter W. Dunwiddie  
RB – Robert Bigelow  
RDN – Ralph & Dorothy  
Naas  
RFD – R.F. Daubenmire  
RG – R. Gibbons  
RGO – Richard G.  
Olmstead  
RGT – Rebecca G. Troth  
RKB – R. Kent Beattie  
RN – Ralph Naas  
RR – Richard Ramsden  
RRH – Richard R. Halse  
RS – R. Saufferer  
RS2 – Reid Schuller  
RSM – Robert S. Rummell  
SC – Sara Crockett  
SF – Stina Freitas  
SFC – Stina Freitas & P.  
Camp  
SFR – Stina Freitas & S.  
Roys  
SG – Sarah Gage  
SH – Steve Heywood  
SR – Shannon Roys  
SR2 – Sharon Rodman  
SRV – Shannon Roys & S.  
Vatheuer  
SW – Steve Wagstaff  
THS – T.H. Scheffer  
TL – Tom Lease  
TP – T. Patten  
VHY – V.H. Young  
WCM – W.C. Muenscher  
WT – Warren Tanaka

WWE – W.W. Eggleston

## Appendix 5. Location data in field [AREA] of OK4.DB

Field [AREA] in OK4.DB is used to hold location data for observed and collected plants. The data is meant to incorporate locations within watershed boundaries, for determining the local flora within those watersheds. [AREA] includes two types of source data as follows:

- A leading semicolon in front of a character string indicates the characters represent the code for a broad area survey.
- A leading dash (“-”) in front of a character string indicates the characters represent the code for a subwatershed or basin.

### Mapping the flora within broad areas

The codes contained in [AREA] representing the broad area surveys listed below, along with the authors of the surveys. These are only partially segregated into watersheds because they overlap more than one basin.

**;CHEL** – Flora of the Chelan–Sawtooth Mountains by Alverson and Arnett (1986). This survey was a botanical reconnaissance of the Lake Chelan–Sawtooth Ridge area published by the Washington Native Plant Society.

**;GRZ** – North Cascades grizzly bear ecosystem evaluation by Almack and others (1993). Special codes for this study set are as follows:

- GRZ-O – Present in Okanogan County within the Griz database.
- GRZ-R or GRZ-OQ – Present in Okanogan County within Griz database, but observation is questionable (Q).
- GRZ-Z or GRZ-OX – Present in Okanogan County within Griz database, but discounted as incorrect (X).
- GRZ-F – Present on lands administered by the Okanogan National Forest (as determined by overlap of USGS quads), but not in Okanogan Co.
- GRZ-S or GRZ-FX – As above, but sighting discounted.
- GRZ-T or GRZ-FQ – As above, but sighting questionable.

**;HB** – Horseshoe Basin Plant List and subsequent refinements – George Wooten.

**;NC** – Naas, Dorothy, R. Naas and E. Burnett (1990). A checklist of vascular plants of the North Cascades, Washington. North Cascades National Park, Sedro Wooley, Washington, 1990. This is combined with the North Cascade check list (June, 1992), by the same authors. Special non-blank characters stand for plants in the herbarium, are given below. Special codes for the NC set are signified by an added dash and a letter as follows:

- NC-B – Private land near Twisp
- NC-D – Department of Wildlife land near Winthrop (Sullivan Pond area)
- NC-K – Winthrop and Tonasket (Freezeout Ridge)
- NC-M – Twisp and Winthrop District
- NC-O – Okanogan River area
- NC-R – Twisp District

- NC-S – Similkameen, Loomis, Sinlahekin, Conconully
- NC-T – Tonasket District
- NC-V – Private land near Winthrop
- NC-W – Winthrop District

;NOX – Okanogan County Noxious weed list, 2006, verified by specialist Anna.

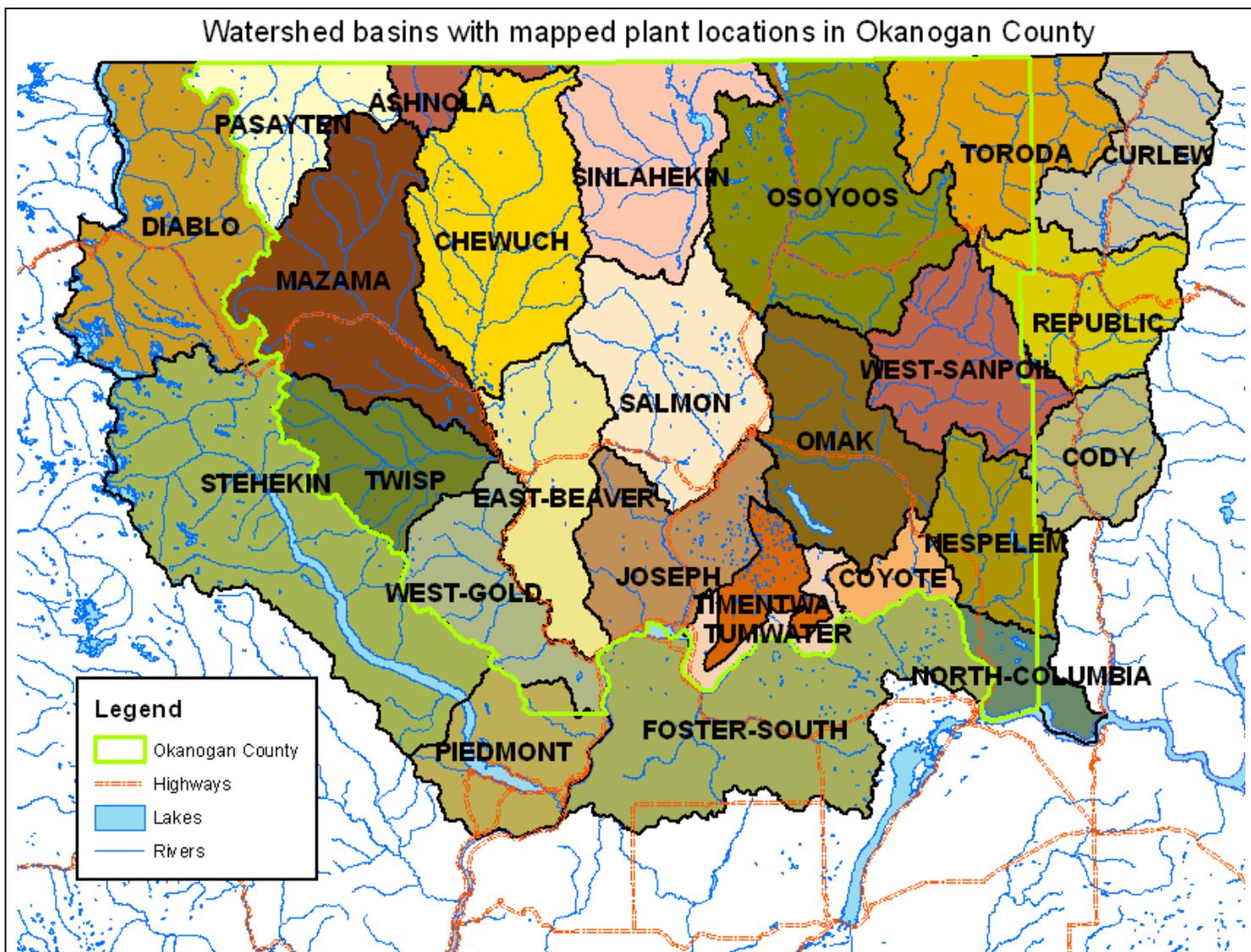
### **Mapping the flora by watershed**

The field [AREA] indicates locations of plant observations and collections by the name of the watershed where the record was observed or collected, referred to here as basins. Codes for the basins are preceded by a dash (“-”) character.

The basis for the watershed boundaries is the 2000 online Water Resource Inventory Areas (WRIA) maintained by Washington Department of Ecology. These watersheds were originally derived from a base layer of Watershed Administrative Units (WAU) courtesy of Department of Natural Resources. In creating the boundaries of the basins, the watershed boundaries were modified to allow more detailed mapping needed for plant location mapping.

The Ashnola watershed was segregated from the Pasayten watershed along the separating ridgeline. The Tumwater watershed was segregated from the Foster watershed. Just above the Tumwater watershed, the Joseph WRIA was split to account for drainage and soil patterns on arising on Okanogan Plateau.

The following map illustrates the locations of the basins used to locate plant observations and collections in the Okanogan flora.



The following table lists the names of the watersheds and basins used in the Flora of Okanogan County, along with the codes listed in [AREA] and the modifications made to the watershed used to derive the boundaries of the basins. Surveys used as sourced data are coded in the column "Included surveys". The codes for the surveys are given below the table.

Code	Basin name	WRIA name	Changes from watersheds to basins	Included surveys (see below)
ASH	ASHNOLA	ASHNOLA	This was split out of the Pasayten watershed along the ridgeline.	
CHE	CHEWUCH	METHOW	This was renamed from "CHEWACK".	-CHER -GRAN -NBOU -TIF -THU
COD	CODY	SANPOIL		
COY	COYOTE	FOSTER		

CUR	CURLEW	KETTLE		
DIA	DIABLO	UPPER SKAGIT		
EBEA	EAST-BEAVER	METHOW		-BEA -BEN -TICE
FOSS	FOSTER-SOUTH	FOSTER	This was split from the FOSTER WRIA along the Columbia River.	
JOS	JOSEPH	OKANOAGAN		-CHIL -DAV
MAZ	MAZAMA	METHOW		-ARR -COP -FAW -HART - HID -LBHS -MAZ -METU - WHI -MAZ
NES	NESPELEM	NESPELEM		
NCOL	NORTH-COLUMBIA	LOWER LK ROOSEVELT	Name changed from NORTH SHORE	
OMA	OMAK	OKANOAGAN		
OSO	OSOYOOS	OKANOAGAN		
PAS	PASAYTEN	PASAYTEN	The Ashnola Watershed was split out along the ridgeline.	-PAY
PIE	PIEDMONT	CHELAN		
REP	REPUBLIC	SANPOIL		
SAL	SALMON	OKANOAGAN		-POI
SIN	SINLAHEKIN	OKANOAGAN		-CHOP -SINL -SJ
STE	STEHEKIN	CHELAN		
TIM	TIMENTWA	OKANOAGAN	This was split from both the FOSTER WRIA and the OKANOAGAN WRIA following the basalt lithology.	-TIM
TOR	TORODA	KETTLE		
TUM	TUMWATER	FOSTER	This was split from the FOSTER WRIA along the Columbia River.	
TWI	TWISP	METHOW		
WSAN	WEST-SANPOIL	SANPOIL	Name changed from WEST FORK	
WGOL	WEST-GOLD	METHOW		-LIB

The following list briefly describes the surveys that were aggregated into basins within the field [AREA].

[ARR] – Arrowleaf proposed resort.

[BEA] – Beaver Creek.

[BEN] – Benson Creek property managed by Trust for Habitat Conservation.

[CHER] – Chewuch RNA Survey 1996, George Wooten

[CHIL] – Wooten, G. F. (1987). Chiliwist Canyon Plant List. Combined with Davis Canyon RNA Plant list compiled by Linda Mycek, Okanogan Chapter of the Washington Native Plant Society, May, 1985.

[CHOP] – Burnett, E., R. Naas and D. Naas (1987). Checklist of Flora of Mt. Chopaka area, Okanogan County,

Washington. Compiled from notes made in 1978 by George Douglas, David Wagner, M. Denton, W. Tanaka, A. R. Kruckeberg, with additions in 1987 by E. Burnett, R. Naas and D. Naas. Additions are marked with (A) from Washington Natural Heritage Program Survey Record, ca. 1990.

[COP] – Copper Pass Survey near Washington Pass – G. Wooten

[DAV] – Dunwiddie, Peter (1982). Davis Canyon Natural Preserve, Floristic Checklist. Appendix I in xxx, Nature Conservancy.

[FAW or FAWN] – Fawn Creek Forest Service rare plant survey.

[GRAN] – Basabe, T. Plant species list for the Granite Mountain Environmental Impact Statement.

[HART] – Species list – Hart's Pass (this is a list of alpine and upper subalpine species at Hart's Pass, starting at the first set of big open subalpine meadows, with additional notable lowland species added and marked with an L. The sources of the compilation are:

1. Notes from classes by Ron Taylor.
2. Flora of Hart's Pass and Vicinity, Okanogan Chapter Washington Native Plant Society, field trips to Hart's Pass and also during the Annual Chapter Bot-A-Thon. Names and dates of persons attending WNPS functions were: Virginia Hassinger & Co. (91) Steve Havas (90, 91) Karen Hinman (90) Dave Hopkins (90) Susie Kowalski (86) Ernie & Verena LeVon (90) Mary Lockman family (91) Eric Mohr (91) Linda Mycek (86) John and Debbie Nickell (91) Gary Ott (90) Leslie Roussan (90, 91) Dave & Marilyn Sabold (86, 90) Lanette Smith (86, 90, 91) Sierra and Forest Thompson (86) Dave Tracy (90) George Wooten, Sr. (86, 91) George Wooten, Jr. (86, 90, 91) Linda Zbigley (86). Dates and locations of these visits were:
  - 2a. August 4, 1986 – Slate Peak, and PCT.
  - 2b. July 20–22, 1990 – South and east side meadows.
  - 2c. August 3–4, 1991 – PCT North and South from the Pass including the big Hart's Pass Meadow, Slate Peak, and wet meadows below Tatle Peak.
3. Botany Washington Field trip July 12, 1997, organized by Art Kruckeberg.

[HID or HIDDEN] – Hidden Lakes Survey 1996 – G. Wooten

[LBHS] – Plant survey on Liberty Bell High School property.

[LIB or LIBBY] – Libby Creek Survey 1996 – G. Wooten

[MET] – Wooten, G., L. E. Smith and R. Crandall (1992). Plants of the Methow Trail, with additions from the Heath Ranch. Contracted by John Hayes for preliminary surveys relating to state acquisition of the Heath Ranch on the Methow River, Washington, and in planning for the Methow Trail through private lands.

[METU or METUP] – Survey of upper Methow by George Wooten.

[NBOU] – Basabe, T. (1995). Biological Evaluation for sensitive plants in the Boulder Analysis Area. Appendix B.

[PAY or PASAYT] – Pasayten Llama Pack trip before Hidden Lakes Survey 1996 – G. Wooten.

[POI or POISON] – Poison Lakes survey (Okanogan WNPS).

[SINL] – Sinlahekin Survey – D. Visalli, 2003.

[SJ] – Harold St. John (1924), A botany survey of Epsom Lake (Hot Lake). This was an early botany foray from WSU in the 1920s, from his personal notes at WSU.

[TICE] – Survey of Tice Ranch.

[TIF or TIFFAN] – The main plant list is based on Elvander (1979). Additions to the list are coded with a “-A” from Coleman Leuthy (1999); Brown Meadows Survey by Herb and Florence Wagner, George Wooten,

Christina Bauman, Linda Knight (1996); Okanogan WNPS loop tour led by Emmett Kinkade, with George Wooten Sr., G. Wooten, Jr., Carol Adams, John Adams, Denny O'Callaghan, Marilyn O'Callaghan (1996); Rock Mountain Botrychium survey, George Wooten, Elroy Burnett (1993); Okanogan Chapter WNPS hike with Dorothy and Ralph Naas, Elroy Burnett, Mildred Arnot, Marilyn, Ben, and Dave Sabold, Jim Barrett, Leah Swayze, Lanette Smith, George Wooten (1988); Wooten / Smith survey (1988); Okanogan Chapter WNPS hike (1987); surveys by Tony Basabe (1979, 1980); survey by R & D Naas (1979).

[TIME] – Timentwa (Okanogan Plateau).

[THU or THUND] – Thunder Mountain fire boreal ecology studies, 1994–2000, George Wooten, Mary Poss

[WHI or WHITEF] – Whiteface post-fire survey 1995, 1996 – G. Wooten

[WOL or WOLF] – Forest Service survey of Wolf Creek, G. Wooten.

The following surveys were available but were not used except for some of the suspected observations or for rare plants.

[BB] – A floristic study of Big Beaver Valley by Vanbianchi and Wagstaff (1988), published by the Washington Native Plant Society.

[COL] – Proposed Columbia Basin Project, Washington (INT-FES-76-8), Final Environmental Statement, appendix 7 and 8, Bureau of Reclamation, Dept of the Interior, Gilbert Stamm, Commissioner, Feb 27, 1976. A review of the Columbia Basin Project, including the building of Grand Coulee Dam, begun in 1933.

[DD] – Douglas and Douglas collection, herbarium unknown.

[ENT] – Entiat Ranger District Survey by Dana Visalli.

[EW] – A compilation of plants on the Eastern Okanogan National Forest by Margaret Willets

[GDOU] – A preliminary biological survey of the North Cascades National Park by Douglas (1969).

[HANF] – Hanford Reach of the Columbia River, Comprehensive river conservation study and Environmental Impact Statement, Final – June 1994, Volume 1, Appendix I., Animal and plant species (partial list), pp. 333–339.

[KET] – Annable, Carol R., and P. M. Peterson (1988). Vascular plants of the Kettle Range, Ferry County, Washington, pp. 62–92 in *Plant life of Washington state: Big Beaver Valley and the Kettle Range*.

Douglasia Occasional Papers, Volume 3, Washington Native Plant Society, University of Washington.

[NAC] – Naches RD by Dana Visalli.

[WWE] – W.W. Eggleston, *Plants Collected in Washington* (1916).