

# Review of LMH 77 Skunkcabbage Forests

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This script is designed to review the site series within each BGC, primarily to identify where site series do not sufficiently differentiate and need to be reviewed. The script also identifies site series with too few plots or with low diagnostic potential for review and interpretation of the quantitative analysis. The script generates a table list of site unit pairs that exceed a threshold similarity and a dendrogram of the cluster analysis of site units for each BGC.

## 1 Historic BEC correlation approach

## 2 Evaluate site series within each BGC

### 2.1 Read in data

Vegetation data is read in from saved .RDS file generated from the BECMaster cleaning scripts. A compiled SU table is build from all BGC \_SU tables stored in the coast guide Vpro database. Taxonomy is read in from the species taxonomy database. A species lumping code table is read in from the Correlation2\_Spp\_lump.accdb database and the vegetation data is lumped using the lump\_species function.

### 2.2 Examine site series within each BGC

1. Identify site series that have fewer than 5 plots (difficult to quantitatively analyse)
2. Identify site series that have low diagnostic potential (review units for membership consistency).

0.17 sec elapsed

Table 1: Site Units with Fewer than 5 Plots

Table 2: Site Units with Low Diagnostic Potential

Table 3: paste0("Site Series pairs with poor differentiation (BEC.sim >= .93)")

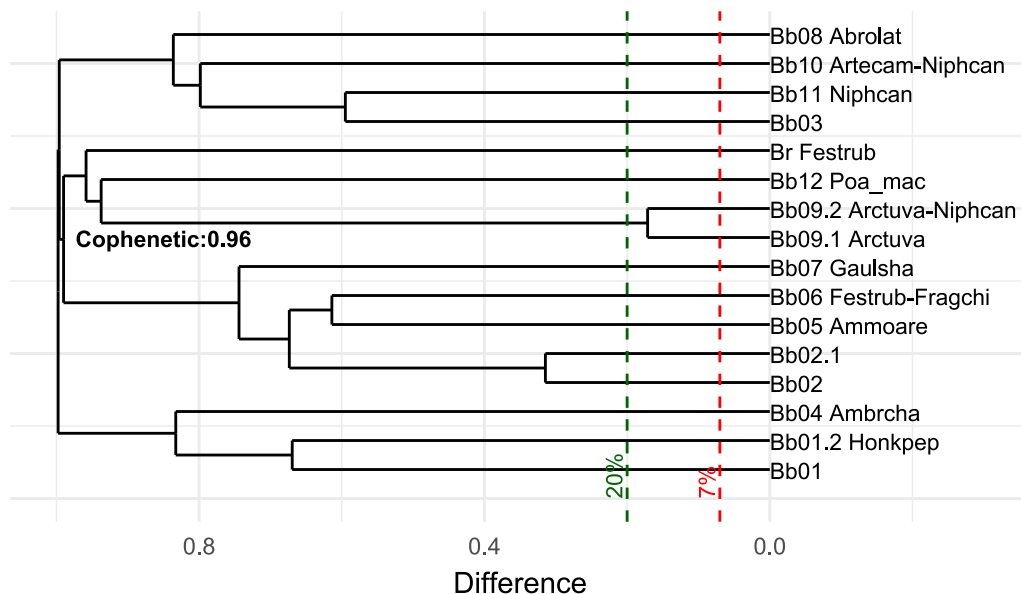
### 3 Compare site series within each BGCs

This section is to identify site series that do not differentiate adequately and require review.

#### 3.1 Dendrogram of cluster analysis by BGC

The dendrogram is an approximate representation of the similarity matrix. It is constructed using agglomerative hierarchical clustering which merges site units from the bottom up. The red line represents the minimal dissimilarity required to separate units into different site series. Any splits to the right of the red line should be considered for merging into the same site series (possibly as phases). Current threshold is set at 7% but assessment is required. Splits that occur between the green association threshold and the red minimum threshold will likely be merged at the sub-association level in the hierarchy. The green line represents the dissimilarity threshold for an association. Site unit 'leaves' to the right of this threshold will fall under the same association in the hierarchy. Current threshold is set at 17% but assessment is required.

#### Cluster Dendrogram of Site Units



```

Call:
agnes(x = dis.matrix, diss = TRUE, stand = TRUE, method = "average")

Cluster method      : average
Distance            : unspecified
Number of objects: 16

```

### 3.2 Generate comparative veg summary report

```

# su2 <- su %>% mutate(bgc = str_extract(SiteUnit, "[^_]+"))
#unit.list <- unique(su$SiteUnit)
unit.choose <- c("Bb01", "Bb01.2 Honkpep", "Bb02", "Bb02.1", "Bb03", "Bb04
Ambrcha", "Bb05 Ammoare", "Bb06 Festrub-Fragchi")
su.choose <- su %>% filter(SiteUnit %in% unit.choose)
table.name1 <- "Beach1"
vegSum <- create_veg_sum_all(vdat = veg.dat2, siteUnits = su.choose,
minimportance = 0)
##determine order of species by unit
indic.order <- build_species_ordering_all(vdat = veg.dat2, vsum = vegSum,
code.lump=lump, siteUnits = su.choose)
veg.sum.table1 <- format_veg_table2(vsum = vegSum, spp = taxon.lifeform)
create_VGS_table(veg.sum.table1, table.name = table.name1)

```

# Beach1

Summary Vegetation Table

Layer	Scientific name	Bb01	Bb01.2 Honkpep	Bb02	Bb02.1	Bb03	Bb04 cha	Ambr-	Bb05 moare	Am-	Bb06 Festrub-Fragchi	Common name
	n Plots	25	12	26	27	14	6		14		7	
Herb	Cakile edentula	nnn	n	v	I	I	III		I			American searocket
Herb	Honckenya peploides	v	nnn	v	v				v			seabeach sandwort
Herb	Leymus mollis	I	v	nnnnn	nnn	I	vv		nn		nnn	dune wildrye
Herb	Lathyrus japonicus	v	v	IIII	I	v	v		nnn		v	beach pea
Herb	Carex macrocephala			vv	v	nnnn	vvv		I		v	large-headed sedge
Herb	Ambrosia chamissonis	v		v	v	v	nnnnn					silver burr ragweed
Herb	Achillea millefolium			v	v	v	vv		v		nn	common yarrow
Herb	Ammophila arenaria	v		vv	v				nnnnn			European beachgrass
Herb	Fragaria chiloensis			vv	v	v			n		nnnnn	coastal strawberry
Herb	Tanacetum bipinnatum			v	v				v		nnn	dune tansy
Moss	Kindbergia praelonga		v	v					nn		III	slender beaked moss

```

unit.choose <- c("Bb07 Gaulsha", "Bb08 Abrolat", "Bb09.1 Arctuva", "Bb09.2
Arctuva-Niphcan", "Bb10 Artecarn-Racomit", "Bb11 Niphcan", "Bb12 Poa_mac")
su.choose <- su %>% filter(SiteUnit %in% unit.choose)
table.name2 <- "Beach2"
vegSum <- create_veg_sum_all(vdat = veg.dat2, siteUnits = su.choose,
minimportance = 0)
##determine order of species by unit
indic.order <- build_species_ordering_all(vdat = veg.dat2, vsum = vegSum,
code.lump=lump, siteUnits = su.choose)
veg.sum.table2 <- format_veg_table2(vsum = vegSum, spp = taxon.lifeform)
create_VGS_table(veg.sum.table2, table.name = table.name2)

```

## Beach2

Summary Vegetation Table

Layer	Scientific name	Bb07 Gaulsha	Bb08 Abrolat	Bb09.1 Arctuva	Bb09.2 Arc-tuva-Niphcan	Bb11 Niphcan	Bb12 Poa_mac	Common name
	n Plots	10	10	9	6	8	12	
Tree	Tsuga heterophylla			ll	v			western hemlock
Tree	Picea sitchensis	v		l	v			Sitka spruce
Shrub	Gaultheria shallon	nnnnn		ll	v			salal
Herb	Leymus mollis	nnn	v	v		v	vv	dune wildrye
Herb	Equisetum hyemale	vv		l	v		v	common scouring-rush
Herb	Abronia latifolia		nnnn				v	yellow sand-verbena
Herb	Rumex acetosella		nn	v		nn	v	sheep sorrel
Herb	Arctostaphylos uva-ursi			nnnnn	nnnnn	v		kinnikinnick
Herb	Carex macrocephala	vv	v	v		nn	v	large-headed sedge
Herb	Hypochaeris radicata	v	v	v	v	nn	v	hairy cat's-ear
Herb	Poa macrantha		v	l	n	v	nnn	dune bluegrass
Herb	Glehnia littoralis		v		v		n	American glehnia
Moss	Leptogium palmatum			n	v	v		antlered lichen
Moss	Peltigeraceae			vv	nn			NA
Moss	Stereocaulon tomentosum				lll	vv		eyed lichen
Moss	Cladoniaceae			l	n	v		clad lichens
Moss	Niphotrichum canescens		vv	vv	nnnnn	nnnnn	v	grey rock moss
Moss	Polytrichum spp.			v	v	ll		haircap mosses

```
# unit.choose <- c("Bb13 Rumefue", "Bbd01 Poa_mac", "Bb_Festrub",
# "Bb_Calysol", "Bb_Grinsti", "Br_Festrub", "HwSs-Gaulsha", "HwSs-Kindpra")
# su.choose <- su %>% filter(SiteUnit %in% unit.choose)
# table.name3 <- "Beach3"
# vegSum <- create_veg_sum_all(vdat = veg.dat2, siteUnits = su.choose,
# minimimportance = 0)
# ##determine order of species by unit
# indic.order <- build_species_ordering_all(vdat = veg.dat2, vsum = vegSum,
# code.lump=lump, siteUnits = su.choose)
```

```

# veg.sum.table3 <- format_veg_table2(vsum = vegSum, spp = taxon.lifeform)
# create_VGS_table(veg.sum.table3, table.name = table.name3)

vegsum.wbk <- createWorkbook()
openxlsx::addWorksheet(vegsum.wbk, sheetName = table.name1)
openxlsx::writeData(vegsum.wbk, sheet = table.name1, veg.sum.table1)
openxlsx::addWorksheet(vegsum.wbk, sheetName = table.name2)
openxlsx::writeData(vegsum.wbk, sheet = table.name2, veg.sum.table2)
# openxlsx::addWorksheet(vegsum.wbk, sheetName = table.name3)
# openxlsx::writeData(vegsum.wbk, sheet = table.name3, veg.sum.table3)
saveWorkbook(vegsum.wbk,      "./vegsum.tables/LMH77_draft_beach_table.xlsx",
overwrite = TRUE)

```

```

# ss_x_bgc <- su %>% select(SiteUnit, bgc) %>% group_by(SiteUnit, bgc) %>%
summarise(n = n()) %>% pivot_wider(names_from = SiteUnit, values_from = n,
values_fill = 0) %>% ungroup() %>% mutate_if(is.numeric, as.character) %>%
arrange(bgc)
# ss_x_bgc[ss_x_bgc == 0] <- "-"
# # low.diff <- gt::as_gtable((gt::gt(ss_similar) |> gt::fmt_number(decimals
= 2)|> gt::tab_options(table.font.size = 10) |> gt::cols_width(Site.Units ~
gt::px(250))), plot = TRUE, text_grob = gridtext::richtext_grob)
#      gt::gt(ss_x_bgc)      |>      gt::fmt_number(decimals      =      2)|>
gt::tab_options(table.font.size = 10)

```