

Review of LMH 77 Beachlands

William H MacKenzie

2025-08-09

Contents

1 Historic BEC correlation approach	1
2 Evaluate site series within each BGC	1
2.1 Read in data	1
2.2 Examine site series within each BGC	1
3 Compare site series within each BGCs	2
3.1 Dendrogram of cluster analysis by BGC	2
3.2 Generate comparative veg summary report	3

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).

0.2 sec elapsed

Site Unit	Number of Plots
Bb08	3
Bb08.2	4

Table 1: Site Units with Fewer than 5 Plots

Site Unit	Diagnostic Potential
Bb01.1	4.11
Bb02.1	9.71
Bb02.2	6.49
Bb02.3	17.78
Bb02.4	19.04
Bb03	7.98
Bb04	10.95
Bb06	18.16
Bb07.1	15.13
Bb07.2	23.35
Bb09	29.02
Bb10	4.90
Bb11	11.53
Bb01.2	5.19

Table 2: Site Units with Low Diagnostic Potential

Similarity	Site Units
------------	------------

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

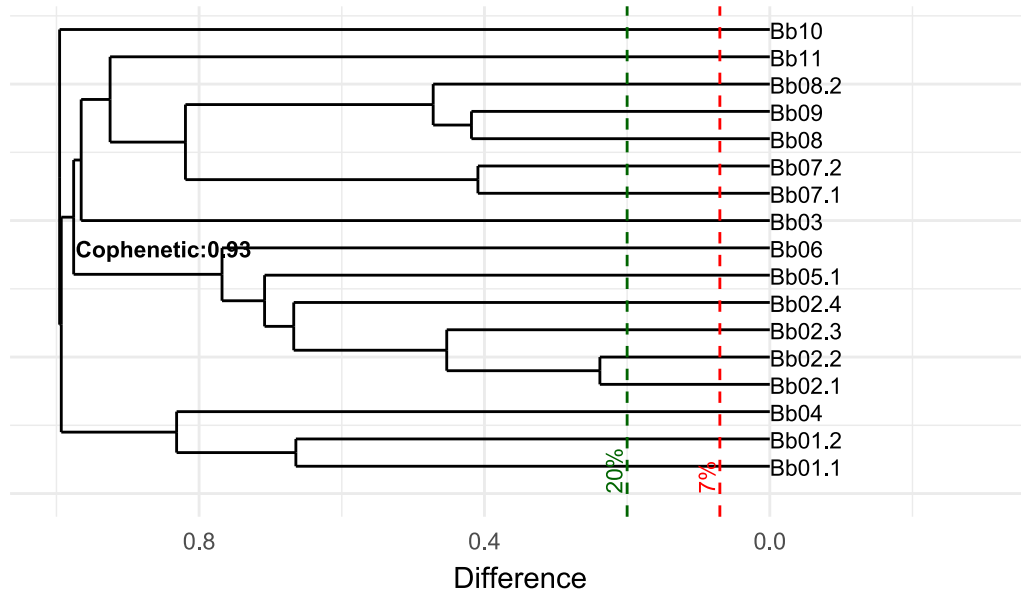
3 Compare site series within each BGCs

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: 17

3.2 Generate comparative veg summary report

```
# su2 <- su %>% mutate(bgc = str_extract(SiteUnit, "[^_]+"))
#unit.list <- unique(su$SiteUnit)
unit.choose <- c("Bb01.1", "Bb01.2", "Bb02.1", "Bb02.2", "Bb02.3", "Bb02.4",
"Bb03", "Bb04")
su.choose <- su %>% filter(SiteUnit %in% unit.choose)
table.name1 <- "Beach1"
vegSum <- create_veg_sum_all(vdat = veg.dat2, siteUnits = su.choose,
minimportance = 0, minconstancy = 50, noiseconstancy = 25)
##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	Bb01.1	Bb01.2	Bb02.1	Bb02.2	Bb02.3	Bb02.4	Bb03	Bb04	Common name
	n Plots	25	11	14	26	13	14	14	6	
Herb	<i>Cakile edentula</i>	nnn	n	v	l		l	l	lll	American searocket
Herb	<i>Honckenya peploides</i>	v	nnn							seabeach sandwort
Herb	<i>Leymus mollis</i>	l	v	nnnnn	nnn	nnnnn	nn	l	vv	dune wildrye
Herb	<i>Festuca rubra</i>			vvv		ll		v		red fescue
Herb	<i>Poa macrantha</i>					v	l	v		dune bluegrass
Herb	<i>Lathyrus japonicus</i>		v	v	l	nnnn	nnn	v	v	beach pea
Herb	<i>Fragaria chiloensis</i>				v	vv	n			coastal strawberry
Herb	<i>Ammophila arenaria</i>						nnnnn			European beachgrass
Herb	<i>Aira caryophyllea</i>						l			silver hairgrass
Herb	<i>Hypochaeris radicata</i>					v	l			hairy cat's-ear
Herb	<i>Carex macrocephala</i>					vv	l	nnnn	vvv	large-headed sedge
Herb	<i>Aira praecox</i>						l	vv	vv	early airgrass
Herb	<i>Ambrosia chamissonis</i>								nnnnn	silver burr ragweed
Herb	<i>Achillea millefolium</i>			l		v			vv	common yarrow
Moss	<i>Kindbergia praelonga</i>					vv	nn			slender beaked moss
Moss	Peltigeraceae						l			NA

```
unit.choose <- c("Bb05", "Bb05.2", "Bb06", "Bb07.1", "Bb07.2", "Bb08", "Bb08.2",
"Bb09", "Bb10", "Bb11")
su.choose <- su %>% filter(SiteUnit %in% unit.choose)
table.name2 <- "Beach2"
vegSum <- create_veg_sum_all(vdat = veg.dat2, siteUnits = su.choose,
minimportance = 0, minconstancy = 50, noiseconstancy = 25)
##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	Bb06	Bb07.1	Bb07.2	Bb08	Bb08.2	Bb09	Bb10	Bb11	Common name
	n Plots	11	9	6	3	4	8	12	10	
Tree	<i>Tsuga heterophylla</i>	vvv	ll	v						western hemlock
Tree	<i>Thuja plicata</i>	vv	l	vv						western redcedar
Tree	<i>Picea sitchensis</i>	vv	l	v						Sitka spruce
Shrub	<i>Gaultheria shallon</i>	nnnnn	ll	v						salal
Shrub	<i>Cytisus scoparius</i>					nnnnn	v			Scotch broom
Herb	<i>Leymus mollis</i>	nn				nnn		vv	v	dune wildrye
Herb	<i>Equisetum hyemale</i>	vv	l	v						common scouring-rush
Herb	<i>Arctostaphylos uva-ursi</i>	vv	nnnnn	nnnnn						kinnikinnick
Herb	<i>Luzula multiflora</i>		l							many-flowered woodrush
Herb	<i>Artemisia campestris</i>				nnnn					field wormwood
Herb	<i>Grindelia stricta</i>				l					Puget Sound gumweed
Herb	<i>Aira caryophyllea</i>				ll	n			v	silver hairgrass
Herb	<i>Bromus</i> spp.				nn	v	vv			bromes
Herb	<i>Aira praecox</i>	v	l	l	nn	nn	nn			early airgrass
Herb	<i>Festuca rubra</i>				nn	nnn				red fescue
Herb	<i>Hypochaeris radicata</i>	v	v	v	n	nn	nn	v	v	hairy cat's-ear
Herb	<i>Anthoxanthum odoratum</i>				l	nnnn	v			vernal sweetgrass
Herb	<i>Rumex acetosella</i>		v		nn	nn	nn		nn	sheep sorrel
Herb	<i>Carex macrocephala</i>		v		l		nn	v	v	large-headed sedge
Herb	<i>Holcus lanatus</i>					nn	v			common velvetgrass
Herb	<i>Poa macrantha</i>		l	n				nnn	v	dune bluegrass
Herb	<i>Glehnia littoralis</i>			v				n	v	American glehnia
Herb	<i>Abronia latifolia</i>								nnnn	yellow sand-verbena
Herb	<i>Polygonum paronychia</i>		v					v	ll	black knotweed
Moss	Peltigeraceae		vv	nn						NA
Moss	<i>Kindbergia praelonga</i>	lll	lll	vv		vvv				slender beaked moss
Moss	<i>Leptogium palmatum</i>		n	v						antlered vinyl lichen
Moss	<i>Dicranum</i> spp.	v	l							heron's-bill mosses
Moss	<i>Stereocaulon</i> spp.			lll						foam lichens
Moss	<i>Kindbergia oregana</i>				l					Oregon beaked moss
Moss	<i>Syntrichia ruralis</i>				nn				vv	sidewalk screw moss
Moss	<i>Racomitrium</i> spp.		vv	nnnnn	nnnnn	nnn	nnnnn		vv	rock mosses
Moss	<i>Polytrichum</i> spp.	v	v	v	l	v	ll			haircap mosses
Moss	<i>Cladonia</i> spp.		l	n	n	n	nn			pixie lichens

```
# 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,
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.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)
```