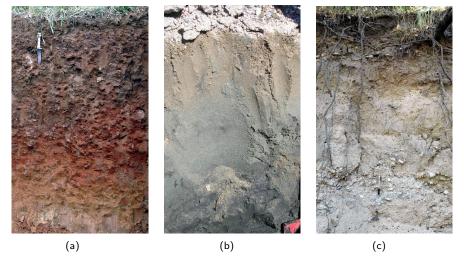
A generalized algorithm for determining pair-wise dissimilarity between soil profiles

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Quantitative (pair-wise) Comparison of Soils



"is **a** more like **b**, as compared to **c**?"

ideally transcending horizonation and description style

Numerical Soil Classification

essentially: an evaluation of "distance" in property space

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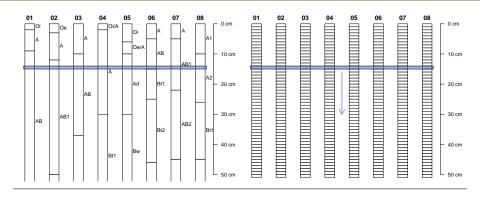
Examples

- ordination of soil properties (Hole and Hironaka, 1960)
- horizon "matching" between profiles (Rayner, 1966)
- depth-intervals, depth func. coeff., transition mat. (Moore et al., 1972)
- allocation to "reference horizons" (King and Girard, 1998)
- k-means, several "distance" metrics (Carre and Jacobson, 2009)

Issues, Assumptions, Limitations

- soil depth not always parameterized
- reference profiles required
- profile-scale (aggregation) vs. hz-scale properties
- algorithm complexity ↔ parsimony
- allocation vs. pair-wise dissimilarity
- distance metric selection & continuous vs. categorical variables

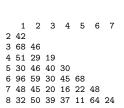
Pair-wise dissimilarity along depth-slices (Moore et al, 1972)

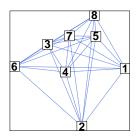


soil properties at slice 15

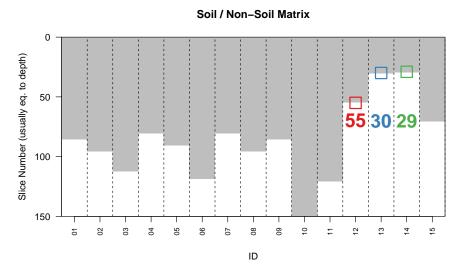
clay vcs ln_tc cec A
1 6.4 21.5 -1.5 3.8 8.1
2 10.6 17.6 -1.5 5.9 4.9
3 8.8 10.5 -0.2 7.5 6.0
4 9.1 12.6 -0.8 5.6 5.9
5 6.8 16.2 -0.5 5.0 8.2
6 17.9 11.0 -0.1 9.4 5.2
7 7.0 11.7 -0.4 4.7 6.3
8 6.3 17.0 -0.1 4.7 7.9

pair-wise dissimilarity at slice 15



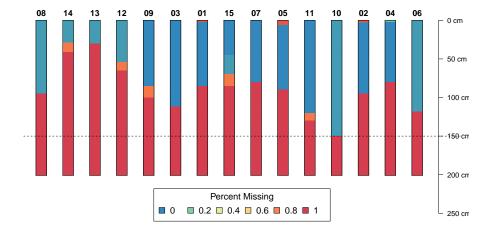


Soil Depth: comparisons between "soil" and "not soil"



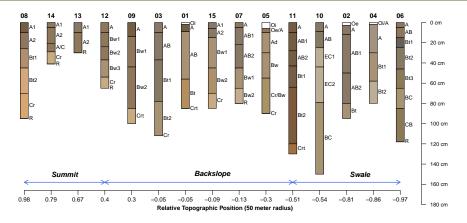
Pair-wise dissimilarities are only accumulated to the deepest of two profiles.

Warning: missing data will bias results!



Real data are often sprinkled with missing values \rightarrow D(6, NA) = NA. Estimate or constrain the dissimilarity calculation to a chunk of non-missing data.

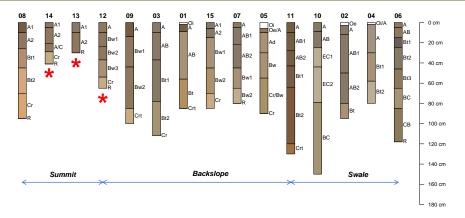
Example: Residual Soils formed on Granite



- summit: Lithic Haploxerolls, Typic Haploxerolls, Mollic Haploxeralfs
- backslope: Typic Haploxerepts, Ultic Haploxerepts
- swale: Oxyaquic Haploxerolls, Typic Argixerolls

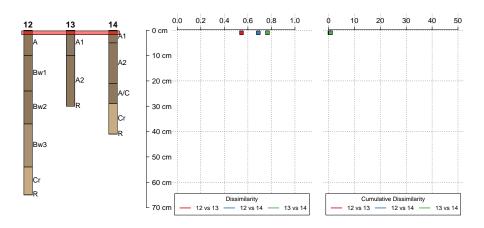
slice-wise comparison via: clay, VCS, CEC, pH

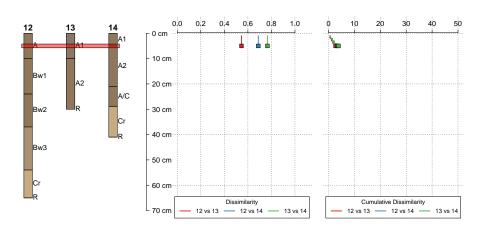
Example: Algorithm Applied to Subset

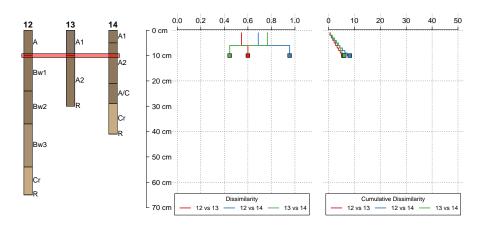


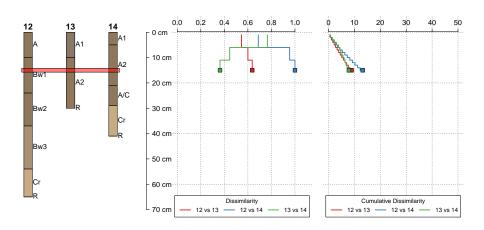
- summit: Lithic Haploxerolls, Typic Haploxerolls, Mollic Haploxeralfs
- backslope: Typic Haploxerepts, Ultic Haploxerepts
- swale: Oxyaquic Haploxerolls, Typic Argixerolls

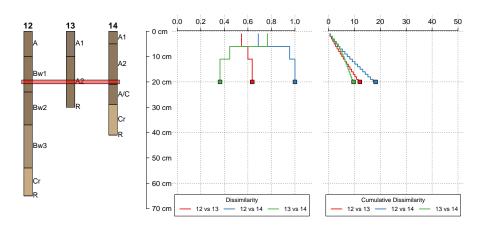
slice-wise comparison via: clay, VCS, CEC, pH

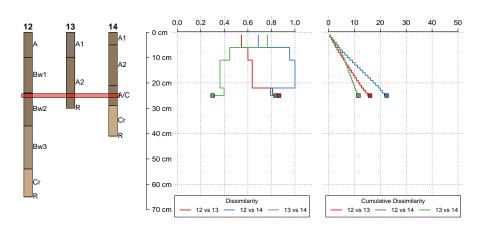


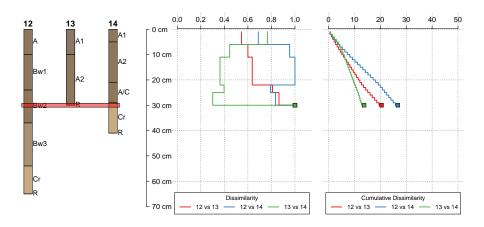


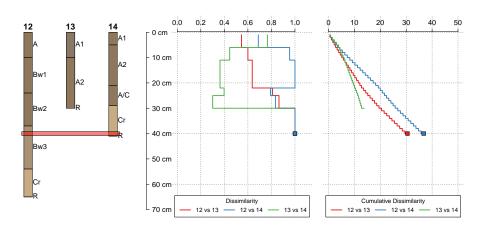


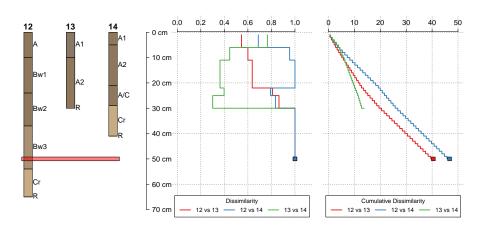


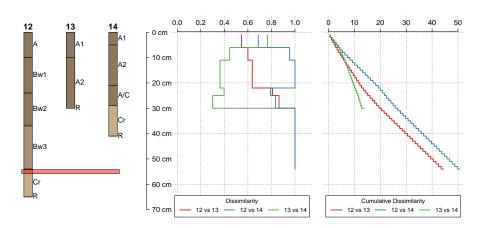




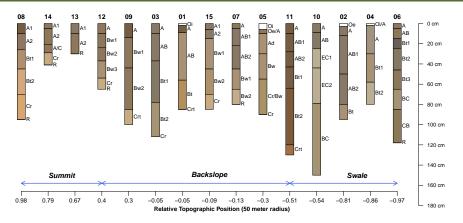








Example: Algorithm Applied to Entire Collection



- summit: Lithic Haploxerolls, Typic Haploxerolls, Mollic Haploxeralfs
- backslope: Typic Haploxerepts, Ultic Haploxerepts
- swale: Oxyaquic Haploxerolls, Typic Argixerolls

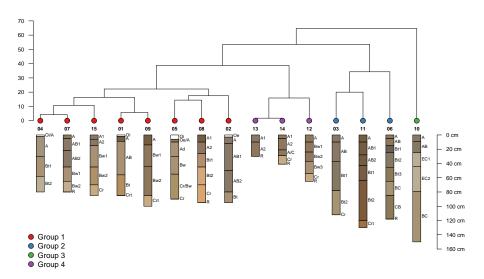
slice-wise comparison via: clay, VCS, CEC, pH

Results: Pair-Wise Dissimilarities

01	02	03	04	05	06	07	80	09	10	11	12	13	14
+													
02 25													
03 41	33												
04 22	25	35											
05 19	23	38	24										
06 68	49	42	60	64									
07 20	27	35	7	22	61								
08 30	27	39	27	22	63	25							
09 9	28	43	20	22	72	20	30						
10 71	68	50	67	68	70	68	67	69					
11 53	48	31	51	53	53	47	51	54	68				
12 32	46	57	32	39	77	29	44	29	84	61			
13 50	60	70	44	56	83	42	55	48	100	74	24		
14 51	60	71	44	56	83	41	55	49	100	75	25	3	
15 25	34	44	17	29	70	15	32	24	75	51	21	33	35

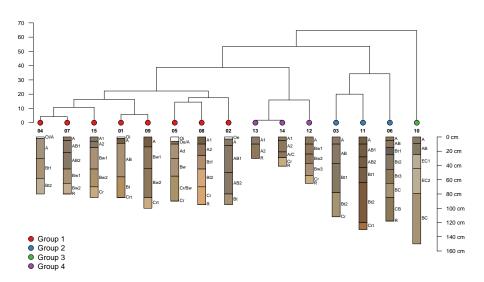
how is this useful?

Results: Dendrogram Representation



divisive, hierarchical clustering

Results: Dendrogram Representation



divisive, hierarchical clustering what does it mean?

Conclusions, Ideas, Caveats

Innovation(?) Relative to (Moore et al., 1972) and Others

- direct parameterization of soil depth
- accomodation of binary/nominal/ordinal/ratio variables: Gower's Distance
- simple implementation, readily scaled to HPC
- integration of hz-scale and pedon-scale variables: $D = \frac{w_{hz}D_{hz}w_pD_p}{2}$

Possible Applications

- similar/dissimilar decisions (map unit composition / OSD house-cleaning)
- automated allocation / identification of outliers
- bridging classification systems
- distance between taxa (Inceptisol <<<< Alfisol << Ultisol)
- evaluation of functional differences

Caveats

- fundamental assumption: comparison along depth-slices makes sense
- \blacksquare missing data heavily bias results \rightarrow limit application

