Costs for multidomain sequence analysis

Setting costs for multidomain sequence analysis

Gilbert Ritschard

Institute of Demography and Socioeconomics, University of Geneva http://mephisto.unige.ch/traminer

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- 2 Costs for combined states
- 3 Toy example
- Illustration: Cohabitation and working status, Switzerland

5 Conclusion





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Costs for multidomain sequence analysis Introduction

Multidomain sequences

Multidomain sequences (MDseq)

When elements in sequences reflect combination of states from different domains

- Family life sequences may combine marital status with parenthood
- Professional careers may combine education, domain of activity, rates of activity, roles.
- Life sequences may combine family, work, health, ...
- Linked lives: status of one person and status of partner

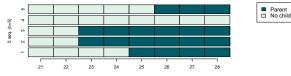
Interest of considering multidomain sequences:

• Studying relationships between domains



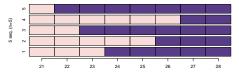
Costs for multidomain sequence analysis Introduction

Toy example of multidomain sequences



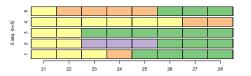
Parenthood















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Costs for multidomain sequence analysis Introduction

Distance between MDseq

Strategies for distances between MDseq

- Extended alphabet : combine alphabets, e.g. Child * Single, Child * Married
 - Combining dimensions may generate big alphabets
 - Consequence for edit distances: dramatic increase of number of substitution (and possibly indel) costs.
 - Trick for edit distances : derive multichannel costs from costs of each channel (Pollock, 2007; Gauthier et al., 2010).
- Sum (linear combination) of distances computed on the different channels.
- Other approaches: e.g. GIMSA (Robette et al., 2015)



Costs for multidomain sequence analysis Costs for combined states

Costs for combined states

How to set costs for combined states?

- Proceed as for regular sequences
 - unique, theoretically-based, data-driven, ...
- Additive trick (AT): MD costs defined as sum (average) of costs of individual domains
 - Example:

sc(child + single, nochild + married)
= sc(child, nochild) + sc(single, married)



Additive trick and state dependent indels

• For single state independent indel per channel, additive indel:

 $\mathsf{indel}_{MD} = \mathsf{indel}_{parenthood} + \mathsf{indel}_{marital}$

- OM and related methods work as well with a vector of state dependent indels:
- Straightforward extension: additive state dependent indels

indel(child, married) = indel(child) + indel(married)



Costs for multidomain sequence analysis Costs for combined states

Pro and cons of AT costs

- AT reduces number of independent costs to set. Computationally, this is not an issue.
- Interpretation: AT-based MD costs get an nice interpretation:
 - When SC is same (constant) in all channel, the AT cost is proportional to the number of channels on which the two MD states differ.
- However, deriving MD costs by summing (averaging) costs of each channel has a severe flaw.
 - Supposes independence of domains, while MD analysis is of interest to study the dependence between domains.



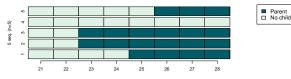
Costs and interaction between domains

- A priori, no reasons to have
 - sc(nochild + single, child + married) = sc(child + single, nochild + married)
 - which automatically follows when applying the additive trick
- In particular, likelihood of having child may depend on marital status such that
 - *nochild* + *single* more common than *child* + *single*
 - *child* + *married* more common than *nochild* + *married*
- and, because of this interaction, we would expect:
 - sc(nochild + single, child + married) < sc(child + single, nochild + married)



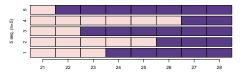
Costs for multidomain sequence analysis Toy example

Toy example of 5 MD sequences

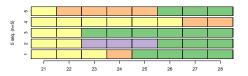


Marital status

Parenthood









Single

Married



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INDELSLOG, extended alphabet vs additive trick

True multichannel INDELSLOG costs

	c.m	c.s	n.m	n.s
c.m	0.00	0.98	0.89	0.75
C.S	0.98	0.00	1.15	1.01
n.m	0.89	1.15	0.00	0.92
n.s	0.75	1.01	0.92	0.00
Indel	0.36	0.62	0.53	0.39

AT costs based on additive trick (symmetry around both diagonals)

	c.m	C.S	n.m	n.s
c.m	0.00	0.58	0.58	1.15
C.S	0.58	0.00	1.15	0.58
n.m	0.58	1.15	0.00	0.58
n.s	1.15	0.58	0.58	0.00
Indel	0.54	0.64	0.51	0.61



Costs for multidomain sequence analysis Illustration: Cohabitation and working status, Switzerland

Illustration: Cohabitation and working status, Switzerland

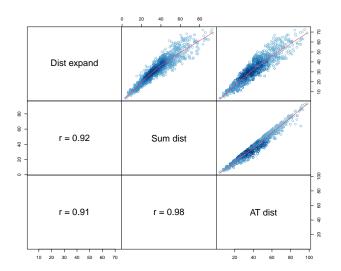
- Biographic data from Swiss Household Panel (SHP)
- 2 domains: Living arrangement (8 states + NA), Working status (8 states + NA)
- Expanded alphabet: 71 states (2485 sc costs, 71 indel costs)
- 1990 life sequences of length between 41 and 60 years $\left(\frac{n(n-1)}{2} = 1,979,055 \text{ dissimilarities}\right)$



Costs for multidomain sequence analysis Illustration: Cohabitation and working status, Switzerland

Plot of distances (random sample of 1000 pairs)

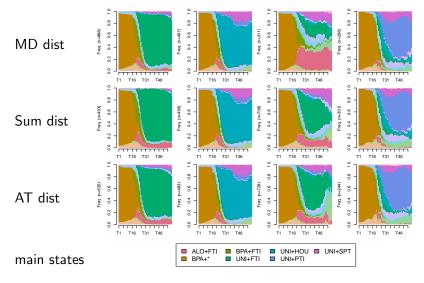
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Costs for multidomain sequence analysis Illustration: Cohabitation and working status, Switzerland

Clusters (chronograms of combined states)



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Costs for multidomain sequence analysis Conclusion

Conclusion

- Multidomain sequence analysis (MDSA) primarily concerns the study of relationships between domains
- MDSA of interest for linked domains only
- Additive trick (AT) for setting MD costs assumes independence between domains. Therefore, not recommended.
- Sum of distances computed independently on each channel assumes independence of domains too. Also not recommended.



Costs for multidomain sequence analysis Conclusion

Thank you!



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Costs for multidomain sequence analysis References

References I

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- Pollock, G. (2007). Holistic trajectories: A study of combined employment, housing and family careers by using multiple-sequence analysis. *Journal of the Royal Statistical Society A 170*(1), 167–183.
- Robette, N., X. Bry, and E. Lelièvre (2015). A 'global interdependence' approach to multidimensional sequence analysis. *Sociological Methodology* 45(1), 1–44.



Toy example of 5 MD sequences

	21	22	23	24	25	26	27	28	
1	n	n	n	n	С	С	С	С	
2	n	n	С	С	С	С	С	С	
3	n	n	С	С	С	С	С	С	
4	n	n	n	n	n	n	n	n	n no child
5	n	n	n	n	n	С	С	С	c child
	21	22	23	24	25	26	27	28	
1	S	S	S	m	m	m	m	m	s single
2	S	S	S	S	S	m	m	m	m married
3	S	S	m	m	m	m	m	m	
4	S	S	S	S	S	S	m	m	
5	S	m	m	m	m	m	m	m	



Costs for multidomain sequence analysis References

INDELSLOG costs

We illustrate with INDELSLOG data-driven costs

INDELSLOG method

- Indel and substitution costs are state dependent
- $indel(x_i) = log(2/(1 + f_i))$

where f_i is relative frequency of state x_i in data set.

• $sc(x_i, x_j) = indel(x_i) + indel(x_j)$

 $indel(x_i)$ decreases with frequency f_i of state x_i



Costs for multidomain sequence analysis References

INDELSLOG costs: main differences

We observe:

- Using true MD INDELSLOG costs
 - Low cost (.75) for substituting *c.m* with *n.s*
 - High cost (1.15) for substituting *c.s* with *n.m*
 - Cost (1.01) for substituting *c.m* with *n.s* (diff. on 2 domains) is lower than for substituting *c.s* with *n.s* (diff. on 1 domain)
 - State dependent indel costs: less frequent combined states (*c.s* and *n.m*) get higher indel costs.

• Using AT, i.e. summing single channel INDELSLOG costs

- Same cost (1.15) for substituting *c.m* with *n.s* and for substituting *c.s* with *n.m*
- Cost for substituting *c.m* with *n.s* is approximatively twice the cost for substituting *c.s* with *n.s* (diff. on 1 domain only)
- Similar indel costs for unfrequent and frequent combined states.



Costs for multidomain sequence analysis Toy example with TRATE

Using TRATE costs

TRATE method

- Substitution costs are state dependent
- $sc(i,j) = 2 p(x_{i,t}|x_{j,t-1}) p(x_{j,t}|x_{i,t-1})$

Using TRATE costs, we observe differences between true MD costs (computed on expanded alphabet) and additive MD TRATE costs similar to those observed using INDELSLOG.



TRATE, extended alphabet vs additive trick

True multichannel TRATE costs

	c.m	C.S	n.m	n.s
c.m	0.00	1.67	1.67	1.93
C.S	1.67	0.00	2.00	1.93
n.m	1.67	2.00	0.00	1.79
n.s	1.93	1.93	1.79	0.00
Indel	1.00	1.00	1.00	1.00

AT costs based on additive trick (observe double symmetry)

	c.m	c.s	n.m	n.s
c.m	0.00	1.71	1.80	3.51
C.S	1.71	0.00	3.51	1.80
n.m	1.80	3.51	0.00	1.71
n.s	3.51	1.80	1.71	0.00
Indel	1.75	1.75	1.75	1.75

