

Testing DTW by simulating phyllotaxis sequences and segmentation errors

1. initial sequences

Real biological values

intervals	angles	internodes
1	1	164
2	2	167
3	3	134
4	4	127
5	5	144
6	6	133
7	7	102
8	8	118
9	9	131
10	10	128
11	11	149

2. measures_type1

e.g. manual measures

2'. measures_type2

e.g. automated measures

2''. segmentation_errors

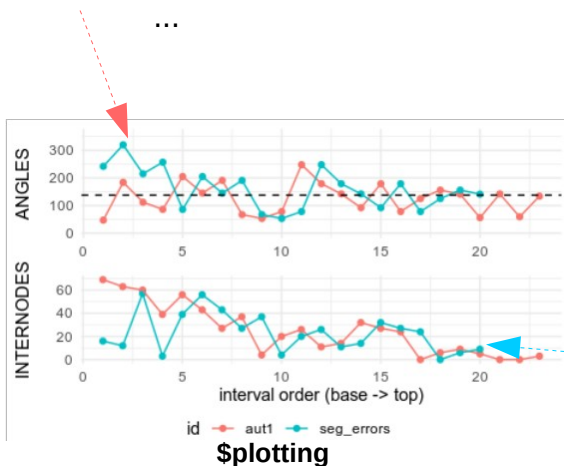
e.g. organs gained / lost

DTW
alignment1

DTW
alignment2

Eval DTW
prediction
quality

Eval DTW
sensitivity
to measure
precision



intervals	angles	internodes
1	242	16
2	320	12
3	215	57
4	257	3
5	86	39
6	205	56
7	145	43
8	191	27
9	67	37
10	52	1

\$values

reference	modified	dtw
1	NA	C
2	1	CTM
2	2	CTM
3	3	M
3	4	M
4	5	~
5	6	~
6	7	~
7	8	~

\$interval_alignment