

A modification of the Smith-Waterman algorithm to align sequences of numeric data

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2 Smith-Waterman modification

Numeric Smith-Waterman | Marcus Vollmer



1. Motivation



For heart rate analysis an ECG is non-invasively measuring heart activity.

Research questions:

- Is expensive medical equipment superior to consumer products in terms of signal quality?
- How does the quality change with physical and mental workload?
- Which devices are superior in terms of usability?



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Signal quality can be expressed by the ability of standard algorithms to detect the R peaks from the ECGs.

1. Motivation Experimental Setup





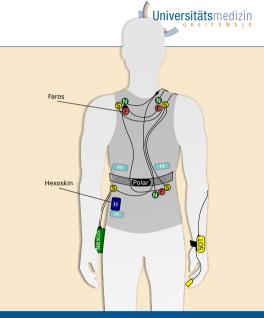
- ▶ 5 min standing rest
- 5 min walking on treadmill (1.2 m/s)
- cognitive test (2-back audio test)
- 5 min walking on treadmill (1.2 m/s, 15% gradient)

In between: NASA Task Load Index to measure individual strain

Conference paper 2019 [3] Data set 2020 [4, 1] • PhysioNet

1. Motivation Experimental Setup

- eMotion Faros 360° | 1000 Hz
- SOMNOtouch NIBP | 512 Hz
- NeXus-10 MKII | 8000 Hz
- 🕨 Polar RS800 Multi | 1000 Hz
- Hexoskin Smart Shirt Hx1 | 256 Hz



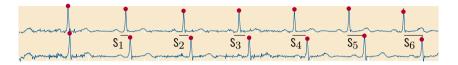




	eMotion Faros 360°	Hexoskin Hx1	NeXus-10 MKII	Polar RS800 Multi	SOMNOtouch NIBP
	2017	2015	2016	2007	2015
Follow-up	Bittium Faros	Hexoskin Smart Shirt	-	Polar Watch V800 + Polar H10	-
Supplies	ECG electrodes	Skin preparation gel	ECG electrodes	-	ECG electrodes
Sampling rate	1000 Hz	256 Hz	8000 Hz	1000 Hz	512 Hz

1. Motivation Linear Adjustment of Sampling Frequencies

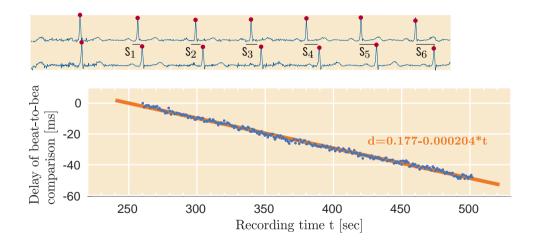




Pairwise differences s_i are linear decreasing or increasing with time

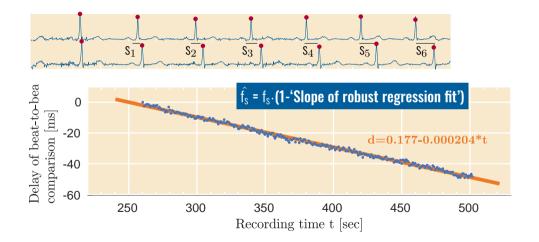
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Linear Adjustment of Sampling Frequencies





1. Motivation Linear Adjustment Factors



Manufacturer's specifications and actual sampling frequency (Hexoskin served as a reference with constant f_s). Two Faros' devices in use, $\hat{f_s}$ splitted according to device ID.

Recording Device	f _s	Mean $\hat{f_s}$	min	max
SomnoTOUCH NIBP	512	511.97	511.97	511.97
NeXus-10 MKII	8000	7999.67	7999.67	7999.68
eMotion Faros 360°, ID1	1000	1000.29	1000.19	1000.36
eMotion Faros 360°, ID2	1000	1000.18	1000.15	1000.21
Polar RS800 Multi	1000	999.91	999.87	999.95

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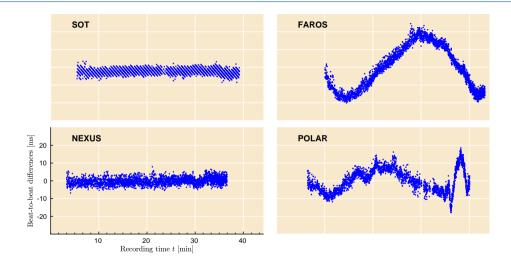


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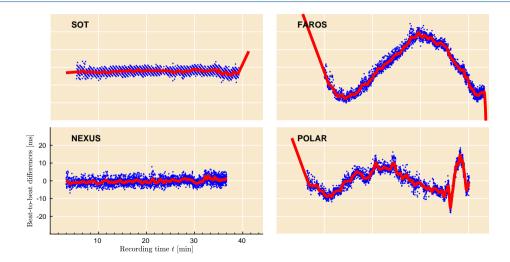
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2. Smith-Waterman modification



RR intervals is the sequence of the durations between successive R peaks of the heart cycle. Any error in these intervals is the reflection of errors in the beat detection.

Alignment and comparison of RR intervals:

- Polar RR interval sequences were generated by an in-house algorithm
- RR intervals were generated for all other devices using a standard detector applied to the ECG
- Reference intervals (ground truth) were generated by experienced researchers based on all signals



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Is there an efficient method to align and evaluate the quality of RR intervals?



Smith-Waterman [2] published a well-known algorithm to perform **local sequence alignment of nucleic** acid sequences or protein sequences.

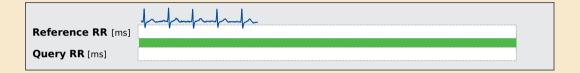
Sequence 1: AAG-GCCAAGGAG ..| ||| .|| Sequence 2: TTGTGCC-TGG

The alignment is composed of **matches**, **mismatches** (mutations) and **gaps** (insertions, deletions). The overall score of an alignment is a sum of individual scores (match=10, mismatch=-2, gap=-7):

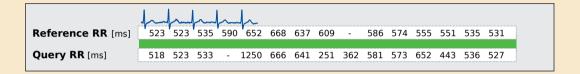
Score = 6 * 10 + 3 * -2 + 2 * -7 = 40

Dynamic programming is used in the matching process to find the optimal local alignment with respect to the scoring system being used.

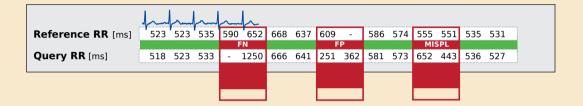








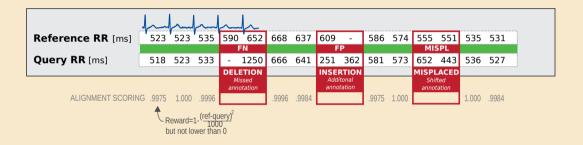




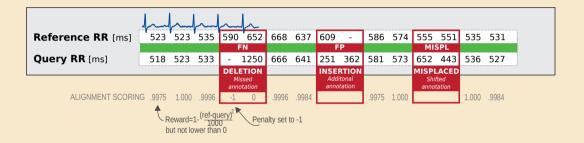


	Ind	لسم	لسم	~	h											
Reference RR [ms]	523	523	535	590	652	668	637	609	-	586	574	555	551	535	531	
					FN		FN		F	FP			MISPL			
Query RR [ms]	518	523	533	-	1250	666	641	251	362	581	573	652	443	536	527	
				DEL	TION			INSE	RTION			MISPI	ACED			
				ssed				tonal				fted				
				anno	otation			anno	tation			anno	tation			

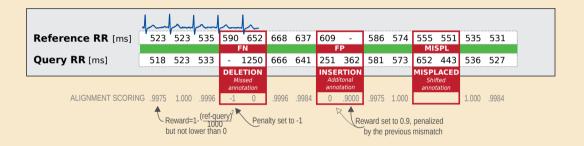




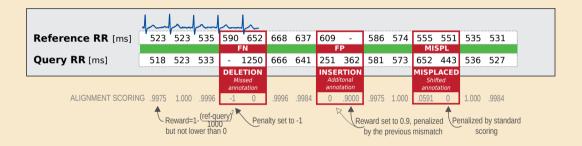




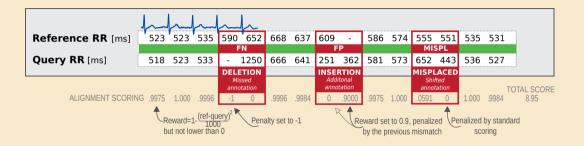












2. Smith-Waterman modification Scoring definition for RR interval alignment



Eq 1 and Eq 2 shows the definition of the scoring matrix H of sequences a and b having m and n values respectively. Function s of Eq 3 defines the reward of matched RR intervals allowing for minor deviations (reward=1 for 0 ms difference, reward=0.9 for ± 10 ms difference, reward=0.6 for ± 20 ms difference):

$$\begin{split} \mathsf{H}(\mathsf{i},\mathsf{j}) &= \max \begin{cases} 0 & \mathsf{No \ similarity} \\ \mathsf{H}(\mathsf{i}-1,\mathsf{j}-1) + \mathsf{s}(\mathsf{a}_\mathsf{i},\mathsf{b}_\mathsf{j}) & \mathsf{Match}/\mathsf{Mismatch} \\ \mathsf{H}(\mathsf{i}-1,\mathsf{j}) - 1.0 & \mathsf{Deletion} \\ \mathsf{H}(\mathsf{i},\mathsf{j}-1) + 0.9 & \mathsf{Insertion} \end{cases} \rbrace, \ 1 \leq \mathsf{i} \leq \mathsf{m}, 1 \leq \mathsf{j} \leq \mathsf{n} \qquad \texttt{(2)} \\ \mathsf{s}(\mathsf{a}_\mathsf{i},\mathsf{b}_\mathsf{j}) &= \max \begin{cases} 0 & \mathsf{capped \ score} \\ 1 - \frac{(\mathsf{a}_\mathsf{i}-\mathsf{b}_\mathsf{j})^2}{1000} & \mathsf{RR \ interval \ deviation} \end{cases}, \ \mathsf{a}_\mathsf{i} \ \mathsf{and} \ \mathsf{b}_\mathsf{j} \ \mathsf{in \ ms} \qquad \texttt{(3)} \end{split}$$



Adapted code from Needleman-Wunsch implementation:

- Source code: https://github.com/meicaljohnjones/Needleman-Wunsch
- Author: Michael John Jones



	Overall	P1 – Rest	P2 – Walking	P3 – 2-back	P4 – Uphill
total reference beats	42364	5623	6235	6106	9222
avg. peak heart rate	-	93.6 bpm	$103.3{ m bpm}$	$105.2{ m bpm}$	$153.7\mathrm{bpm}$
avg. median breathing rate	-	$14.5{ m min}^{-1}$	$24.1{ m min}^{-1}$	$24.3{ m min}^{-1}$	$27.1\mathrm{min}^{-1}$
FP FN Misplaced using Sn					
eMotion Faros 360°	5 0 19	0 0 0	0 0 0	0 0 0	0 0 6
Hexoskin Hx1	85 10 765	3 0 5	114 0 204	11 0 14	29 1 270
NeXus-10 MKII	40 5 765	0 0 0	3 0 4	15 0 40	0 1 309
SOMNOtouch NIBP	63 0 202	0 0 0	8 5 134	0 0 2	0 0 65
Polar RS800 Multi	28 29 333	0 3 18	6 0 57	3 3 66	0 0 11

Table: QRS detection performance through RR interval alignment using the modified Smith-Waterman algorithm for numericals. Errors are expressed by false positive counts (FP), false negative counts (FN), and the number of misplaced annotations from unsynchronized data (50 ms tolerance).





We are able to rate the performance and to classify beat detection error:

- Insertions represent RR intervals that are splitted into smaller sub-intervals due to a false positive beat location
- Deletions can be interpreted as missing beat locations
- Mutations represent inaccurate RR intervals due to misplaced beat locations

The SW-approach represents an efficient way of quantifying errors due to poor signal quality and weaknesses in heartbeat detection.

Efficiency is expressed by:

- No need to synchronize signals or frequency correction
- Automated handling of alterations of sampling frequencies during long-term measurements
- Signals are allowed to interrupt or stop for a period





* Bigillum

I am happy to answer questions

A. L. Goldberger, L. A. N. Amaral, L. Glass, J. M. Hausdorff, P. C. Ivanov, R. G. Mark, J. E. Mietus, G. B. Moody, C.-K. Peng, and H. E. Stanley.

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