Deep Learning Model for Base Calling of MinION Nanopore Reads

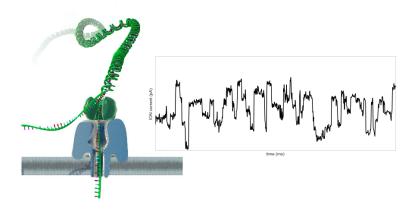
Marko Ratković Associate Profesor Mile Šikić, PhD

University of Zagreb Faculty of Electrical Engineering and Computing

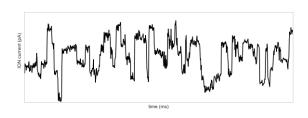


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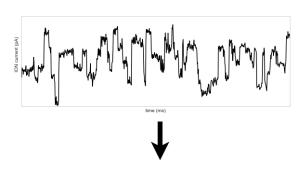
Technology



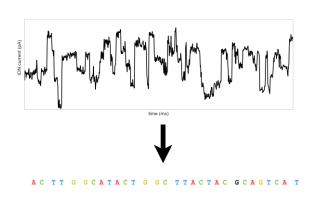
Basecalling



Basecalling



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Basecalling options

Metrichor

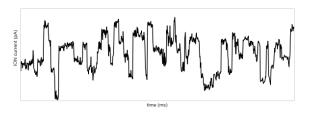
- only basecaller for ONT data
- proprietary software
- available as a cloud service

Goals

- local basecalling
- open-source
- speed, accuracy

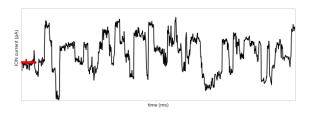
- Third-party: DeepNano, NanoCall
- Official: MinKNOW, Nanonet, Albacore, Scrappie

- Signal segmentation event detection
- RNN, HMM (older version of *Metrichor* and *NanoCall*)



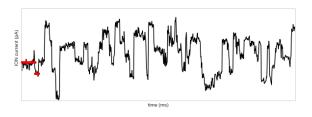
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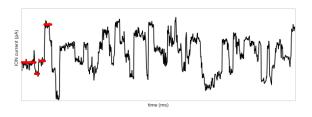
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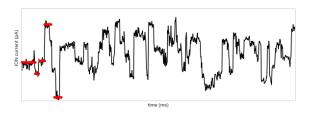
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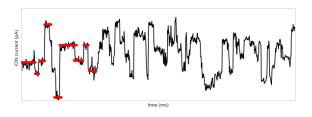
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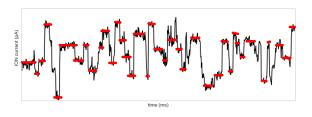
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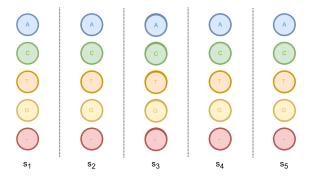


Proposed solution

end2end, CNN, CTC loss speed, paralelization, sequental, eliminate shit variable length loss function

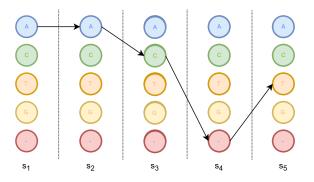
Idea: decode sequence from fixed-width output (softmax over alphabet)

Figure 1: Path "AAC-T"



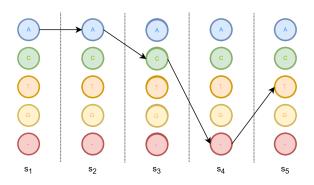
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Figure 1: Path "AAC-T"



Idea: decode sequence from fixed-width output (softmax over alphabet)

Figure 1: Path "AAC-T"



$$P(\pi|X) = \prod_{t=1}^{m} s_t(\pi_t) \tag{1}$$

Idea: decode sequence from fixed-width output

$$ACT = \begin{cases} decode(A, A, A, C, T) \\ decode(A, A, C, -, T) \\ decode(-, A, C, T, T) \\ decode(-, -, A, C, T) \\ decode(A, C, C, C, T) \\ \vdots \\ decode(A, C, T, -, -) \end{cases}$$

$$(2)$$

Idea: decode sequence from fixed-width output

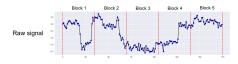
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$$(2)$$

$$P(Y|X) = \sum_{\pi \in decode^{-1}(Y)} P(\pi|X)$$
(3)

Given the dataset $D = \{(X_i, Y_i)\}$, training objective is the maximization of the likelihood of each training sample which is the same as the minimization of negative log likelihood:

$$L(D) = -\sum_{(X,Y)\in D} InP(Y|X) \tag{4}$$











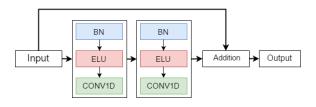
Model

• Residual CNN

Model

- Residual CNN
- 72 blocks, 2M parameters

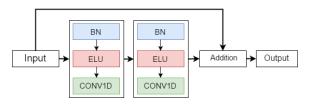
Figure 2: Residual block



Model

- Residual CNN
- 72 blocks, 2M parameters
- Maxpool every 24 blocks, reduction of dimensionality by factor 8

Figure 2: Residual block



Ground truth? Per read metrics

Table 1: Alignment specifications of E. Coli R9 basecalled reads

	Match % (median)	Mismatch % (median)	Insertion % (median)	Deletion % (median)
DeepNano	90.254762	6.452852	3.274420	11.829965
Metrichor	90.560455	5.688105	3.660381	8.328271
Nanonet	90.607674	5.608912	3.652791	8.299046
MinCall	91.408591	5.019141	3.477739	7.471608

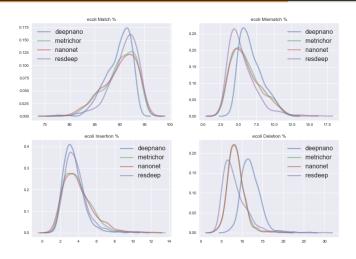


Figure 3: KDE plot of alimnment operations for E. Coli

Consensus from pileup

```
...CCAGAAACTGGCTCAGTTTGCCTTCCTCCGTGTCCTCCATGCTGACT...}

AGAAACTGGCT

GGCTCAGTT

CAGTATGCCTTGCTC

AGTATGCCTTTCCTC

AGTATGCCTTCCTC

AGTATGCCTTCCTC

AGAAACTGGCTCAGT

AGAAACTGCTTCCTCCGTGTCCTC

AGAAACTGCTTCCTCCATGCTGA

AGAAACTGCTCAGTATGCCTTCCTCCATGCTGA

Consensus
```

Figure 4: Consensus from pileup

Consensus from pileup

Table 2: Consensus specification of E. Coli R9 basecalled reads

	Total called [bp]	Correctly called [bp]	Match %	Snp %	Insertion %	Deletion %
DeepNano	1510244.0	1493242.0	98.8742	1.0044	0.1214	0.9041
Metrichor	1515893.0	1502588.0	99.1223	0.7464	0.1313	0.6300
Nanonet	1414237.0	1385515.0	97.9691	1.5700	0.4609	1.5158
MinCall	1517828.0	1506233.0	99.2361	0.6474	0.1165	0.5510

Consensus from de novo assembly obtained using assembler ra^1 and compared to the reference using dnadiff present in the Mumer²

¹https://github.com/rvaser/ra

²https://github.com/garviz/MUMmer

Consensus from de novo assembly obtained using assembler ra^1 and compared to the reference using dnadiff present in the Mumer²

Table 3: Assembly and consensus results for E. Coli

	Metrichor	resdeep	Nanonet
Aln. bases ref. (bp)	4639641(100.00%)	4639612(100.00%)	4639031(99.99%)
Aln. bases query (bp)	4604787(100.00%)	4614351(100.00%)	4599745(99.99%)
Avg. Identity	98.76	99.06	98.47
Edit distance	60418	46686	74341

¹https://github.com/rvaser/ra

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Results - basecalling speed

Table 4: Base calling speeds measured in base pairs per second³

	resdeep	Nanonet	DeepNano
Speed CPU(bp/s)	1363.34	897.49	692.37
Speed GPU(bp/s)	6571.76	3828.39	-

 $^{^3} Tested$ on server with two 8-core Intel(R) Xeon(R) E5-2640 v2 CPUs, NVIDIA Titan X Black GPU, 6GB

• Scaled Exponential Linear Units (SELU), Jun 2017

• Scaled Exponential Linear Units (SELU), Jun 2017

Figure 4: Implementation

```
def selu(x):
    with ops.name_scope('elu') as scope:
        alpha = 1.6732632423543772848170429916717
        scale = 1.0507009873554804934193349852946
        return scale*tf.where(x>=0.0, x, alpha*tf.nn.elu(x))
```

- Scaled Exponential Linear Units (SELU), Jun 2017
- Facebook Al Research (FAIR) team: Convolutional Sequence to Sequence Learning, May 2017

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• ..

End

Thank you for your attention!

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Any questions?