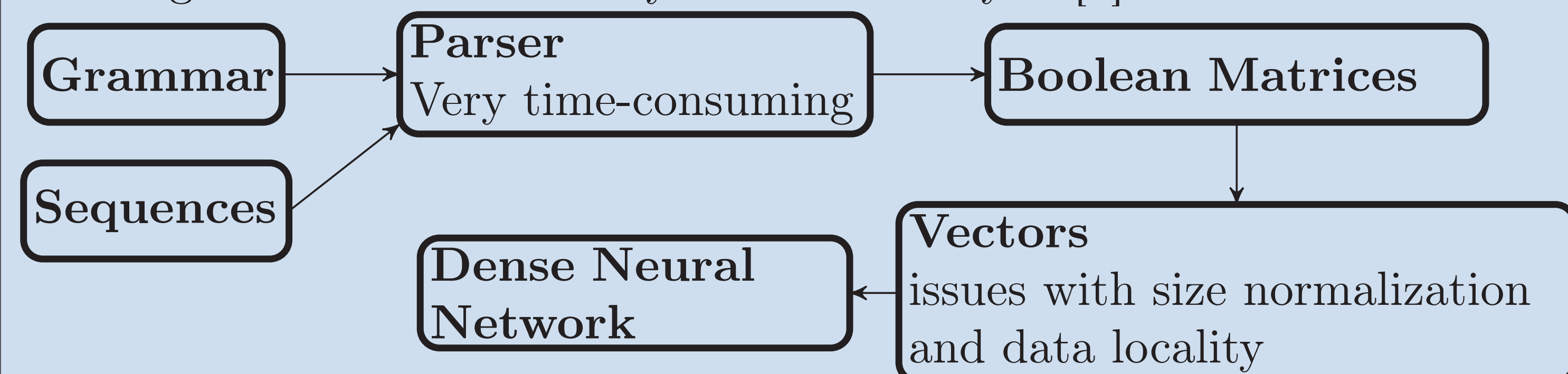




Motivation

Existing solution for secondary structure analysis [1]:



Questions:

- Is it possible to move parsing to network training step?
- Is it possible to use convolutional neural networks for parsing result processing?

Results: tRNA classification

- 2 classes: eukaryotes and prokaryotes (EP).
- 4 classes: archaea, bacteria, fungi and plants (ABFP).

Classifier	EP		ABFP	
Approach	Vectors	Images	Vectors	Images
Base model accuracy	94.1%	96.2%	86.7%	93.3%
Extended model accuracy	97.5%	97.8%	96.2%	95.7%
Total samples (train:valid:test)	20000:5000:10000		8000:1000:3000	

Sequences from open databases [2, 3].

Parsing elimination

We solve this problem by using two-staged learning.

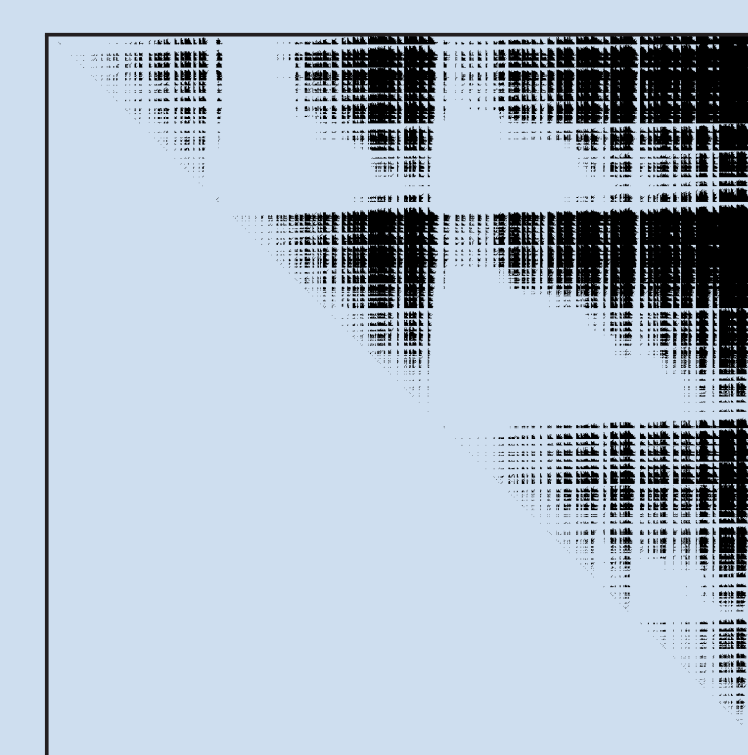
1. Train a network which takes parsed data as an input (**base model**).
2. Extend the trained network with a number of layers that convert the nucleotide sequence into a parsing result (**extended model**).

Parsing is required only for the network training.

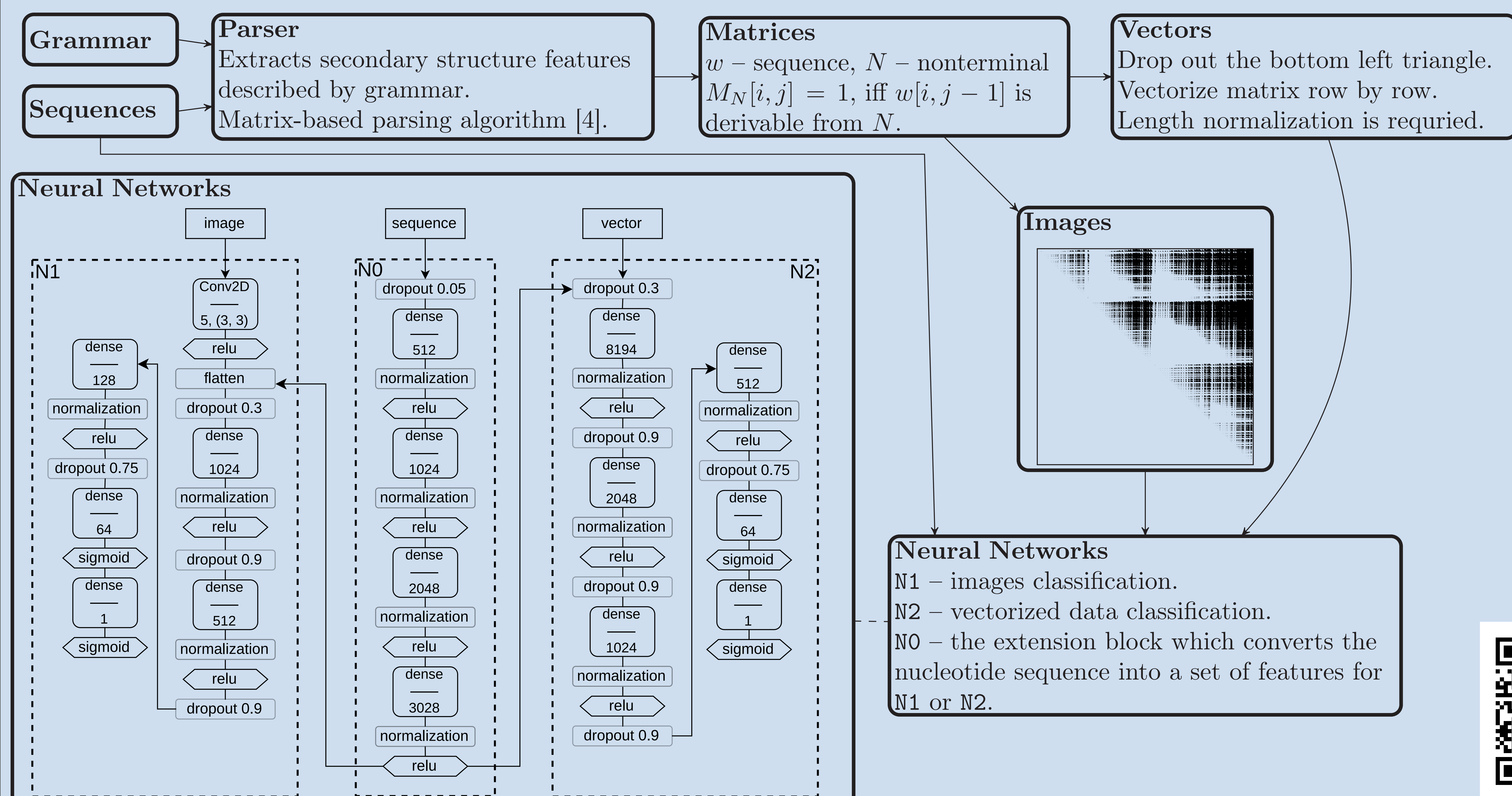
Convolutional networks

Matrices can be treated as bitmaps.

- Images can be easily resized.
- Data locality is preserved.
- We can use convolutional networks.



Solution Overview



Future Research

- 16s rRNA processing and chimeric sequences filtration.
- Proteomic sequences processing, proteins functions prediction.
- Generative networks for sequences secondary structure prediction.

Acknowledgments

The research was supported by the Russian Science Foundation grant 18-11-00100 and a grant from JetBrains Research.

Information

Trained models and other materials are published at GitHub: <https://github.com/LuninaPolina/SecondaryStructureAnalyzer>.

References

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