



# Формальные грамматики и искусственные нейронные сети для анализа вторичной структуры

Семестровый проект на осень 2019

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Санкт-Петербургский государственный университет  
Математико-механический факультет

14 сентября 2019г.

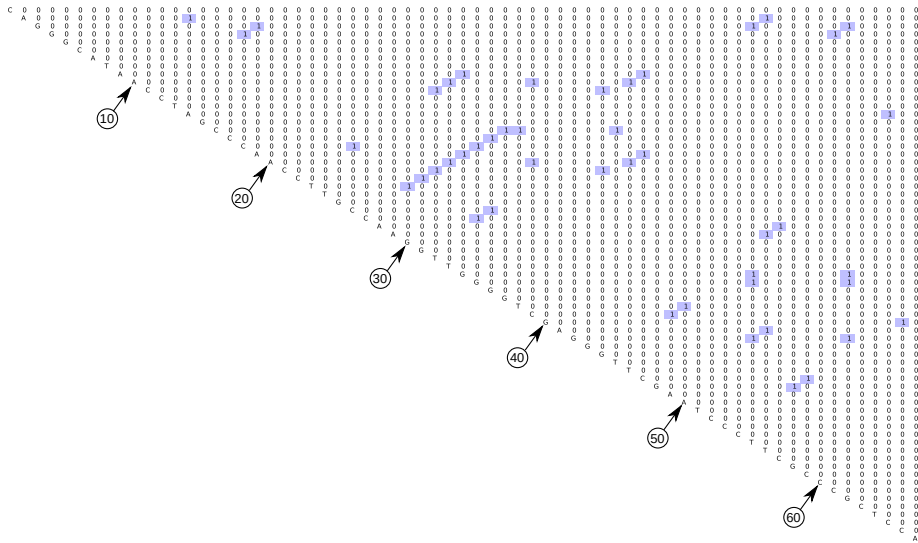
- Исследовательская группа на Математико-Механическом факультете СПбГУ
- Исследовательская группа в лаборатории языковых инструментов JetBrains Research
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  - ▶ semyon.grigorev@jetbrains.com
  - ▶ <https://research.jetbrains.org/researchers/gsv>

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- Сферы интересов
  - ▶ Теория формальных языков
  - ▶ **Применение теории формальных языков для решения прикладных задач**

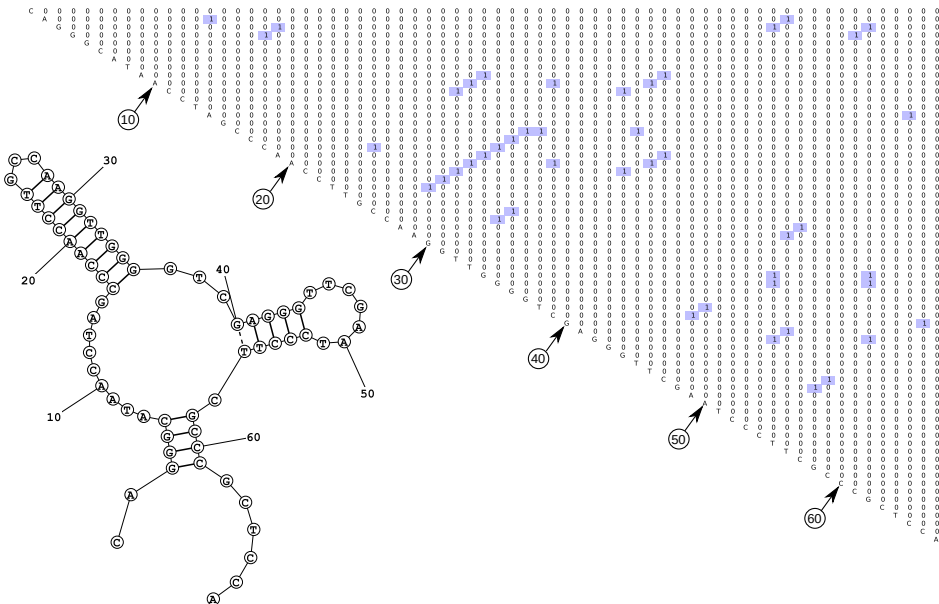
# Анализ вторичной структуры: синтаксический анализ + искусственные нейронные сети

- Формальная грамматика — способ описать особенности вторичной структуры
  - ▶ А не смоделировать структуру всей цепочки
  - ▶ Используем обыкновенные грамматики, а не вероятностные
- Синтаксический анализ — способ извлечь особенности вторичной структуры
- Искусственная нейронная сеть — вероятностная модель для обработки извлечённых особенностей

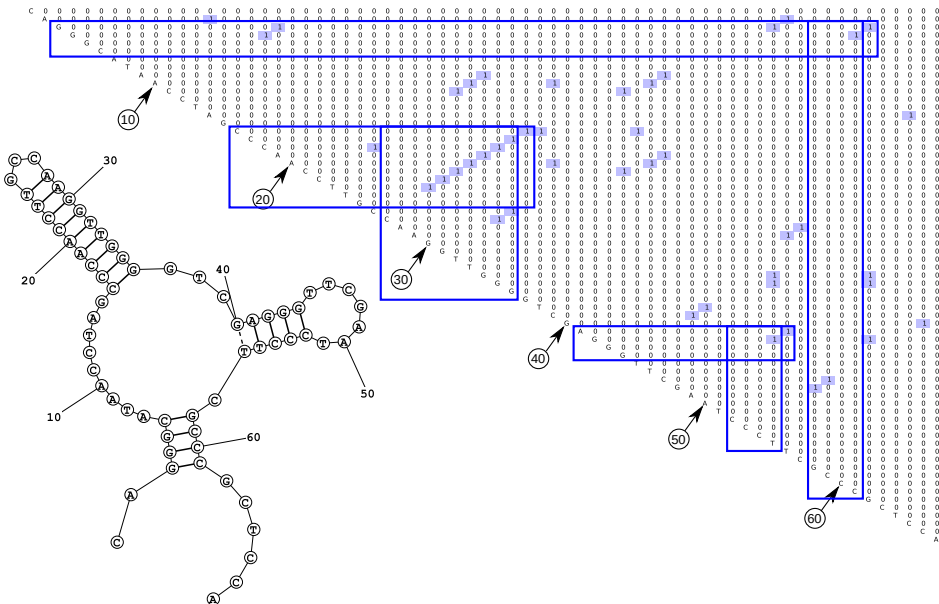
# Example 3: real tRNA



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- Подготовка данных для обучения нейронных сетей
  - ▶ Поиск и анализ баз РНК-цепочек
  - ▶ Подготовка набора данных для обучения: фильтрация, сбор метаданных, приведение к общему формату



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  - ▶ Подготовка набора данных для обучения: фильтрация, сбор метаданных, приведение к общему формату
- Подготовка инструментария для анализа вторичной структуры
  - ▶ Анализ и сравнение существующих инструментов предсказания вторичной структуры РНК последовательностей
  - ▶ Выбор лучшего и его интеграция в процесс обучения нейронных сетей

# Требования к кандидатам

- Знание Python (потребуется для автоматизации процесса)
- Знание C/C++ и сопутствующего инструментария (потребуется при работе с инструментами)

- Создание и обучение моделей для различных задач: предсказание вторичной структуры, классификация, фильтрация химер
- Применить аналогичный подход к белковым цепочкам
- Курсовая/диплом/публикация

```
s1: stem<s0>
any_str: any_smb*[2..10]
any_smb: A | T | C | G
stem1<s>:          \\ stem of height exactly 1
             A s T | T s A | C s G | G s C
stem3<s>:          \\ stem of height exactly 3
             stem1< stem1< stem1<s> > >
stem<s>:           \\ stem of height 3 or more
             A stem<s> T
             | T stem<s> A
             | C stem<s> G
             | G stem<s> C
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    | C stem<s> G
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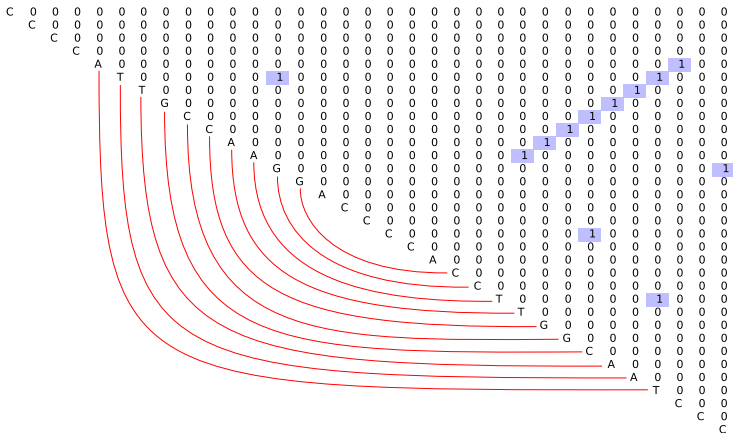


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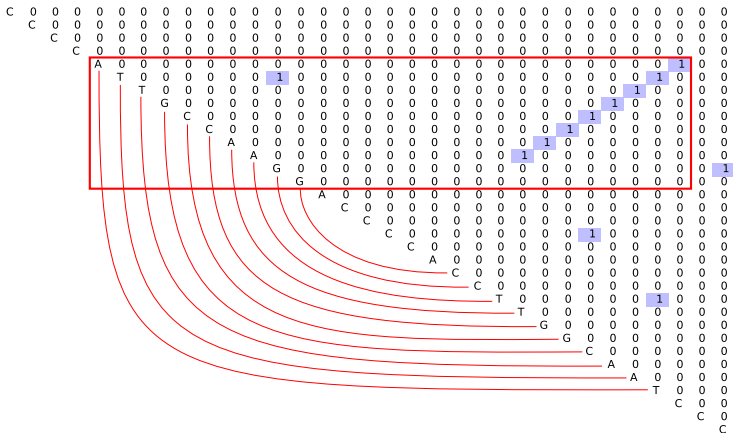
# Пример 1: Stem

CCCCATTGCCAAGGACCCACCTTGGCAATCCC



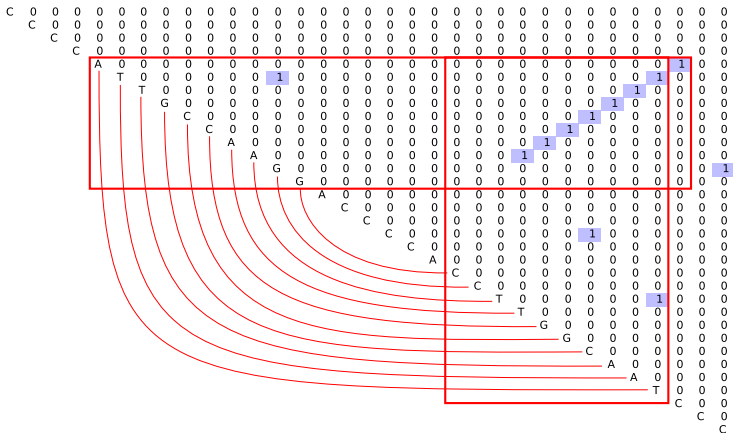
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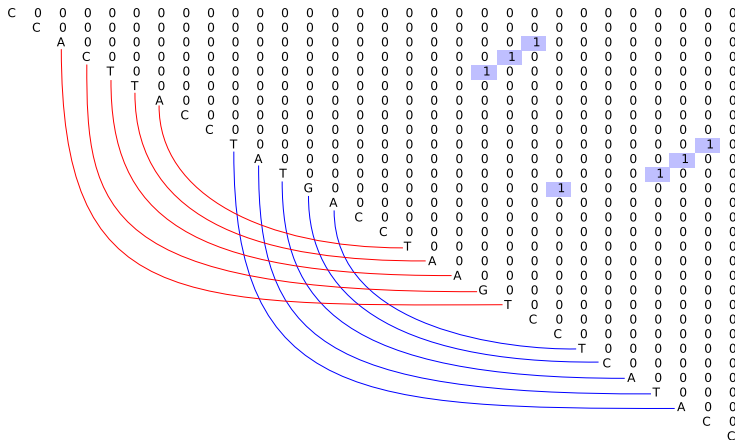
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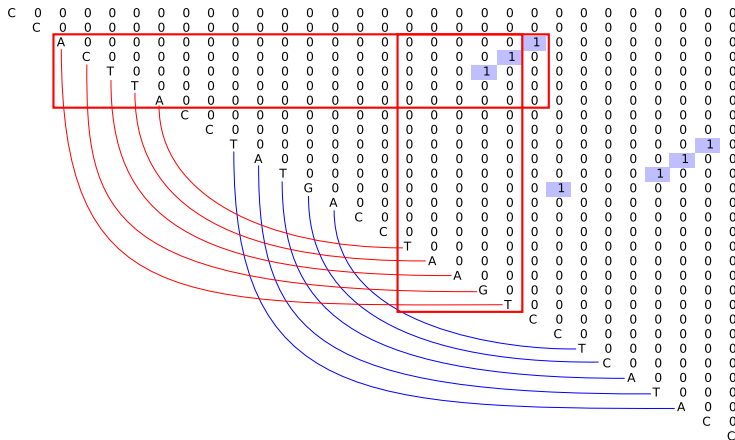
## Пример 2: псевдоузел

CCACTTACCCTATGACCCTAAGTCCATACCT



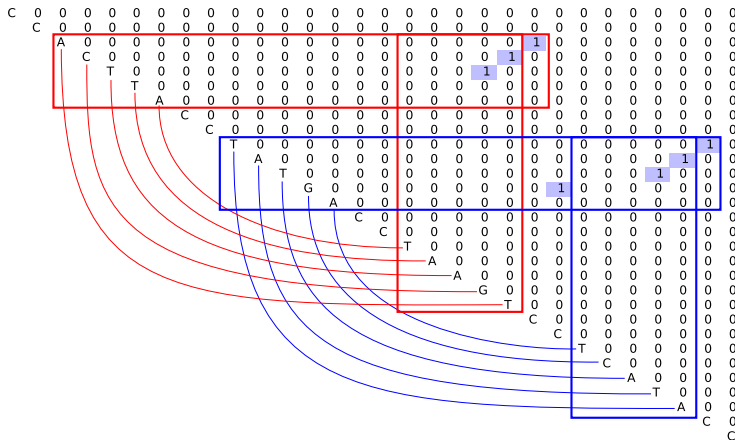
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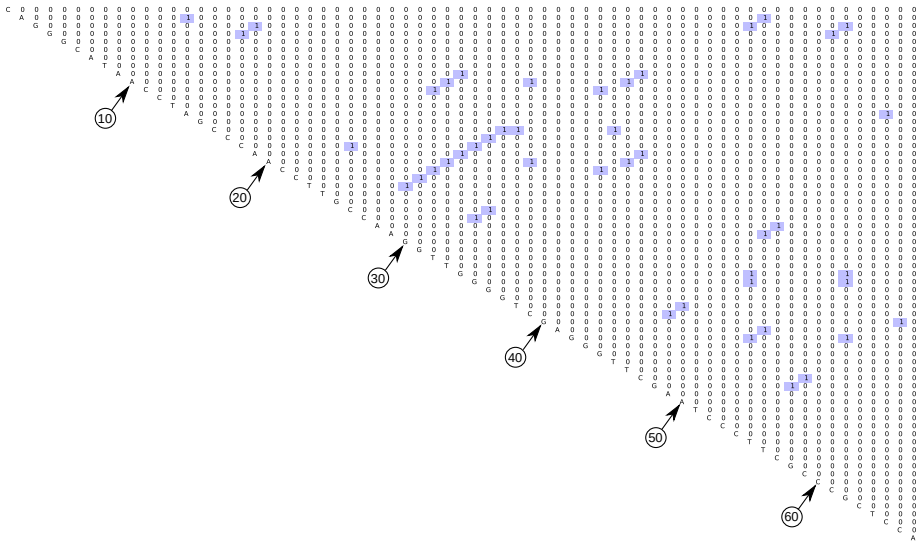


## Example 3: real tRNA

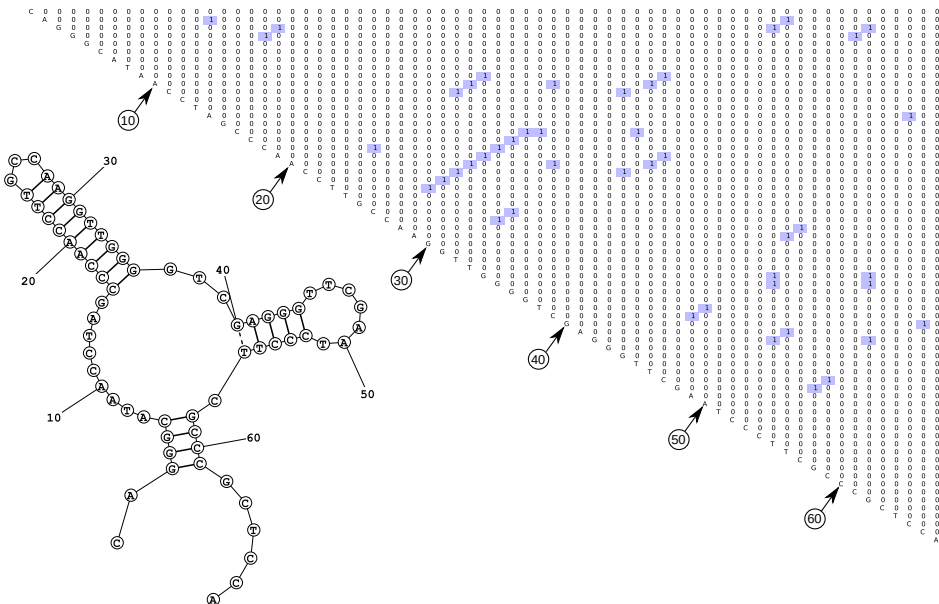
CAGGGCATAACCTAGCCCAACCTTGCCAAGG  
TTGGGGTCGAGGGTTCGAATCCCTTCGCCCCTCCA

- *Novosphingobium aromaticivorans* DSM 12444  
chr.trna57-GlyGCC(268150-268084) Gly (GCC) 67 bp Sc: 22.9, from  
GtRNAb
- Predicted secondary structures are given by using the Fold Web Server  
with default settings

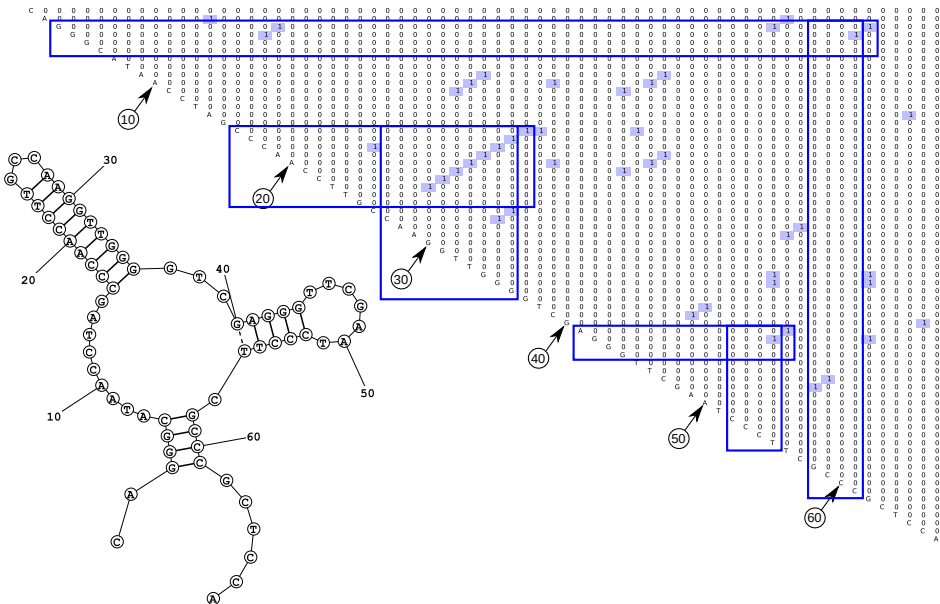
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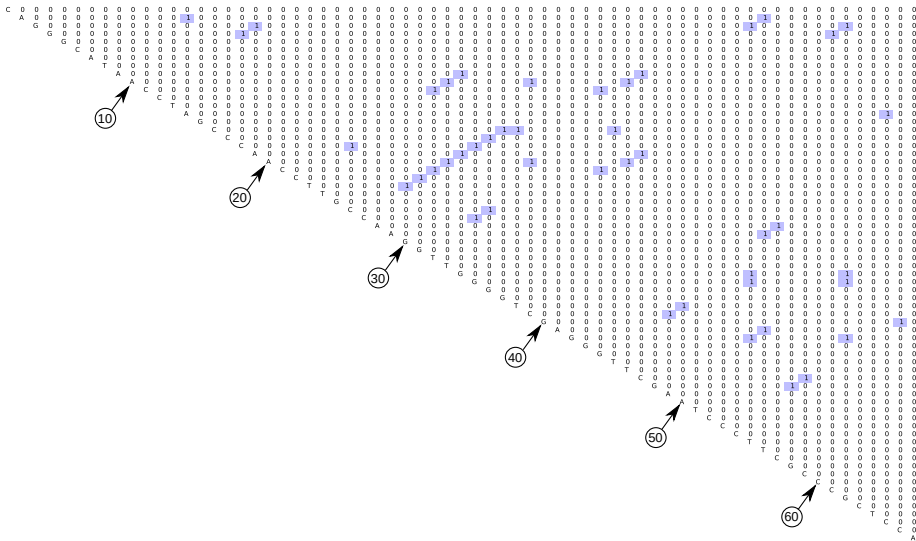
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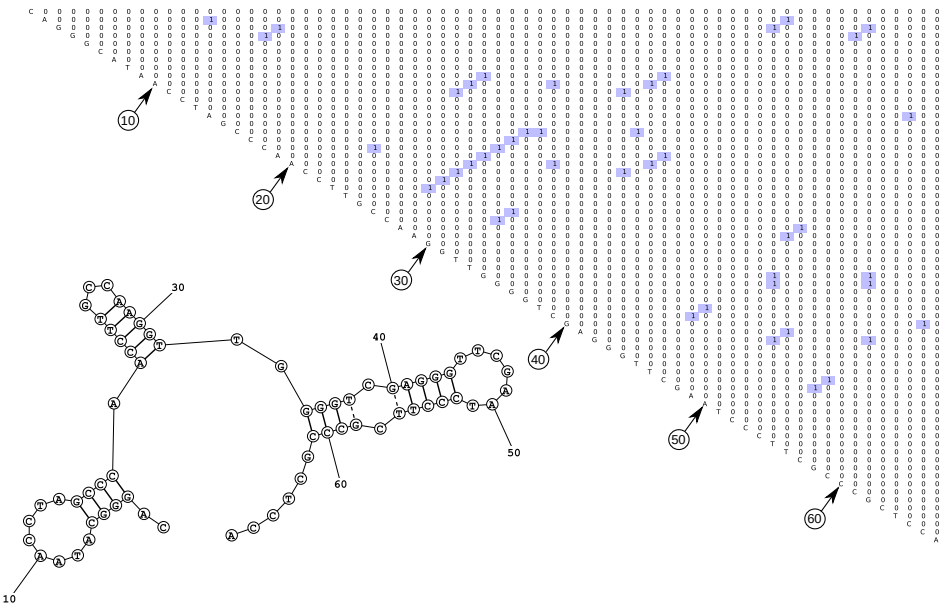
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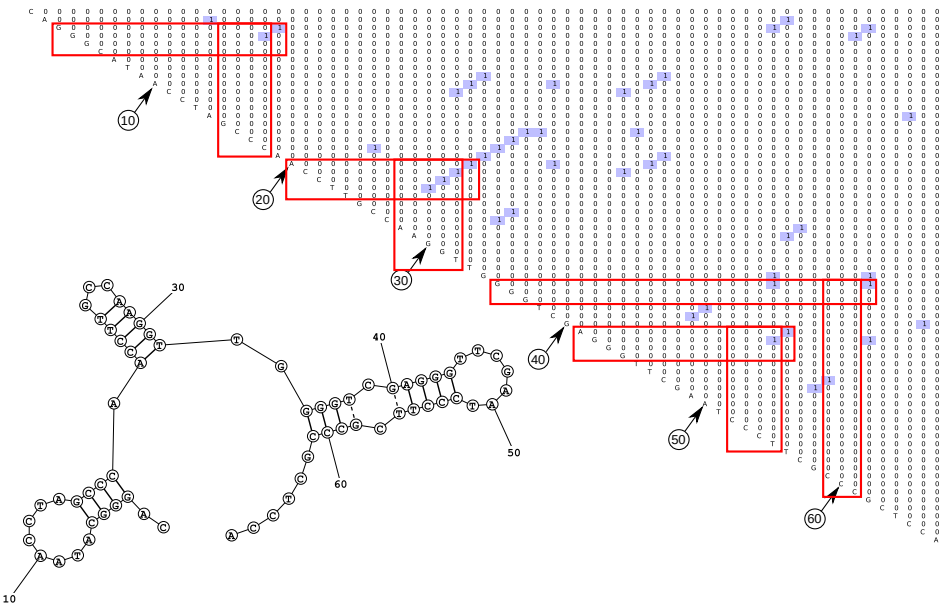
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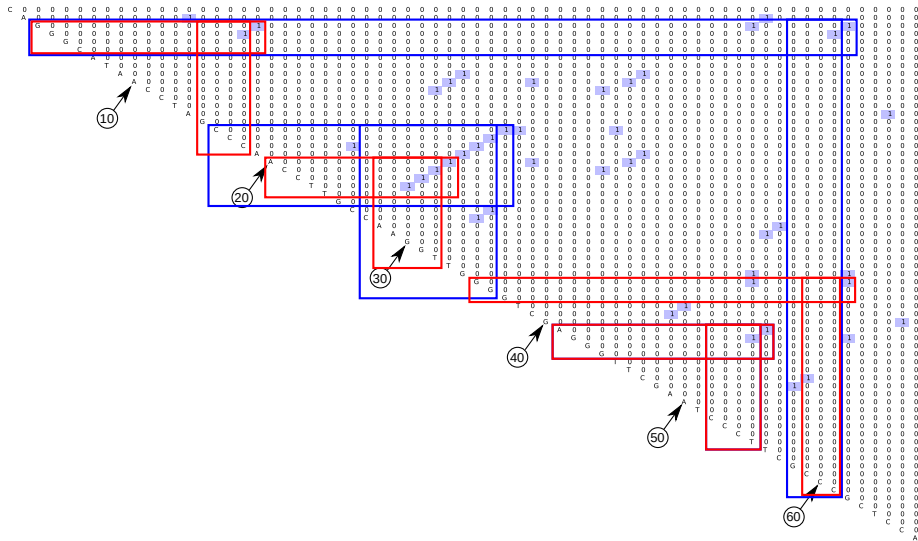
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# Solution Structure

## Grammar

Fixed formal grammar (not necessarily context-free) describes features of secondary structure and can be tuned to increase the quality of result.

## Sequences

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## Result of classification

## Parser

Parser extracts features of the given sequence secondary structure. Implementation of parsing algorithm is based on matrix multiplications (Valiant, Okhotin) and utilizes GPGPU.

## Neural Network

Dense neural network with more than 10 dense layers. Aggressive dropout and batch normalization for learning process stabilization. Typical building block:

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## Matrices

$$\begin{pmatrix} 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

Parsing result is (0-1) matrix  $M$  which represents secondary structure features for sequence  $\omega$ :

$$M[i, j] = 1 \iff s1 \xrightarrow{*} \omega[i, j], \text{ and } 0 \text{ otherwise.}$$

## Vectors

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