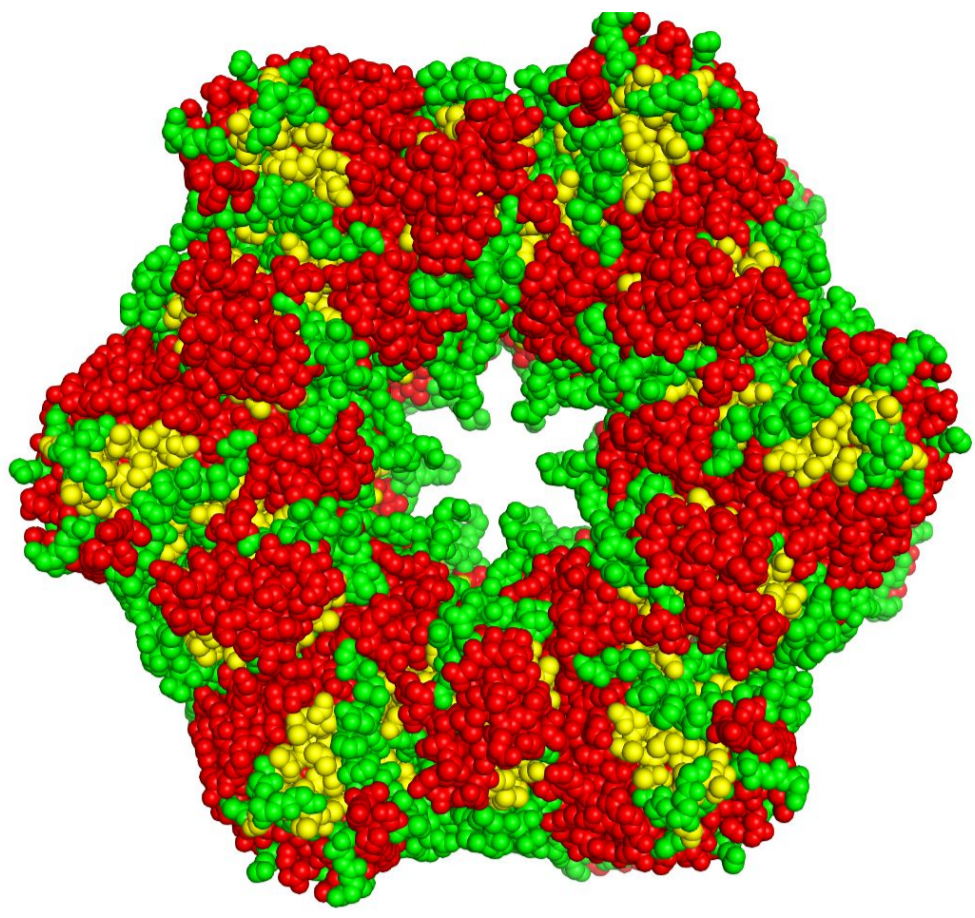
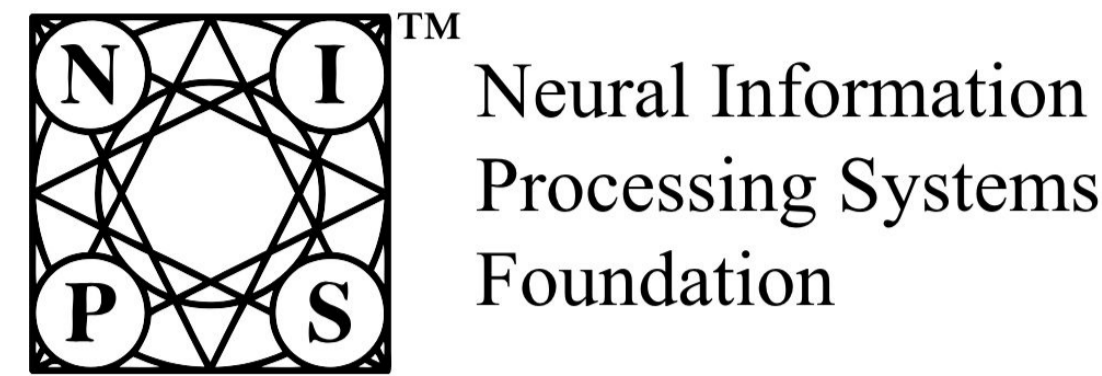
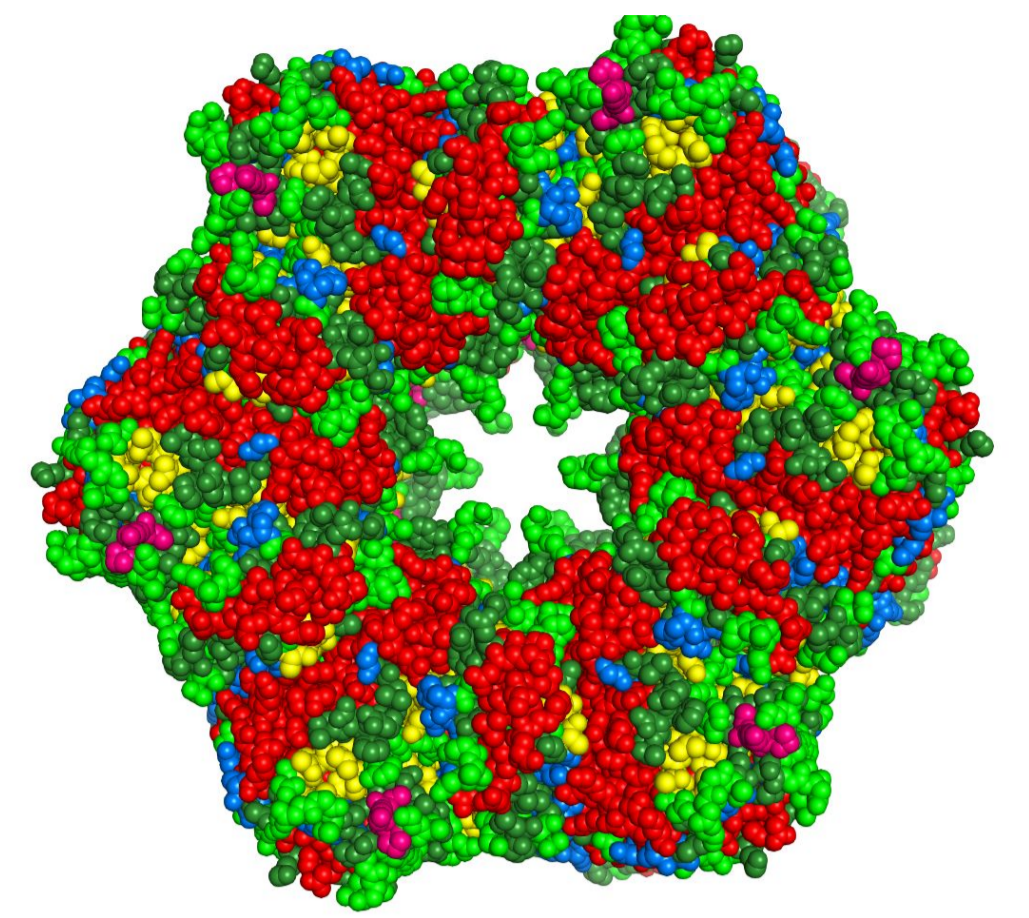


High Quality Protein Q8 Secondary Structure Prediction by Diverse Neural Network Architectures

Iddo Drori, Isht Dwivedi, Pranav Shrestha, Jeffrey Wan, Yueqi Wang, Yunchu He, Anthony Mazza, Hugh Krogh-Freeman, Dimitri Leggas, Kendal Sandridge, Linyong Nan, Kaveri Thakoor, Chinmay Joshi, Sonam Goenka, Chen Keasar, Itsik Pe'er



Q3 of 1F52

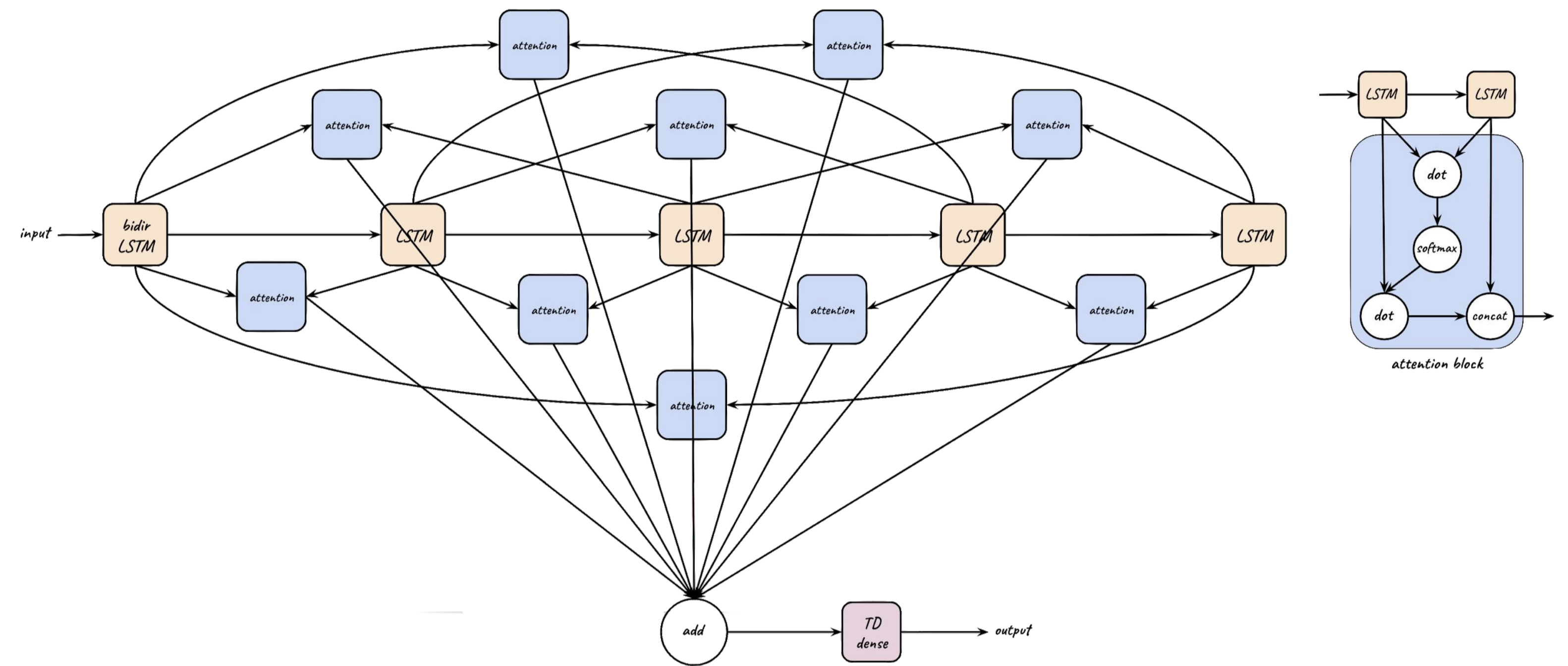


Q8 of 1F52

Data, Models, and Code: github.com/idrori/cu-ssp

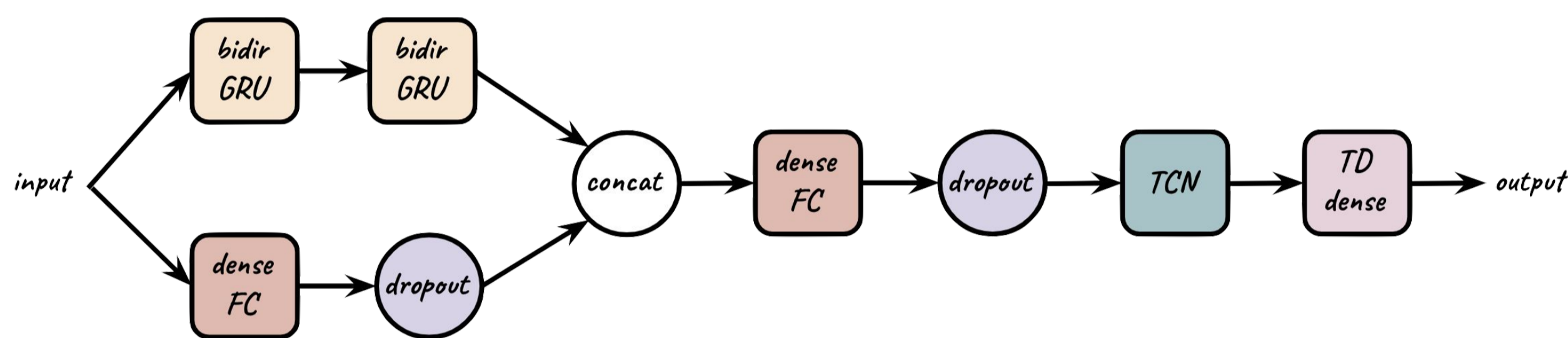
Diverse Neural Network Architectures

Ensemble	70.7
Bidirectional GRU with convolution blocks	69.8
U-Net with convolution blocks	69.2
Temporal convolutional network	68.7
Bidirectional LSTMs with attention	68.4
Convolutions and bidirectional LSTM	67.8
Bidirectional GRUs	67.4

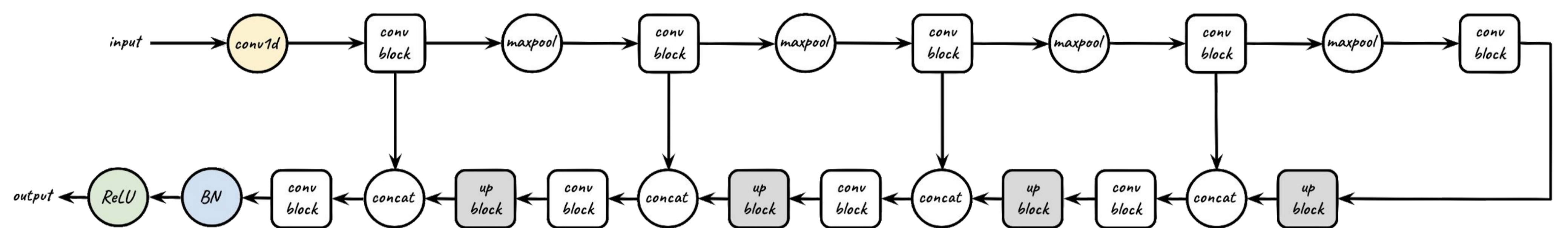
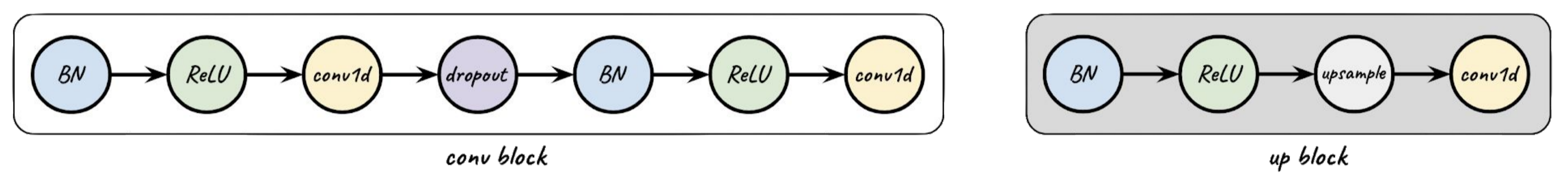


Bidirectional LSTM with attention

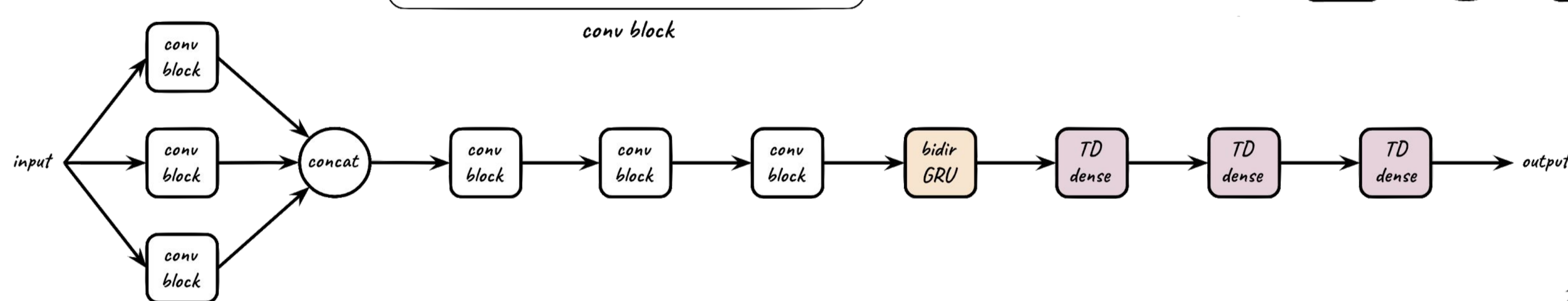
Q8 mean accuracy of our models and their ensemble on CB513



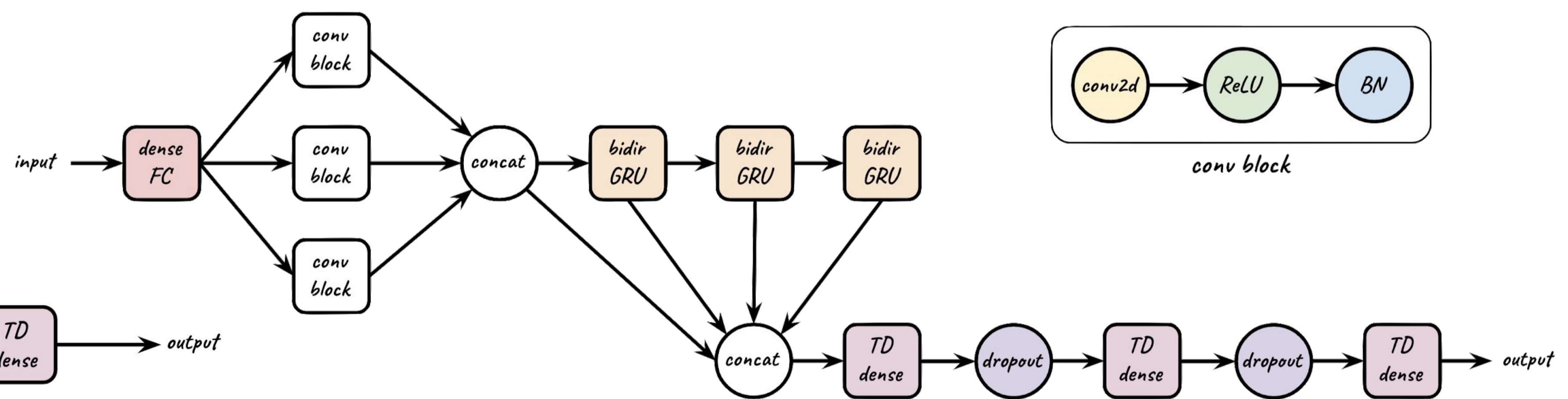
Temporal Convolutional Network



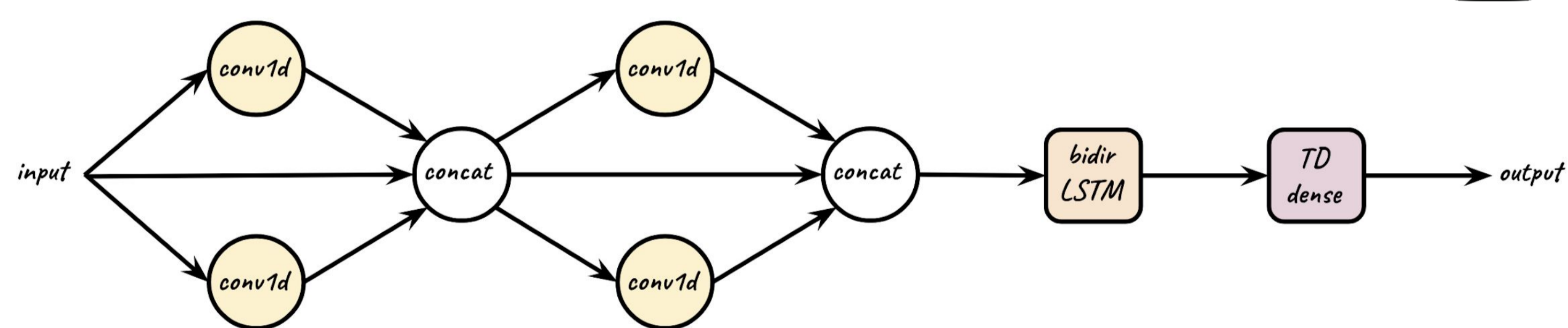
U-Net with convolution blocks



Bidirectional GRU with convolution blocks



Bidirectional GRUs



Convolution and bidirectional LSTM

Results

Models on CB513	Best Single	Ensemble
MUFOLD-SS [11]	70.5	70.6
NCCNN [3]	70.3	71.4
biRNN-CRF [17]	69.4	70.9
DeepMSCNN [2]	70.0	70.6
DCRNN [21]	69.4	69.7
BLSTM [28]	67.4	N/A
GSN [40]	66.4	N/A
DeepCNF [33]	N/A	68.3
Ours	69.8	70.7

Models on CB6133	Best Single	Ensemble
GSN [40]	72.1	N/A
DCRNN [21]	N/A	73.2
biRNN-CRF [17]	73.4	74.8
CRRNN [38]	N/A	74
Ours	75.4	76.3

	L	B	E	G	I	H	S	T
L	11,828	618	1,880	629	4	738	3,192	1,619
B	7	31	6	0	0	3	4	0
E	3,167	316	15,419	234	2	334	997	565
G	134	8	24	851	0	233	109	328
I	0	0	0	0	0	0	0	0
H	762	77	216	777	22	24,126	554	1,585
S	871	49	201	78	0	77	2,039	502
T	1,151	82	270	563	2	646	1,421	5,414

Confusion matrix for each of the Q8 structures on CB513 dataset

Acknowledgements

We thank the 100 Columbia University graduate students of the Fall 2018 Deep Learning course for participation in in-class protein secondary structure prediction competition.