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There have been a number of related attempts to address the general sequence to sequence learning problem with neural networks. Our approach is closely related to Kalchbrenner and Blunsom [18] who were the first to map the entire input sentence to vector, and is very similar to Cho et al. [5].

Sequence to Sequence Learning with Neural Networks

Sequence to Sequence Learning with Neural Networks Ilya Sutskever Google ilyasu@google.com Oriol Vinyals Google vinyals@google.com ... In this paper, we present a general end-to-end approach to sequence ... model stops making predictions after outputting the end-of-sentence token. Note that the LSTM reads the

Sequence to Sequence Learning with Neural Networks

We present Model-based Analysis of ChIP-Seq data, MACS, which analyzes data generated by short read sequencers such as Solexa's Genome Analyzer. MACS empirically models the shift size of ChIP-Seq tags, and uses it to improve the spatial resolution of predicted binding sites. MACS also uses a dynamic ...

Model-based Analysis of ChIP-Seq (MACS)

We derived the transcriptome profiles from a real RNA-seq dataset with widespread splicing changes (E-MTAB-1147; knockdown of splicing factor HNRNPC in the HeLa cell line) and plugged them into ...

Deep-learning augmented RNA-seq analysis of transcript ...

Model and normalization. The starting point of a DESeq2 analysis is a count matrix K with one row for each gene i and one column for each sample j . The matrix entries K_{ij} indicate the number of sequencing reads that have been unambiguously mapped to a gene in a sample. Note that although we refer in this paper to counts of reads in genes, the methods presented here can be applied as well to ...

Moderated estimation of fold change and dispersion for RNA ...

We present Model-based Analysis of ChIP-Seq data, MACS, which analyzes data generated by short read sequencers such as Solexa's Genome Analyzer. MACS empirically models the shift size of ChIP-Seq tags, and uses it to improve the spatial resolution of predicted binding sites. MACS also uses a dynamic Poisson distribution to effectively capture local biases in the genome, allowing for more ...

Model-based Analysis of ChIP-Seq (MACS) - Genome Biology

MACS website by Tao Liu. Model-based Analysis for ChIP-Seq About. Next generation parallel sequencing technologies made chromatin immunoprecipitation followed by sequencing (ChIP-Seq) a popular strategy to study genome-wide protein-DNA interactions, while creating challenges for analysis algorithms.

MACS - Model-based Analysis for ChIP-Seq

All of the results in the paper can be replicated in at most 1 hour on a single Cloud TPU, or a few

hours on a GPU, starting from the exact same pre-trained model. SQuAD, for example, can be trained in around 30 minutes on a single Cloud TPU to achieve a Dev F1 score of 91.0%, which is the single system state-of-the-art.

GitHub - google-research/bert: TensorFlow code and pre ...

Estimation of Sequential Search Model Jae Hyen Chung Pradeep Chintagunta Sanjog Misra July 27, 2018 Abstract In this paper, we propose a new likelihood based estimation method for the sequential search

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