自动生物实体关系抽取技术对于构建生物领域知识库，知识图谱，提高搜索引擎检索效率具有重要意义。通过总结现有工作，本文由浅入深，从三个方面进行自动实体关系抽取。

1. 基于规则的关系抽取。在句子句法分析和依存分析的基础上，通过观察动词和介词在生物实体关系中的重要作用，本文首先构建了一个相互作用词词表，然后制定了两条通用的策略来判断一对实体之间是否存在关系。同其他基于规则的关系抽取系统相比较，本文提出的基于规则的系统在LLL-challenge数据集上取得了第二好的效果。
2. 基于核函数的机器学习算法的关系抽取。在句子依存分析基础上，可以发现，实体对在依存分析中的最短路径一般包含足够的信息去判断这对实体是否存在关系，本文在最短依存路径的基础上，提出了一种编辑距离核函数和余弦核函数相结合的核函数。该混合核函数能充分抓住数据的结构信息以及单词层面的信息。实验结果表明，同其他基于核函数的系统相比，本文提出的方法在BioInfer标准数据集上取得了最优的结果。
3. 基于神经网络的关系抽取。为了避免特征工程，缓解生物关系抽取领域数据稀少问题。本文结合词向量以及神经网络结构，提出了一个用于实体关系抽取的框架。在CNN和RNN这两种结构下，本文提出了multi-CNN以及单通道RNN两个模型，实验结果表明，提出的模型在DDIExtarction，Aimed以及BioInfer数据集上都取得了最优结果。

进一步，在实际应用方面，本文将基于规则的关系抽取系统应用到了同“breast cancer”的相关文献上，通过分析抽取到的关系，可以构建出同乳腺癌相关的基因关系图，通过图的分析算法，可以找出同乳腺癌最相关的基因。

Automatic biological entity relation extraction technology is of great significance to construct the knowledge database, knowledge graph and further improve the efficiency of search engine retrieval in the field of biological. By summarizing the existing work, this paper introduce the entity relation extraction technology from three aspects as follow：

Rule-based relation extraction. On the basis of sentence syntax analysis and dependency analysis, by observing the important role of verbs and prepositions in biological relation extraction, this paper first constructs an interactive word list, and then develops two general strategies to judge whether there is a relationship between a pair of entities. Compared with other rule-based relational extraction systems, the method proposed in this paper achieves the second best performance on the LLL-challenge task.

Kernel-based relation extraction. Based on sentence dependency analysis, we can observe that the shortest dependency path between two entities generally contains enough information to judge whether there is a relationship between two entities, on the basis of this observation, in this paper, we propose a kernel function that combines the edit distance kernel and cosine kernel, the proposed hybrid kernel function can fully grasp the structure of the data structure and word level information. The experimental results show that compared with other kernel function-based systems, the proposed method achieves the best results on the BioInfer standard data set.

Neural network-based relation extraction. To avoid data sparseness and feature engineering problems in traditional relation extraction systems, by integrating convolutional neural network (CNN) and recurrent neural network (RNN), in this paper, we propose two models for biological relation extraction: multi-CNN and single-channel RNN. The experimental results show that the proposed models achieve the best results on DDIExtraction, Aimed and BioInfer data sets.