虽然人工生命(AL)领域与人工智能(AI)领域的确有明显的重叠区，但他们有截然不同的初衷和演生史。以研究是否以及如何实现模拟智能的人工智能研究，早在计算机诞生后的初期就已经兴起，然而以试图澄清emergent behaviors的本质的人工生命的研究者们，可以说一直不知其他人在做类似的工作而孤军作战，直到80年代末，这个领域才正式的诞生，在2010年之后才逐渐兴起研究热潮。

While there is a clear overlap between the research field of artificial life (AL) and artificial intelligence (AI), but they have very different Intentions and Evolutionary histories actually. The research of Artificial intelligence is about how to achieve analog intelligence has been rise since the early days of computer Technology history. But the artificial life research about trying to clarify the nature of artificial life, the emergent behaviors, it can be said, that no one else is doing similar work and alone until the late 1980s, the AL research field was officially born, and began growing from year 2010.

理论上，只要我们能够设计一个足够复杂，包含有相对完善的反馈回环的网络模型，然后对这个网络模型进行模拟运行之后，emergent behaviors将会诞生于这个网络模型之中，我们也就成功的让一个人工的生命系统诞生在这个世界上了。GCModeller项目的诞生就是为了帮助人们更加方便的进行这种复杂的生命系统网络的设计。

Theoretically, as long as we can design a network model that it is complex enough to contains a relatively complete feedback loops, and then we run the simulation of this network model, the emergent behaviors will Appear in this complex network model. Which means we have succeeded bring an artificial life system born in our world. The GCModeller project was created to help people design this complex network of artificial life systems more easily.

在目前的如何进行生命系统设计的探索工作中，我们目前存在着两种方向的工作来完成一个生命系统的改造设计： 正向工程以及逆向工程。

In the exploration of how to carry out the design of artificial life system, we currently have two directions of work to finish an artificial life system transformation design: forward engineering and reverse engineering.

在合成生物学领域内，一份基因组的完整的全长DNA序列是我们进行生命系统设计的目标产物，所需要的生物学性状都被编码为DNA序列存放于基因组之中，从而编译成为了一份生命系统应用程序。对于这个生命系统的存储数据DNA序列的合成设计分析工作中，存在有：

In the field of synthetic biology, a full-length DNA sequence of a genome is the target product of our artificial life system design work, and the desired biological phenotype are encoded as DNA sequences stored in the designed genome, thus compiling into an artificial life system application. For the synthetic design analysis of the DNA sequence in artificial life system, we could:

1. 正向工程指的是通过CAD软件平台，基于我们所需要的目标，向细胞模型容器之中填充产生所需要的生物学性状特性所需要的蛋白组件，最终在这些填充的蛋白质组件的基础上,完成模拟， 并达到我们的预期之后，对这些蛋白组件逆向生成对应的基因组序列，再将调控关系填充在基因序列之间来完成目标全基因组DNA序列的生成。

1. Forward engineering refers to Fill the cellular model container with protein components needed to produce the required biological phenotype through the CAD AL design software platform, based on the objectives we expected. And then run the simulation of this filled cellular model. After we have achieved our expectations, then these protein components reverse-generated to their corresponding genome sequences including their expression regulatory components to finish the generation of a complete whole genome DNA sequence.

2. 逆向工程是我们目前用于研究分析目标基因组的一种非常常用的方法，通过逆向工程，我们对目标基因组进行蛋白质组件的功能注释操作，然后在这些完成注释的蛋白质组件的基础上构建出一幅生物学功能的蓝图，在这份蓝图的基础上进行突变体的组学分析，从而来了解变化的产生原因以及变化所带来的影响。

2. Reverse engineering is a very common method we currently use to study and analyze the target genome. Through reverse engineering, we perform functional annotation of protein components in the target genome, and then build a blueprint (which is so called pathway) for biological functions based on these annotated protein components. Based on this blueprint, High throughput omics technology like genomics, proteomics and metabonomics analysis of mutants is performed to understand the causes of change and the impact of change.

在上面所提到的两个方向上的生命系统设计分析工作之中，GCModeller尝试提供下列的一个完整的工具链：

In the analysis of artificial life system design in these two direction that mentioned above, GCModeller attempts to provide a relative complete CAD tool chain of following:

1. 进行细胞组件的注释方法

2. 在所完成的细胞组件注释结果基础之上，装配出一个完整的细胞数据模型

3. 提供一个对完成注释的细胞模型的模拟计算的环境

4. 提供一个进行存储整个模拟过程数据的存储程序

5. 提供一系列组学分析工具可以使用户可以通过对所保存的数据进行分析来明确自己的设计是否有效

6. 将目标设计所得到的细胞模型导出为一个完整的染色体DNA序列，用于全长DNA的人工合成或者野生型突变实验设计

1. Annotation protocols for the cell components

2. Assemble a complete cell data model based on the results of the cell component annotation results

3. Provide an environment for simulated calculations of the annotated cell model

4. Provide a storage program for storing data for the entire simulation process

5. Providing an analysis tools allows users to determine whether their design is effective by analyzing the saved simulation data.

6. Export the cell model from the target design into a complete chromosomal full-length DNA sequence for synthetic or wild mutation experimental design