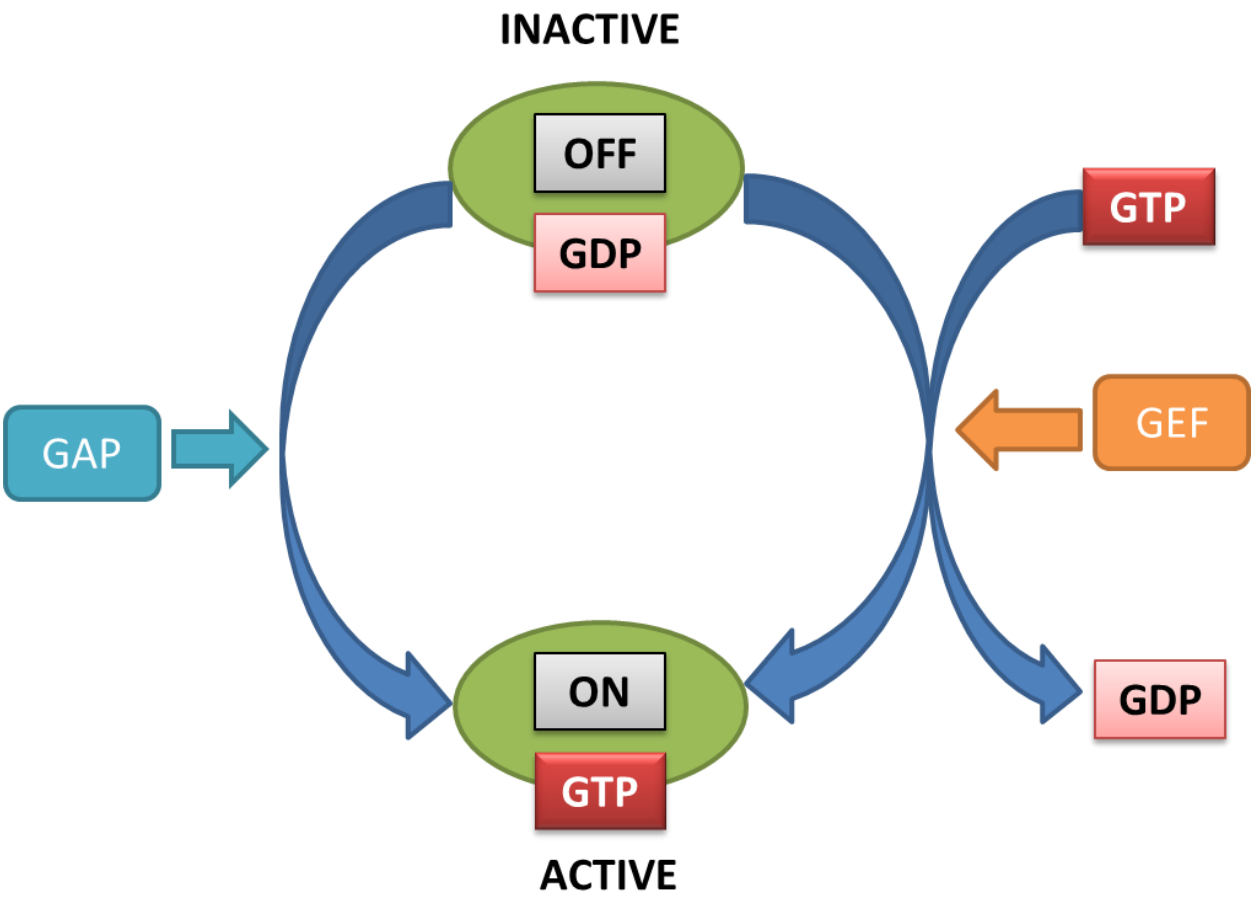
Introduction

Transport proteins are proteins interacted in cell membrane to bind and carry atoms and small molecules within cells and throughout the body. There are many different kinds of transport proteins, they are critical to the growth and life of all living organisms. Membrane trafficking is the important process in transport protein, in which proteins and other macromolecules are transferred to various destinations inside and outside of the cell. This process uses membrane-bound vesicles and vesicular transporters as mediates transport to establish the absorption of molecules within a vesicle.

To implement membrane trafficking, G-proteins are activated to be recruited to membrane vesicles by interacting with specific effector proteins. This below figure shows the process of G-protein in membrane trafficking. As shown in this figure, G-protein operates as a molecular switch between GDP-bound inactive state and GTP-bound active state. These two states are controlled by guanine nucleotide exchange factors (GEFs) and GTPase activating proteins (GAPs). If G-protein binds GTP, it will be activated and involved in membrane trafficking. A number of studies determined that a functional loss of GTP binding sites in membrane trafficking has been implicated in a variety of human diseases (i.e., neurodegenerative, cancer, Parkinson [1-4] … So there is a need to develop techniques such as computational techniques for identifying GTP binding sites in membrane trafficking (especially in vesicular transport protein).



The current study proposes an approach based on PSSM profiles and SAAPs for identifying GTP binding sites in transport proteins. We applied the independent data set to evaluate the performance of the proposed method, which demonstrated an accuracy of 98.7%. Compared with the general GTP binding predictor developed by the others, the proposed method exhibited a higher improvement in accuracy and Matthew's correlation coefficient (MCC). The proposed method also increases the number of true positives significantly and offers useful information for biologists. This study can serve as an effective tool for predicting GTP binding sites in transport proteins and can help biologists understand transport proteins function, particularly those of GTP binding sites.