

(For JSPS Fellow)

Form B-5

Date (日付)

01/02/2016

(Date/Month/Year: 日/月/年)

**Activity Report -Science Dialogue Program-**

(サイエンス・ダイアログ事業 実施報告書)

- Fellow's name (講師氏名): TAMBI RICHA (ID No. P15080)

- Participating school (学校名): Yamanashi Prefectural Tsuru High School

- Date (実施日時): 29/01/2016  
(Date/Month/Year: 日/月/年)

- Lecture title (講演題目): (in English) Proteins on computers: Analyzing protein structures using bioinformatics tools

(in Japanese)

コンピュータ上のタンパク質: バイオインフォマティクスツールを使用したの分析タンパク質構造

- Lecture summary (講演概要): Please summary your lecture 200-500 words.

**Proteins are one of the most important biological molecules. Misfolding diseases may occur if a protein fails to attain its proper three-dimensional(3D) structure. Researchers are performing both wet lab and in silico experiments on proteins to gain more and more insight about its structure and function. In this lecture I tried to give an overview of protein bioinformatics. I explained different computational methods that can be used to study the 3D structure of protein. My talk was divided into four sections as described herein. In section 1 [10 min] I introduced myself and give an overview of my country. In section 2 [10 min] I defined bioinformatics and also discussed its applications. I started with the description of proteins in section 3 [30 min]. I explained the importance of proteins as food source and their multi-fold use in human body. Furthermore, I also discussed the structural hierarchy of proteins. I then connected proteins with bioinformatics and introduced students to the basic bioinformatics databases and algorithms used for sequence and structural analysis of proteins. I demonstrated how one can use NCBI (National Center for Biotechnology Information: <http://www.ncbi.nlm.nih.gov/>) and PDB (Protein Data Bank: <http://www.rcsb.org/>) databases and do BLAST (Basic Local Alignment Search Tool: <http://blast.ncbi.nlm.nih.gov/Blast.cgi>) for finding similar protein sequences. Finally, in section 4 [20 min] I briefly discussed my current research work. I am developing algorithm using machine learning tool to analyze the structure of proteins. I explained**

how proteins can be defined in terms of feature such as hydrophobicity, amino acid composition and so on. Moreover, the ways in which these features can be used for classifying the structural regions (ex. domains) of proteins were also described. I concluded my lecture by telling the students about various new and interesting sub-fields of protein bioinformatics.

- Language used (使用言語): English

- Lecture format (講演形式):

◆Lecture time (講演時間) 70 min + Two 10min break (分), Q&A time (質疑応答時間) 10 min (分)

◆Lecture style (ex.: used projector, conducted experiments)

(講演方法 (例: プロジェクター使用による講演、実験・実習の有無など))

Powerpoint presentation

◆Interpretation (ex.: assistance by accompanied person, provided Japanese explanation by yourself) (通訳 (例: 同行者によるサポート、講師本人による日本語説明))

NONE

◆Name and title of accompanied person (同行者 職・氏名)

NONE

◆Other note worthy information (その他特筆すべき事項):

NONE

- Impressions and opinions from accompanied person (同行者の方から、本事業に対する意見・感想等がありましたら、お願いいたします。):