BIOMOD

2023 Quick Guide

Saturday, November 4th 8:00 – 17:00

Sunday, November 5th 9:00 – 11:30

Tokyo Institute of Technology (Tokyo Tech.)
Ookayama Campus
Multi-Purpose Digital Hall, West Bldg. 9,
2-12-1 Ookayama, Meguro-ku, Tokyo, Japan

Co-organized by

BIOMOD FOUNDATION

molbot

BIOMOD Foundation and the Molecular Robotics Research Group, Japan (CBI Society)

Sponsored by

Molecular Cybernetics

SPRINGER NATURE

Molecular Cybernetics, JSPS Grant-in-Aid for Transformative Research Areas (A) and Springer Nature Applied Sciences

Schedule (all based on JST, Japan Standard Time)

Friday, November 3rd, 2023 from 16:00 to 19:45

- Pre-Team Check-In at Tokyo Tech
- Practice session, 15 minutes per team (by prior arrangement, see page 4)

Saturday, November 4th, 2023

08:00	**Doors Open @ Multi-Purpose Digital Hall,– Please do not arrive earlier than 08:00**
08:00–09:00	**Team Check-In (Breakfast available to all registered participants)** **Connection check by online presenters (Team #1 and #2)**
09:00–09:10	Welcome — Opening Remarks
09:10–09:30	Team #1 — BIOMOD QUERÉTARO **[Online]**
09:30–09:50	Team #2 — Cargo Code-Breakers **[Online]**
09:50–10:10	Team #3 — FUNDNA
10:10–10:30	**Group Photo**
10:30–11:00	**Break**
11:00–11:20	Team #4 —Team NoKo
11:20–11:40	Team #5 — Team SeaSon
11:40–12:00	Team #6 — Team Kansai
12:00–13:30	**Lunch Break**
13:30–13:50	Team #7 — YOKABIO
13:50–14:10	Team #8 — XMU-Bionova
14:10–14:30	Team #9 — Team Sendai
14:30–14:40	**Short Break**
14:40–15:00	Team #10 — Tokyo Alliance
15:00–15:20	Team #11 — USYD UFOLD
15:20–15:40	Team #12 — Nano-JLU
15:40–15:50	**Short Break**
15:50–16:10	Team #13 — Team Tokyo Tech
16:10–16:30	Team #14 — UBC BIOMOD
16:30–16:45	**A word from our sponsor (Springer Nature)**
16:45–16:50	Closing Remarks
17:30–	Banquet @ Tsubame Terrace (New Cafeteria) Tokyo Tech.

Sunday, November 5th, 2023

09:00	**Doors Open @ Multi-Purpose Digital Hall,– Please do not arrive earlier than 09:00**
09:00–10:00	**Breakfast available to all registered participants**
10:00–11:30	**Awards & Closing Ceremony**
(11:30–12:30)	(BIOMOD Mentors & Committee Members Meeting)

Presentation Details

All team presentations will take place in Multi-Purpose Digital Hall, Build. #9 at Tokyo Institute of Technology (Ookayama Campus). *Please note that, with the exception of bottled water, food and drinks are not allowed in the Multi-Purpose Digital Hall at any time.* You may drink and eat outside of the hall (catering area).

The **TOTAL** time allotted to each team is **20 minutes**. This includes laptop setup (**1 min**), present slides (**10 min**), audience questions (**~7 min**), and exiting the stage + buffer time (**2 min**). The time limits will be strictly enforced, so rehearsing in advance is strongly recommended to avoid being cut off. The room is equipped with a projector and screen. *Please remember to bring your PC, laser pointers, converters, adapters, cables, etc., as these will **not** be provided by BIOMOD.* (Please note that each team needs to use your PC and connect to WiFi for your presentation.)

Teams are required to **share screen via Zoom** for the presentation slides. (See page 6 for Wi-Fi information.) A shared screen will be projected in the hall. A camera crew will also live broadcast the presentation on-site.

Zoom Address (Friday-Sunday)
https://kyutech-ac-jp.zoom.us/j/89280454781?pwd=aWGemV0hdbayxeJuSZ0KinTGQcRQ8X.1

Practice Session (Friday)
You may sign up for a practice session at the hall from the form below (first-come, first-serve basis; **for on-site presentation teams**):
https://docs.google.com/spreadsheets/d/1T91MC_Ccp1JtzYUK5gHRyx2xnnUk3Ni-cd6Zls-t4JQ/edit?usp=sharing
Please enter your team name in a desired time slot (please do not edit/move other team's information without permission). Practice sessions are strictly limited to **15 minutes per team**. Thanks in advance for arriving on time, and finishing in the time allotted.

For **online presentation teams**, we will test your connection and screen sharing on **Saturday morning (8:00 JST)**, so please join the Zoom address above.

Registration/Check-in

All teams are required to check-in for BIOMOD on Friday, Nov. 3 or Sat. Nov. 4. The presentation practice session (see above) also secures your check-in time on Friday. Checking in on Friday is preferred; please come and check in by all members of the team at the time specified in the practice slot spreadsheet.

Getting to BIOMOD

Location: Tokyo Institute of Technology (Tokyo Tech)
Ookayama Campus
West Bldg. 9, Multi-Purpose Digital Hall

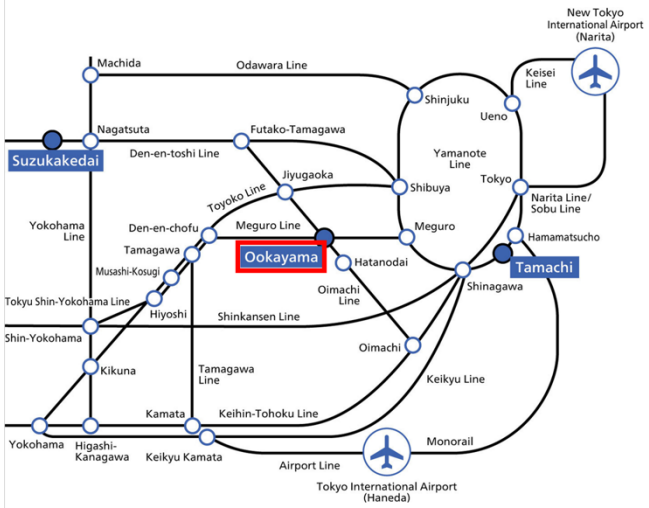
Address: 2-12-1 Ookayama, Meguro-ku, Tokyo 152-8550 Japan

Google Maps: https://maps.app.goo.gl/moy2P3aSZatzkRht6

Transportation to Tokyo Tech

Tokyo Tech (Ookayama campus) is located in the downtown Tokyo area. You may take Tokyu Meguro Line or Tokyu Ooimachi Line and get off at Ookayama Station. The main gate of the university is right in front of the station.
https://www.titech.ac.jp/english/0/maps
https://www.titech.ac.jp/english/0/maps/ookayama

Google Maps' Transit function is quite reliable in the downtown Tokyo area. You may find the fastest route from your hotel to the campus. (There are multiple subway and train corporations in Tokyo, so using such Apps is highly recommended.)



Required time from major stations (lines used are for reference only)
Tokyo: 35 minutes (JR Keihin Tohoku Line → Tokyu Oimachi Line)
Shibuya: 20 minutes (Tokyu Toyoko Line → Tokyu Oimachi Line)
Shinagawa: 20 minutes (JR Keihin Tohoku Line → Tokyu Oimachi Line)
Shin-Yokohama: 25 minutes (Tokyu Shin-Yokohama Line → Tokyu Meguro Line)
Narita Airport: 90 minutes (Skyliner → JR Yamanote Line → Tokyu Meguro Line)
Haneda Airport: 55 minutes (Keikyu Airport Line → Keikyu Main Line
→ JR Keihin Tohoku Line → Tokyu Oimachi Line)

Once at Tokyo Tech Campus – Getting to Multi-Purpose Digital Hall

Once you arrive at Ookayama station, the main gate of Tokyo Tech is right in front of the main station exit (the other side of the crossing). Enter the gate and go through the main pathway. You will find a slight downhill road on the right. Go along with the road, and then you will see the building on the left side.

Building Security

You must wear your BIOMOD ID badge at all times while on campus. *If you forget your BIOMOD ID badge you will have to return to your hotel to get pick it up as additional ID badges cannot be printed on-site.*

Please do not arrive early. Building doors will not be unlocked before 08:00 on Saturday and 09:00 on Sunday.

Network and Wi-Fi

WiFi is available during the BIOMOD Jamboree in the Hall and adjacent areas:

SSID: BIOMOD
Password: QfLhpDF9

Meals

Saturday: On-site breakfast, snacks (morning and afternoon), lunch (bento box), and beverages will be provided. The banquet includes a buffet-style meal.

Sunday: On-site breakfast, snacks, and beverages will be provided.

Update (Oct 24, 2023): Breakfast and lunch will be provided at the Tsubame Terrace (banquet/social event location).

If you have any food allergies that were not noted on your registration, please let us know immediately.

Please be courteous of other BIOMOD participants and take only one serving of food at a time. You will have the chance to come back for seconds after everyone else has been served.

Banquet (Sat. 17:30-) will be held at the Tsubame Terrace, a cafeteria located right next to the hall.

COVID-19

Currently, the Japanese government does not mandate any rules related to COVID-19. However, considering the status, it's advisable for participants to consider a plan in case of infection. In particular, please check in advance whether you will be able to extend your stay (i.e., visa issues and hotels), postpone your return flight, and a potential procedure you might need in order to enter your own country, just in case. Antigen test kits are available for purchase at local pharmacies.

Resources

- Japan National Tourism Organization
- Ministry of Foreign Affairs of Japan
- Cabinet Secretariat

Japanese Phrase Basics (Survival Guide) by Dr. Richard Archer

***Survival tip for eating out** – All convenience stores (7-11, Family Mart, Lawson) will accept credit cards, however, not all restaurants will accept cards. Especially smaller, independently owned places will only take cash.

***Survival tip around the city** – Bins and toilets can often be found in the convenience stores

English - Japanese/(Phonetic pronunciation)

Numbers / phonetic pronunciation									
1	2	3	4	5	6	7	8	9	10
ichi	ni	san	yon	go	roku	nana	hachi	kyu	juu
11	12	13	14	15	16	17	18	19	20
juu-ichi	juu-ni	juu-san	juu-yon	juu-go	juu-roku	juu-nana	juu-hachi	juu-ku	ni-juu

Common Survival Phrases

- Hello – こんにちは　（kon-ni-chi-wa）
- Thank you - ありがとうございます (Ah-ri-ga-tou go-zai-mas)
- Excuse me - すみません (su-mi-ma-sen)
- It is ok - 大丈夫です (Dai-jou-bu-des)
- Is it ok? - 大丈夫ですか？ (Dai-jou-bu-des-ka?)
- Yes – はい (Hai)
- No – いいえ (ii-eh)
- I understand – わかりました (wa-ka-ri-mash-ta)
- I don't understand – わからない(wa-ka-ra-nai)
- Please (accepting)- お願いします – (On-ne-gai-shi-mas)
- Please (go ahead) – どうぞ　(Dou-zo)
- Where is the toilet? - トイレはどこですか？(Toi-le-wa-doko-des-ka?)
- Where is the station? - 駅はどこですか? (Eki-wa-doko-des-ka?)
- This – これ (Kore)
- That – それ (Sore)

Reservations (Hotels and restaurants)

- *Reservation-* よやく (*Yo-ya-ku)*
- *Do you have a reservation? - 予約はありますか？ (Yo-ya-ku wa a-ri-mas ka?)*
- *I have a reservation* 予約してあります- (*Yo-ya-ku o shi-te a-ri-mas)*
- *I don't have a reservation* 予約はありません– (*Yo-ya-ku wa a-ri-ma-sen)*
- *How many people? - 何人? – (nan-nin?)*

1 Person – 1 人 (He-tor-ri)

2 People – 2 人 (Fu-tar-ri)

***x** people - **x** 人 [Number + "nin"] e.g. 5 people would be "go-nin"*

At the convenience store (Combini)

<u>At the counter you might be asked;</u>

- Would you like it heated? 温めますか？- (Ah-ta-ta-mae-mas-ka?)
- Or to directly ask for heating your food - 温めてください (Ah-ta-ta-mae ku-da-sai)
- Would you like a bag? - 袋にお入れしますか? (Fu-ku-ro ni oiresimas ka?)
- Or to ask for a bag – 袋をください (Fu-ku-ro ku-da-sai)
- Do you want chopsticks? - お箸が欲しいですか？ (O hashi ga hoshīdesu ka?)
- Or to ask for chopsticks お箸を下さい(O hashi ku-da-sai)

<u>How to respond:</u>

- Yes please - お願いします (On-ne-gai-shi-mas)
- No thanks - 大丈夫です (Dai-jou-bu-des)

At the restaurants

- *Please wait - お待ちください (O-machi ku-da-sai)*
- Could I get the bill? お勘定 お願いします (O-Kie-ke On-ne-gai-shi-mas)
- Ask for the bill but pay separately - お会計別々で (O-Kie-ke betsu betsu de On-ne-gai-shi-mas)
- Thank you for the food (When leaving) - ご馳走様です (Goch-ii-sou-sama-des)

Japanese Phrase Basics (Survival Guide) by Dr. Richard Archer

Foods we recommend for the Japanese experience.

Rice ball
お握り (onigiri)

Ramen
ラーメン

Miso-soup
味噌汁 (Miso-Shiru)

Sushi
すし

Japanese fried-chicken
から揚げ (kara-ah-ge)

Japanese sake (alcohol)
日本酒 (Ni-hon-shu)

Soup curry
スープカレー

*Northern Japan specialty

Fermented beans
納豆 (Nat-to)

*for the brave

If you have specific food restrictions, you can point to the following;

Vegetarian ベジタリアン (be-ji-ta-ri-an)	Vegan ビーガン (bee-gan)
Does this contain meat? 肉が入っていますか？(Ni-ku ga hai-tte imas ka?)	

Allergies - アレルギ		
Meat 肉 (Ni-ku)	Milk 牛乳 (Gyu-Nu)	Eggs 卵 (Ta-ma-go)
Fish 魚 (Sa-ka-na)	Crab 蟹 (Ka-ni)	Wheat 小麦 (Ko-mugi)
Buckwheat そば (So-ba)	Peanuts 落花生	Shrimp エビ (Ebi)

For Vegan/Vegetarian options: you may also check HappyCow (happycow.net) for local restaurants.

Judging

Our aim is to maintain an open and fair process for evaluating each team's performance. Teams will be scored by judges using a point system. The judging process will have two stages: online content (worth up to **75 points**) and live presentation (worth up to **25 points**).

Online content scoring

- Maximum combined score for online content is **75 points** (= 50 points for wiki + 25 points for internet video)
- Scores will be determined by a range-voting system.
- Five (5) judges will be randomly assigned to each team.
- Judges will evaluate each project according to a rubric (see below) and assign a point value in each category.
- Highest and lowest judges' total scores are excluded to remove outliers.
- Three remaining judges' scores will each weighted by 1/3 and combined to determine the total scores for each category.

Website (up to 50 points)

Project Idea (20 points)

- Relevance: Has the team made a strong case that their project idea is scientifically and/or technologically interesting? **(5 points)**
- Specification: Are the project goals well-defined? (i.e. Does the team explicitly state what criteria need to be met in order to consider the project a success?) **(5 points)**
- Feasibility: Was the proposed solution feasible? (i.e. Was it reasonable to expect that the solution could be implemented by a BIOMOD team in one summer?) **(5 points)**
- Merit: Is the proposed solution a good one? Is it particularly elegant or innovative? **(5 points)**

Project Documentation (20 points)

- Clarity: Is the project description well-written and easy to understand? Does it include the background and motivation of the project, methods, results, and discussion? Are the figures easy to understand? **(10 points)**
- Transparency: Are all of the raw experimental data and source files easily accessible? Would it be straightforward to attempt to reproduce the team's results? **(5 points)**
- Layout: Is the team's project page arranged in a clear and logical fashion? **(5 points)**

Project Execution (10 points)

- Execution: Did the team accomplish what they set out to do? **(10 points)**

YouTube video (up to 25 points) (Updated Oct 24: clarified 3 min. limit in accordance with the detailed description on biomod.net)

- Overall impact: Was the video interesting? Did you want to watch more than once? **(10 points)**
- Clarity: Was the project described in a simple and clear manner that could be easily understood by a wide audience? **(10 points)**
- Production: Was the video duration 3 minutes or less? Was the sound and video high quality? Were the images focused and scaled properly? **(5 points)**

Presentation scoring (up to 25 points)

- Content: Were the slides clear and easy to understand? Did the project narrative have a logical flow, with clearly stated goals and results? **(10 points)**
- Delivery: Did the speaker(s) give a well-rehearsed, well-paced presentation? Did the speaker(s) engage with the audience and maintain good eye contact? **(10 points)**
- Impact: Was the presentation interesting? fun? clever? memorable? **(5 points)**

Judges

- Judges were selected from a pool of BIOMOD faculty mentors and outside experts.
- Mentors will not evaluate their own team.

Award Categories

The following prizes will be awarded:

Top Prizes

- Grand prize = 1st highest total combined points from wiki + video + presentation
- 1st runner up = 2nd highest total combined points from wiki + video + presentation
- 2nd runner up = 3rd highest total combined points from wiki + video + presentation

Category awards

- Best Website = 1st place, 2nd place, 3rd place
- Best YouTube Video = 1st place, 2nd place, 3rd place
- Best Presentation = 1st place, 2nd place, 3rd place
- Audience Favorite = 1st place, 2nd place, 3rd place

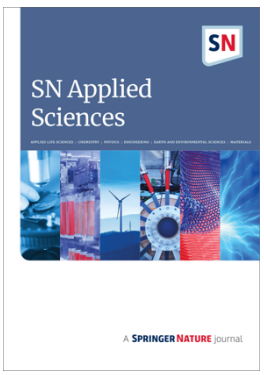
Project awards

- Bronze: Team satisfied all minimum requirements for judging (i.e. Submitted a complete Project wiki and uploaded a YouTube video)
- Silver: Satisfied criteria for Bronze, plus at least one device (part of the system) in the team's design is worked as expected.
- Gold: Satisfied criteria for Silver, and overall point score from Wiki + YouTube + Jamboree presentation are in top 50% of all teams.

Special Awards (Updated Oct 24: Audience Choice merged with category awards; award name correction)

- Molecular Robotics Award
- ~~Audience Choice Award – Best Project~~
- Best ELSI Practice Award
- Best Team T-shirt Award

Springer Nature Travel Award



Courtesy of Springer Nature Applied Sciences Journal, BIOMOD is happy to announce the Springer Nature Travel Award. The grand prize team will receive 200 Euros to help part of the travel fee and other team activities.

Organizer Contact Info.

In case of emergency, please email/call the organizer:

Shogo Hamada
Phone: +81-(0)70-8489-2907
Email: hamada@nanoeng.net, hamada@c.titech.ac.jp

BIOMOD Japan (Steering Committee)
Email: info@biomod.jp

Team Abstracts

Team: BIOMOD QUERÉTARO

Title: Micro-sense: detection of cefotaxime-resistant bacteria through a portable microfluidic device

Abstract

Antibiotic-resistant bacteria have raised concerns among researchers over the past several decades regarding the serious public health problem these represent. These microorganisms have hindered the effectiveness of antimicrobial treatments, increasing the difficulty to find an adequate antibiotic to treat infection-causing bacteria successfully. The *CTX-M-15* allele, present in plasmidic DNA of cefotaxime-resistant bacteria, has been related to the production of enzymes that confer resistance to beta-lactam antibiotics. Accordingly, the use of these antibiotics to treat infections caused by any *CTX-M-15*-containing *E. coli* results ineffective. Identifying the presence of this gene through molecular biology techniques is crucial to avoid utilizing beta-lactam antibiotics when facing this type of bacteria. Therefore, the design of a microfluidic device that conducts the amplification of *CTX-M-15* via loop-mediated isothermal amplification (LAMP) on-field is proposed, representing a cost-effective, portable, reliable, and rapid method to detect beta-lactam antibiotic-resistant bacteria containing the *CTX-M-15* allele. It is expected that, by implementing this device within practical applications, a trustworthy visual result that verifies or discards the presence of the *CTX-M-15* gene could be provided, functioning as solid evidence to facilitate decision-making when addressing antibiotic resistance problematics.

Team: Cargo Code-Breakers

Project Title: Cargo Sorting DNA-Robot

Abstract: DNA nanorobots have the potential to carry out highly specific tasks in molecular factories and can bring us closer to understanding complex cellular trafficking. While existing research has demonstrated a DNA nanorobot sorting cargo on a 2D origami in solution, imaging of the movement of individual robots remains limited. In this BIOMOD project, we use super resolution microscopy to characterize the motion of the robot as it carries out a random walk and sorts cargo. To visualize the robot and the fiduciary markers on DNA origami tracks, we implemented DNA-PAINT, a novel imaging technique utilizing fluorophores to bypass the diffraction limit. Our movie will be critical in the further evolution of molecular robotics, including optimizing the sorting algorithm and scaling up the number of robots with ever increasing complexity to carry out tasks, opening the door to potential applications in nanoelectronics, medicine, and biomolecular factories.

Illuminating the Future of Alzheimer's Diagnosis: Rapid Quantitation of GFAP using Programmable DNA

Abstract

Alzheimer's Disease is a debilitating progressive neurodegenerative disease. As therapies become available, patients need to be diagnosed earlier in order to begin treatment before irreversible neurodegeneration sets in. Our research project addresses the need for an early detection tool for Alzheimer's Disease by identifying key biomarkers from RNAseq databases and designing a rapid DNA-based detection and quantification method for target genes.

Glial Fibrillary Acidic Protein (GFAP) has been shown by multiple studies to be upregulated in patients with Alzheimer's Disease. It has been confirmed to be elevated in both serum and cerebrospinal fluid samples. We analyzed and selected specific nucleotide sequences within the GFAP gene that could be targeted with our DNA-based detection method. We then designed a DNA Displacement Fluorescence Assay that can rapidly calculate GFAP levels. This method could be adapted as an early detection tool that will improve chances of diagnosis and treatment for Alzheimer's patients.

DNA origami is known as an innovative technology that can build various 2D and 3D nanostructures using DNA strands. In conventional procedure, DNA origami is folded in bulk solution such as in a test tube. Here, we present our project “SynthePHERE”, which aims at the folding of DNA origami nanostructures in a small compartment such as in a liposome.

As a first step, giant unilamellar vesicles (GUVs) containing scaffold and staple strands are prepared. The DNA origami nanostructures are folded in GUVs with the temperature control of the solution. Since scaffold and staple strands are inside of a small reaction system of GUVs, faster and efficient DNA origami folding is expected.

Additionally, introduction of staple strands into GUVs through the pores on the membrane surfaces is carried out. A membrane protein streptolysin O(SLO) is used to form pores with ≈ 27 nm diameter on GUV membrane surfaces. Also, SLO can get sealed when calcium ions are added. By closing SLO pores, scaffold and staple strands are expected to be entrapped in GUVs, allowing to fold DNA origami nanostructures inside GUVs.

By introducing different staple strands into a small compartment, various DNA nanostructures can be folded as a response. This input-output system would be applied to liposome-type molecular robots that can respond to outer environments, which could be used as drug delivery system.

A New Method of DNA Nanoassembly - DNA Dumbbell Hybridization

As is well known, a long DNA strand serves as the main strand, and many short strands are added to guide the assembly of this long strand to form a predetermined structure.

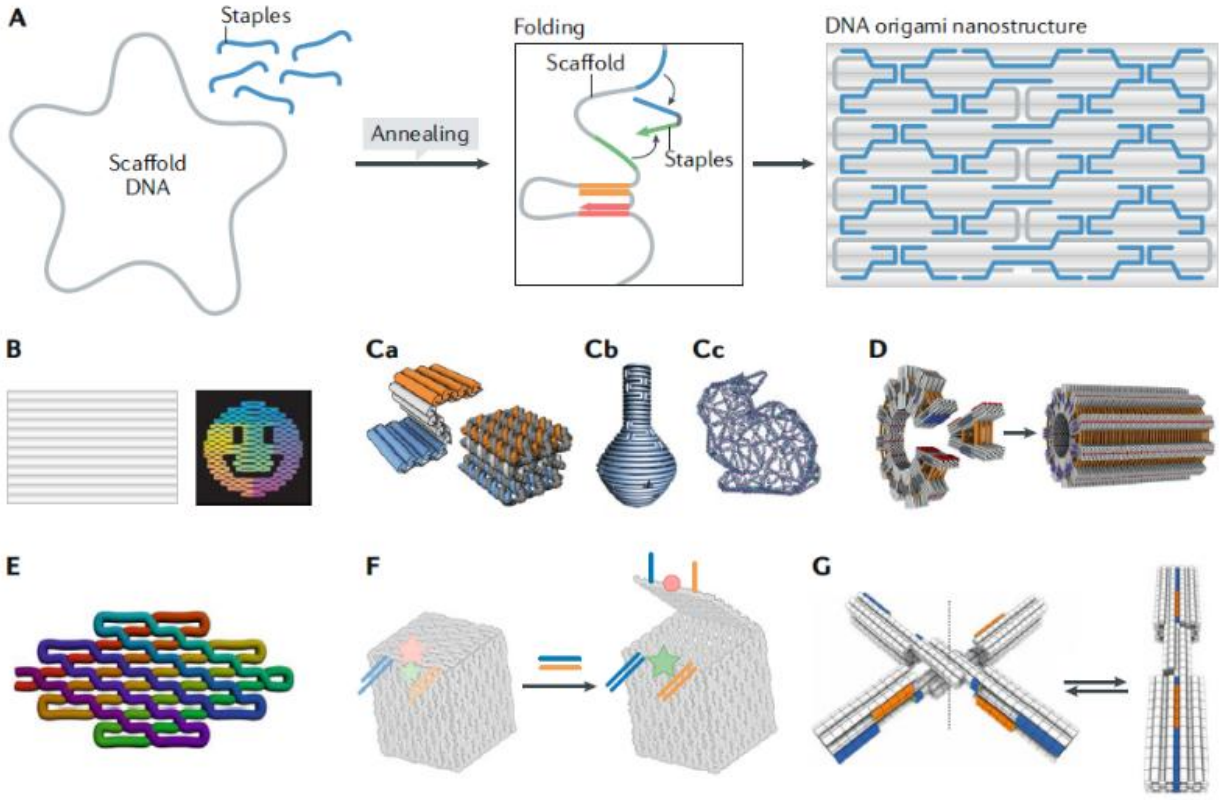


Fig1. DNA Origami, published in the inaugural issue of Nature Methods Reviews Primers

Recently, the OUC-SeaSon team has invented a new assembly technology, which involves designing DNA strands to self connect to form dumbbell rings, which are then hybridized to achieve the purpose of assembly. At the same time, by modifying the sequence, we can change the angle of

hybridization between dumbbells, thereby forming other structures.

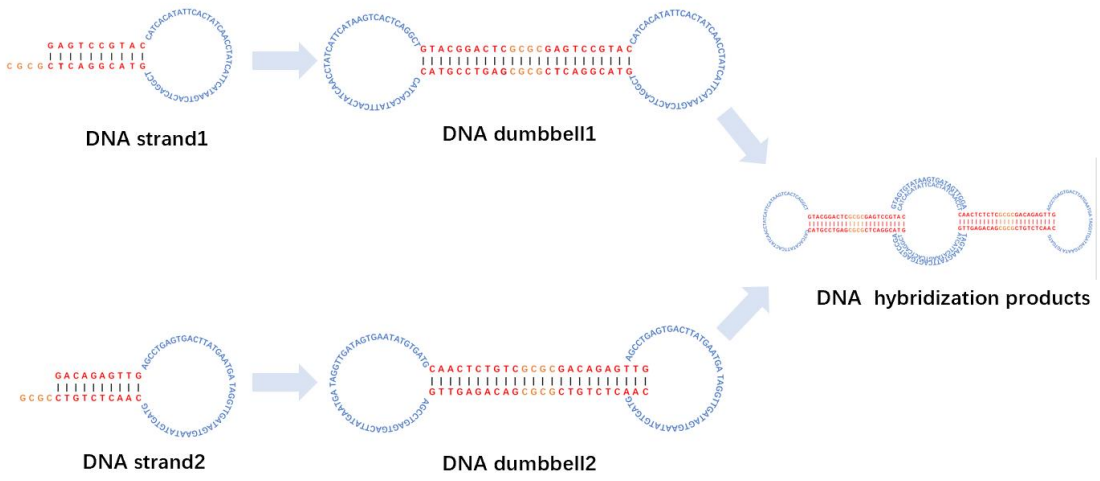


Fig2. DNA strands self connect to form dumbbell rings, and then hybridize them 180 degrees

Due to the structure of Z-DNA produced in the process of dumbbell ring hybridization, we used polyacrylamide gel electrophoresis and domain proteins that can specifically recognize Z-DNA, such as ADAR1, to verify the success of hybridization.

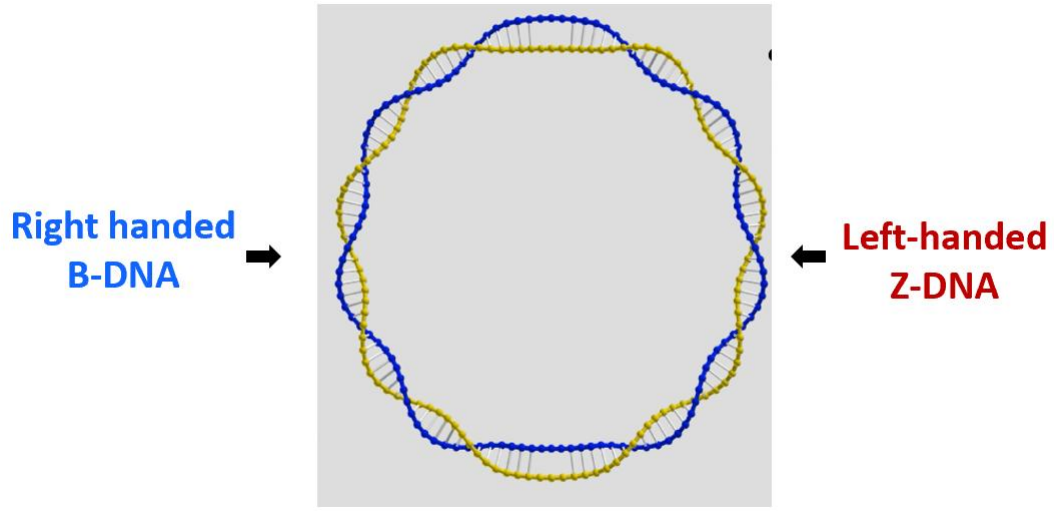


Fig3. DNA hybridization produces z-dna structure

Our project provides a new solution for the assembly of DNA structures, and the assembled structures also provide raw materials for studying Z-DNA and its specific binding proteins.

As of 2018, cancer affects more than 18.1 million people worldwide and kills more than half of those affected.
Cancer is mostly treated with anticancer drugs. Anticancer drugs are prescribed as intravenous infusions, injections, or oral medications, and once inside the body, they travel throughout the body in the bloodstream to attack cancer cells.
Unlike surgery or radiotherapy, anticancer drug therapy is not a local treatment, but acts on the whole body. Therefore, it damages normal tissues and causes side effects.

So, we propose a drug delivery system (DDS) using liposomes and RCA.
In this molecule, DNA is coated around a liposome that encapsulates the drug. In cancer cells, there are tumor markers with specific sequences. The reaction between the tumor markers and their complementary DNA strands with them stuck in the liposome membrane causes the coated DNA to peel off at the target site. When the DNA coating is removed, the liposome breaks down and the encapsulated drugs are released.

The mechanism of action of this molecule requires the realization of three steps:
1. RCA on the liposome membrane.
2. Coat DNA around the liposome.
3. Peel off the coated DNA and break the liposome.

In this project, we examined coating around liposomes with DNA formed by RCA and breaking the liposomes through strand displacement reactions. In the future, our research may contribute to the development of new DDS materials for medical applications.

Geometrical elements of DNA nanostructure are faces, edges, and vertices. Research focusing on the faces and edges has been reported, such as DNA boxes and DNA tweezers. Since no mechanism has been established to change the number and position of vertices, here we propose a new mechanism that controls the shape by swapping the positions of recessed and protruding vertices using the theory of dual polyhedron. The structure consists of a rhombic dodecahedron created using DNA origami wireframe and ssDNA branched from the edges. When Another ssDNA is added as a signal, the corresponding ssDNA reacts and transform the structure. There are three states: a rhombic dodecahedron, a hexahedron, and an octahedron. Therefore, by arranging the structures regularly, it is possible to create crystals whose density can be changed in response to signals, and there is a possibility that this structure is used as a new building material.

The technologies such as DNA origami have made it possible to engineer biological molecules to form defined structures in vitro. However, manufacturing of multiscale-ordered materials in the complex cellular environment remains challenge. Here, through designing the phase separation behaviors of synthetic DNA and protein molecules, our project constructs several ordered DNA-protein condensates in vivo, which are characterized by fluorescent microscopy. Our ribonucleoprotein nanostructures, by turning the "disordered collaboration" state to the "ordered pipeline", enhance the lycopene pathway's flux and final productivity, exampling how the organization of biomolecules could accelerate the life engineering process.

Novel DNA Valve for Light-inducible Gas Exchange

Team Sendai

Various chemical exchange systems exist in nature and are crucial in regulating important phenomena in biology and geochemistry. Attempts at replicating these using DNA nanotechnology have mainly focused on liquid-based systems. There exists no example of a DNA nanostructure that controls movement of molecules in the gas phase, leaving the potential of molecular robots to interact with different microenvironments unexplored. Taking inspiration from plant stomata, we propose a DNA origami polymer that facilitates light-inducible gas exchange through the membrane of a soap bubble.

The monomer is a square plate with a slit similar to a vending machine's coin slot. To span the variable thickness of the membrane, monomers self-stack through shape complementarity, with the slits forming a central tunnel. The inside of the tunnel is lined with cholesterol to realize the hydrophobic environment required for gas transport. The structure has two distinct states that dictate whether gas molecules can pass or not: closed and open, the transition between which is controlled by DNA. When closed, the DNA strands form hairpins that cover the entirety of the tunnel, preventing gas flow. Due to their photoresponsivity, the hairpins unfurl under UV exposure, opening the whole tunnel for gas exchange.

Expansion of our structure’s functionality may enable nanorobots to perform biomimetic photosynthesis, pH control of various environments, and even detection, capture, and subsequent treatment of harmful gases.

DNA Mochi Device

Although self-assembly of DNA origami into larger structures by fractal assembly, etc., has been achieved, there have been no methods of drastic size expansion. We devised combining DNA hydrogels with DNA origami and developing nanoscale devices which transform into gels, which further aggregate into a larger gel. Then, inspired by the softness of gel, we call it DNA-Mochi-Device.
First, the device is two types of nanoscale DNA origami, each has long single-stranded DNA with a complementary sequence to each other produced by Rolling-Circle-Amplification as scaffolds. Second, a strand displacement reaction of specific input DNAs and staples releases the scaffold, it binds to complementary scaffolds of other devices and transitions to a DNA hydrogel. Finally, these gels aggregate to micrometer-scale gels.
Because of this drastic change and input-specific gelation, it could be used as a device which traps substance locally or creates occlusion structures within microscale flow paths such as capillaries.

University of Sydney 2023 BIOMOD team
Team name: USYD UFOLD: Plastic Fanatics

Project title: DNA Cargo Bays for Nanoplastic Capture

Abstract: Nanoplastics are found all around, including in clothes, cosmetics, food, and even in the northern Atlantic air. Consequently, humans inhale and ingest these plastics regularly, where they build up in the body. They are linked to inflammation, oxidative stress, and neurotoxicity in human cells, among others. This results in the challenge of detecting and removing nanoplastics from the human body. The aim of this project is to design a novel DNA structure to eventually detect and capture specific micro- or nanoplastics. These structures, DNA cargo bays, will be produced using the design software CadNano and assembled. Structural verification will be performed using gel analysis, fluorescence testing, and transmission electron microscopy (TEM). The structures will undergo switching between closed and open states, the open structure allowing capture of target molecules inside the cargo bay. This product acts as proof-of-concept for bloodstream nanoplastic detection and capture.

Team members:
Alicia Werlen
Lucy Hing
Markus Williams
Edmund Derwent
PhD mentor:
Karuna Skipper
Faculty Mentor:
Dr Shelley Wickham

Abstract

Team: Nano-JLU

Title: Redefining Drug Resistance Strategy in Cancer Treatment: De Novo Design of a Stimuli-Responsive Peptide-Based Block Copolymer Assembly

Abstract:

Drug resistance poses a persistent challenge in the context of advanced malignant tumor treatment. Within this arena, we report the self-assembly of a peptide-based block copolymer with the unique capability to trigger cell apoptosis across a wide spectrum of cancer cell phenotypes through plasma membrane rupture (PMR) upon stimuli from tumor microenvironment, such as pH and the overexpression of matrix metalloproteinase 2 (MMP2). The block copolymer consists of three distinct components: a hydrophobic poly(tyrosine)-block-poly(histidine) (pTrp-pHis) unit and a hydrophilic polyethylene glycol (PEG-8) segment, intricately linked by a MMP2-sensitive peptide linker (PLGLAG). This resulting block copolymer self-assembles to generate nano-capsules of approximately **100** nm in diameter when introduced into an aqueous solution. The as-prepared nanocapsules maintain structural integrity and exhibit negligible cytotoxicity under normal physiologic condition. However, once the nanocapsules accumulate inside a tumor due to the enhanced permeability and retention (EPR) effect, cleavage of the block-copolymer by MMP2 and protonation of the pTrp-pHis block lead to collapse of the nanocapsules, releasing the cationic pTrp-pHis block into the tumor microenvironment. The released cationic pTrp-pHis blocks egage in stable electrostatic interaction with the negatively charged tumor cell membranes, eventually inducing PMR-mediated tumor cell apoptosis.

Our research unveils an innovative strategy for combating drug resistance in cancer therapy and holds the potential to address broader drug resistance challenges in the treatment of bacterial and fungal infections.

Micro Invader Game

Team Tokyo Tech

Our love of biology and games led us to note the similarities between the Invader Game and the immune system in terms of defeating foreign enemies. We therefore decided to create an immune-like molecular system at the microscale. We call it the "Micro invader game". The invader game is simplified into three components: bullets, a cannon and enemies. The bullets consist of DNA-modified microbeads that roll and move on a flat surface with RNAs for a substrate. The cannon fires the bullets by removing the stopper DNA on the surface that restricts the movement of the bullets. The enemies are made of liposomes, which fluoresce and/or self-destruct when hit by the bullet. The design of the enemies mimics the basic mechanisms of living organisms that respond to external stimuli. We believe our system, especially the sense-response mechanism of the enemy's design, could lead to new insights in the development of artificial life and drug delivery systems.

A BIOMODular Enzyme Delivery Vehicle to Target Biofilms

By: UBC BIOMOD

Biofilms are layers of bacterial communities that can adhere to one another within a self-produced matrix. They can attach to a variety of surfaces including human tissue, causing severe healthcare and environmental issues. Traditional strategies for combating biofilms include the use of antibiotics and interference of bacterial layer formation. However, removing biofilms using these methods can be challenging due to antibiotic resistance and unexpected pathogenic features arising from interference strategies. To address this issue, we aim to create a modular enzyme delivery vehicle. This structure consists of a DNA templated liposome, conjugated with variable enzymes, referred to as an "enzymosome". By forming our liposomes around DNA-origami structures, which can be altered to modify their size and shape, we can create a customizable platform. Among the DNA structures developed – a trihedron, pentahedron, and octahedron – all three demonstrated high stability in CanDo©. Future investigations include testing enzyme synergy with liposomes and validation of the platform *in vitro*. The modularity of the enzymosome can address biofilms present in various environments such as in cystic fibrosis patients, food facilities, and water systems. By changing the cargo type and liposome size, this delivery vehicle provides potential to be used across a wide range of applications.