Preview of Award 2450549 - Annual Project Report

Cover |
Accomplishments |
Products |
Participants/Organizations |
Impacts |
Changes/Problems
| Special Requirements

Cover

Federal Agency and Organization Element to Which Report is Submitted:	4900
Federal Award or Other Identifying Number Assigned by Agency:	2450549
Project Title:	CIRC: Planning C: Community Three-Dimensional Image Infrastructure for Sustainable Innovation in Biofilm Research
PD/PI Name:	Albert E Parker, Principal Investigator Bettina Buttaro, Co-Principal Investigator Joseph Picone, Co-Principal Investigator Heidi J Smith, Co-Principal Investigator
Recipient Organization:	Montana State University
Project/Grant Period:	07/01/2025 - 06/30/2027
Reporting Period:	07/01/2025 - 06/30/2026
Submitting Official (if other than PD\PI):	N/A
Submission Date:	N/A
Signature of Submitting Official (signature shall be submitted in accordance with agency specific instructions)	N/A

Accomplishments

*** What are the major goals of the project?**

The Biofilm Imaging Library (BIL) planning project aims to establish the foundation for an open-access, community-driven repository of standardized, high-quality biofilm images, coupled with the development of computationally efficient, user-friendly tools supported by machine learning. The primary objective of this initial phase is to advance the design and implementation of the BIL while positioning the effort for a larger, collaborative proposal focused on expanding these capabilities. Specifically, the project will (1) establish a robust and scalable BIL framework for the collection and organization of imaging data and metadata; (2) develop open-source computational tools grounded in machine learning and modeling approaches that address current limitations in reproducibility, scalability, and usability in biofilm image analysis; and (3) provide an open-access resource for both research and education by delivering curated datasets, analytical tools, and training materials that support broad participation and hands-on learning. Ultimately, these efforts will drive the development of advanced image analysis methods, predictive models, and integrated data science approaches, thereby establishing a comprehensive image analysis pipeline for biofilm science.

As stated in our proposal, our activities over the last reporting period were:

Activity 1: Prototypes and Standards	Target Completion Date	Percent of Completion
• 1.1: Prototype Data	9/2025	100%
• 1.2: Metadata Definitions	10/2025	100%
• 1.3: External Contributors	12/2025	100%
• 1.4: Licensing and Legal Issues	2/2026	100%
• 1.5: Curation Practices	3/2026	100%
• 1.6: Validation and Constency	6/2026	100%
Activity 2: Outreach	Target Completion Date	Percent of Completion
• 2.1: IEEE SPMB Symposium	12/2025	100%
• 2.2: ASM Biolfilms Meeting	10/2025	100%

• 2.3: CBE Biannual Meetings	7/2025	100%
Activity 3: Grant Planning	Target Completion Date	Percent of Completion
• 3.1: Identify Collaborators	12/2025	100%
• 3.2: Identify Research Themes	6/2026	90%
• 3.3: Proposal Development	12/2026	50%

*** What was accomplished under these goals and objectives (you must provide information for at least one of the 4 categories below)?**

Major Activities: Over the last reporting period we have accomplished three major activities including the development of data prototypes, conducting outreach, and engaging in planning for a future grant submission.

Activity 1: Prototypes and Standards

1.1: Prototype Data – We have employed undergraduate students to annotate 3D image data. These annotations and the original raw 3D image data and meta data have been standardized as an Open Microscopy Environment (OME) formatted multi-plane TIF files and entered into an alpha version of the BIL.

1.2: Define Metadata Criteria - Meta-data are submitted into the BIL as an Excel spreadsheet, including fields for:

- Investigator
- Lab
- Geographic Location
- Date of submission
- Species being imaged
- Stain or Tag used.
- Type of microscope used
- File of view size (µm× µm) in planar dimensions *x* and *y*
- image depth, *z* (µm)
- Pixelation of each z-slice (number of pixels x number of pixels) – many times 512 x 512 or 1024 x 1024
- Voxel (Pixel) Width, $\Delta x = \Delta y$ (um)
- Voxel Height (Depth), Δz (um)

1.3: External Contributors - We have identifed 5 contributors to the BIL, listed with details in Participants section of this report.

1.4: Licensing and Legal Issues

The BIL is based on best practices from other similar activities used by the Neural Engineering Data Consortium. As part of our subscription information, we have users sign a data use agreement that covers issues such as: (1) Contact Information: users provide a name, an institution name, a valid verifiable post office address, telephone number, and an email address at that institution. (2) Date and Signature.

The terms of use are as follows:

(1) The user should acknowledge the provider of this data using the publication listed in the documentation included with the specific corpus (typically found in the AAREADME file released with the data).

(2) The user will not release data to a third party or redistribute the data. Please have the third party contact us directly by sending an

email to help@nedcdata.org.

(3) The user agrees that no attempts will be made to re-identify the subjects, who have been anonymized in this distribution.

(4) The user will not use the data for malicious purposes. This data can be used for research and technology development, but not for uses beyond these broad classifications.

(5) The data recipient will delete the data from all computer systems when finished with the data.

There are no restrictions regarding commercial use of the data - subscribers are free to use the data for research or commercial applications.

If more restrictive agreements are required for specific data sets or requested by the data provider, we can accommodate those constraints as well.

1.5 & 1.6 Curation Practices, Validation and Consistency

All data is created with a versioning system that tracks the version of the release. The downloads page lists the most recent version of the data (e.g., v3.2.1), while the archives also contain previous versions of the data. As we make corrections to specific annotations, the minor version number (least significant digit) is incremented. The major version number (middle digit) is used when significant upgrades are made to the file formats, etc. The highest version number (first digit) is increased when significant additions are made to the amount of data or the type of data.

Data submitted for distribution is reviewed and verified by our IT and annotation teams for conformance to our guidelines. We also typically release a document describing the annotation guidelines, and update this document as our understand of the problem evolves.

Activity 2: Outreach

2.1: IEEE Signal Processing in Medicine and Biology Symposium (SPMB) – Dr Picone and Dr Parker attended. Dr Parker presented “Why do we need a biofilm imaging library? Current limitations when analyzing confocal 3D images” at this meeting on 12/6/2026.

2.2: American Society of Microbiology Biolfilms Meeting (ASM) Biofilms Meeting – Dr Buttaro and Dr Smith attended in November 2026 in Portland OR.

2.3: Center for Biofilm Engineering (CBE) Biannual Meetings –A special session was hosted by Dr’s Parker, Buttaro and Smith to meet with potential BIL users and collaborators. Dr Buttaro presented a group poster “Why do we need a Biofilm Imaging Library? (A Community Discussion – What to study?)”

Activity 3: Grant Planning

3.1: Identify Collaborators

We expanded an interdisciplinary network spanning microbiology, computer science, engineering, and applied mathematics by strengthening existing partnerships and recruiting new collaborators who all have imaging based research needs that cannot be met with current analytical approaches.

3.2 Identify Research Themes

One of the most universal themes was the need for 3D imaging analysis and tools for microbiomes, both human and environmental. Elegant studies have been done looking at spatial and temporal gene metagenomics to probe microenvironments and gene activity. Imaging goes beyond information based on genetics to reveal how spatial organization of the subcommunities drives the function of the community. Having a large collection of images allows for identification of common spatial organizations (e.g., protective, competitive, cooperative). By linking spatial architecture with local metabolic activity and gene expression, machine learning can uncover how distinct subpopulations form, interact, and specialize within biofilms.

A subgroup within microbiomes is those with a special interest in multikingdom interactions, where there are significant image quantitation challenges. This also spans medical, dental, and environment interests. This prompted us to try to develop a fungal quantitation tool.

Another group with significant interest in the BIL were those developing mathematic models to predict and understand biofilm behavior. These groups are interested in biophysical properties driving biofilm attachment and growth as well as resistance to toxic insults. Here large collections of images allow for robust testing of mathematical models using images from multiple environments to discover common 3D spatial themes that may share the same underlying biophysical principles.

Finally, all groups had an interest in how these properties are influenced by the local conditions. These conditions can be time of year, available nutrients, temperature, water, and carbon dioxide. This can include structural environments such as crevices in rocks and polygons in permafrost.

3.3 Proposal Development

For the grant planning phase of this project, we have engaged with multiple program officers (in CISE and BIO) to ensure alignment with agency priorities. As the originally targeted solicitation (to CISE/CIRC) is no longer active, these discussions enabled identification of a new and highly relevant funding opportunity (NSF 23-580 within BIO directorate's Division of Biological Infrastructure). Hence, during this first year we have focused our efforts on laying the groundwork for the submission of a competitive, large-scale interdisciplinary proposal to NSF 23-580 by expanding collaborations, refining research themes, and advancing proposal development.

Specific Objectives: The Biofilm Imaging Library (BIL) planning project seeks to lay the groundwork for an open-access, community-driven repository of standardized, high-quality biofilm images and the development of open-source easy-to-use computationally efficient tools aided by machine learning.

Our activities have identified: (1) an approach to standardizing data for submission to the BIL; (2) an interested community who have used and contributed data to the BIL; (3) already applied (as part of this project) open-source easy-to-use computationally efficient machine learning tools that identify (segment) bacterial and fungal cells from 3D image data – this is an active area of research.

Significant Results: A major objective of the Biofilm Image Library is the creation of high-quality

annotated datasets capable of supporting machine learning methods for automated segmentation of complex three-dimensional biofilm images. Developing an efficient annotation pipeline proved to be one of the most significant technical challenges of the project, requiring substantial optimization to balance annotation quality with scalability.

Our initial workflow relied on exhaustive manual annotation using the open-source visualization tool Napari. Expert annotators manually outlined every visible cell in selected two-dimensional image slices by tracing precise bounding polygons. Restricting the initial effort to single image slices allowed us to refine annotation standards, establish consistent labeling conventions, and evaluate segmentation performance before extending the workflow to full 3D image stacks.

These fully annotated images were then used to train a segmentation model using the open-source StarDist OPP framework. The results are shown in Figure 1 in the Supporting Files. After iterative tuning of model parameters, the resulting segmentation accuracy was encouraging and demonstrated that modern deep learning methods could successfully learn complex cellular morphologies from manually curated examples. Although this validated the overall approach, it also revealed a major practical limitation: complete annotation of every cell in every image required an unsustainable amount of expert effort, making large-scale corpus development impractical.

To overcome this bottleneck, we redesigned the annotation process around partial annotation. Rather than labeling every cell within an image, annotators identify approximately one hundred representative regions of interest that capture the diversity of cell shapes, sizes, densities, and imaging conditions. This dramatically reduces annotation time while preserving the information necessary to train accurate segmentation models. The results are shown in Figure 2 in the Supporting Files.

Implementing this strategy required overcoming a limitation of the StarDist training framework. StarDist assumes that every pixel in each training image has been assigned to either a foreground object or the background. Partially annotated images violate this assumption because large portions of the image remain unlabeled. To address this incompatibility, we developed a preprocessing tool that automatically extracts the annotated regions from each image and assembles them into a single composite training image in which every pixel is assigned a valid label. These collated images satisfy StarDist's labeling requirements while preserving the manually annotated examples.

Experiments demonstrated that models trained using these composite images achieve segmentation performance comparable to models trained on fully annotated images, while reducing manual annotation effort by an order of magnitude. This improvement has transformed the overall workflow by allowing annotated datasets to grow rapidly without sacrificing model quality.

Once an updated segmentation model has been trained, it is applied automatically across every slice of an entire confocal image stack. Since a typical dataset contains approximately 200 slices, automated inference eliminates thousands of manual segmentation operations for every image processed. To further extend the analysis into three dimensions, we have also developed software that tracks segmented cells across adjacent slices and reconstructs them as individual 3D objects. This enables quantitative measurements of cell morphology, volume, and spatial organization throughout the biofilm.

The combination of optimized manual annotation, efficient machine learning training, automated segmentation, and 3D reconstruction provides a scalable pipeline for

generating large, high-quality annotated datasets. Using this workflow, we expect to produce approximately 200 fully processed biofilm images as an initial pilot corpus, providing an important community resource for developing and benchmarking future machine learning methods for biofilm image analysis.

Key outcomes or Other achievements:

The Fungal Quantitation Tool (FQT) was initially developed by an MS student in the laboratory of Dr. Gillian Queisser (Mathematics Department at Temple University). This is an example of another tool that will be made available within the Biofilm Image Library (BIL). The FQT has the capability to identify and quantitate yeast, fungal chains, germ tubes, and hyphae, providing both numbers and volumes. The FQT is being tested and validated by 4 different undergraduate students working on the fungal project in Dr Buttaro's lab. Test images were obtained from Dr Smith's lab at the Center for Biofilm Engineering and from collaborators' laboratories of Dr Abranches and Dr Doran. Further development is underway to identify individual hyphae in intertwined hyphal mats and to assess a method for removing yeast cells from densely packed images. Dr. Katrak, a postdoctoral researcher in Dr Abranches laboratory, has joined the development team and is using the software Dragonfly to separate yeast and hyphae. Dr. Buttaro is presenting a poster on this work at the Center for Biofilm Engineering's Montana Biofilm Meeting in 2026.

*** What opportunities for training and professional development has the project provided?**

The project supported the training of 16 undergraduate students, 13 of them funded at either Temple or CBE, in activities spanning image data collection, annotation, segmentation, and development of computational tools. Students were involved in biweekly group meetings where they presented updates and led group discussions. Through these activities, trainees developed interdisciplinary skills spanning microscopy, quantitative image analysis, and collaborative scientific communication. These student-led findings will be presented at national conferences during the next reporting period.

*** Have the results been disseminated to communities of interest? If so, please provide details.**

The PI team has presented and attended multiple conferences (a primary goal for this planning grant) to support the development of new collaborations and identify community wide resource needs. This includes:

- **IEEE Signal Processing in Medicine and Biology Symposium (SPMB) –** Dr Picone and Dr Parker attended. Dr Parker presented “Why do we need a biofilm imaging library? Current limitations when analyzing confocal 3D images” at this meeting on 12/6/2026.
- **American Society of Microbiology (ASM) Biofilms Meeting –** Dr Buttaro and Dr Smith attended in November 2026 in Portland OR.
- **Center for Biofilm Engineering (CBE) Biannual Meetings –**A special session was hosted by Dr’s Parker, Buttaro and Smith to meet with potential BIL users and collaborators. Dr Buttaro presented a group poster “Why do we need a Biofilm Imaging Library? (A Community Discussion – What to study?)”

*** What do you plan to do during the next reporting period to accomplish the goals?**

We plan to develop a competitive, large-scale interdisciplinary proposal to NSF 23-580 by expanding collaborations, refining research themes, and advancing proposal development.

Supporting Files

Filename	Description	Uploaded By	Uploaded On
segmentation_v00_Figure1.pdf	Figure 1. An example of the supervised training process used in machine learning. A manually annotated image is shown in the left. An automatically annotated image is shown on the right. Our optimized StarDist OPP models were	Albert Parker	06/30/2026

Filename	Description	Uploaded By	Uploaded On
	used for the automatic annotation		
segmentation_v00_Figure2.pdf	Figure 2. An example of the annotation process. The original image appears on the upper left. A manually annotated image appears on the upper right. Automatically annotated images appear in the lower panes that use a model trained on fully annotated data (left) and partially annotated data (right).	Albert Parker	06/30/2026

Products

Books

Book Chapters
A Parker, H Smith, B Buttaro, J Picone (2026). The Biofilm Image Library: Enabling Machine Learning for 3D Biofilm Analysis. *Signal Processing in Medicine and Biology: Applications of Deep Learning to the Health Sciences 2026.* A. Ahmed, J. Picone. Springer. . Status = OTHER; Acknowledgement of Federal Support = Yes ; Peer Reviewed = Yes

Inventions

Journals or Juried Conference Papers
View all journal articles and conference papers currently available in the NSF Public Access Repository for this award.

The results in the NSF Public Access Repository will include a comprehensive listing of all journal articles and conference papers recorded to date that are associated with this award.

Licenses

Other Conference Presentations / Papers
J Picone, B Buttaro, A Parker and H Smith (2026). *Machine Learning Challenges in Biofilm Engineering*. Center for Biofilm Engineering's Montana Biofilm Meeting. Bozeman. Status = OTHER; Acknowledgement of Federal Support = Yes

B Buttaro, H Smith, A Parker, J Picone. (2025). *Poster: Why do we need a biofilm imaging library?*. Center for Biofilm Engineering's Montana Biofilm Meeting. Bozeman, MT. Status = PUBLISHED; Acknowledgement of Federal Support = Yes

A Parker, H Smith, B Buttaro, J Picone (2025). *Why do we need a biofilm imaging library? Current limitations when analyzing confocal 3D images*. IEEE Signal Processing in Medicine and Biology Symposium. Philadelphia. Status = PUBLISHED; Acknowledgement of Federal Support = Yes

Other Products
View all datasets currently available in the NSF Public Access Repository for this award.
The results in the NSF Public Access Repository will include a comprehensive listing of all datasets recorded to date that are associated with this award.

View all workshop reports currently available in the NSF Public Access Repository for this award.

The results in the NSF Public Access Repository will include a comprehensive listing of all workshop report publications recorded to date that are associated with this award.

Other Publications

Patent Applications

Technologies or Techniques
Machine Learning models for use with StarDist OPP to segment individual cells in 3D image data

Thesis/Dissertations

Websites or Other Internet Sites
Biofilm Image Library Resources
http://www.biofilmimagelibrary.org

Periodic announcements of new data releases, users can explore library of images, sign up to receive emails, and provide feedback on the Biofilm Imaging Library

Participants/Organizations

What individuals have worked on the project?

Name	Most Senior Project Role	Nearest Person Month Worked
Parker, Albert	PD/PI	1
Buttaro, Bettina	Co PD/PI	1
Picone, Joseph	Co PD/PI	1
Smith, Heidi	Co PD/PI	1
Beeram, Vinay	Undergraduate Student	1
Beligalage, Thisumi	Undergraduate Student	1
Byrchak, Denys	Undergraduate Student	2
Dennis, Dennes	Undergraduate Student	2
Drobny, Sylvan	Undergraduate Student	1
John, Eleena	Undergraduate Student	1
Kazi, Sami	Undergraduate Student	1
McNutt, Georgia	Undergraduate Student	1
Nunez, Helisa	Undergraduate Student	2
Pasyar, Aryan	Undergraduate Student	1
Potluru, Tanishta	Undergraduate Student	1
Roxas, Erielle	Undergraduate Student	1

Name	Most Senior Project Role	Nearest Person Month Worked
Siddiq, Ayesha	Undergraduate Student	1

Full details of individuals who have worked on the project:

Albert E Parker
Email: albert.parker@montana.edu
Most Senior Project Role: PD/PI
Nearest Person Month Worked: 1

Contribution to the Project: Presented and hosted informational sessions at conferences, helped develop data standardization and research themes, mentored undergraduate students, drafted chapter, drafting proposal

Funding Support: None

Change in active other support: No

International Collaboration: No
International Travel: No

Bettina Buttaro
Email: bbuttaro@temple.edu
Most Senior Project Role: Co PD/PI
Nearest Person Month Worked: 1

Contribution to the Project: Managed data annotation and Fungal Quantitation Tool development and undergraduates. Presented and hosted informational sessions at conferences, helped develop data standardization and research themes, drafting proposal

Funding Support: None

Change in active other support: No

International Collaboration: No
International Travel: No

Joseph Picone
Email: joseph.picone@gmail.com
Most Senior Project Role: Co PD/PI
Nearest Person Month Worked: 1

Contribution to the Project: Managed the development and distribution of data.

Funding Support: None

Change in active other support: No

International Collaboration: No
International Travel: No

Heidi J Smith
Email: heidi.smith@montana.edu
Most Senior Project Role: Co PD/PI

Nearest Person Month Worked: 1

Contribution to the Project: Presented and hosted informational sessions at conferences, helped develop data standardization and research themes, mentored undergraduate students, collected and managed data, drafting proposal

Funding Support: None

Change in active other support: No

International Collaboration: No
International Travel: No

Vinay Deep Beeram
Email: vinay.deep.beeram@temple.edu
Most Senior Project Role: Undergraduate Student
Nearest Person Month Worked: 1

Contribution to the Project: Annotated 3D images to train and test machine learning algorithms for cell segmentation.

Funding Support: None

International Collaboration: No
International Travel: No

Thisumi Anupraba Beligalage
Email: thisumi.beligalage@temple.edu
Most Senior Project Role: Undergraduate Student
Nearest Person Month Worked: 1

Contribution to the Project: Annotated 3D images to train and test machine learning algorithms for cell segmentation.

Funding Support: None

International Collaboration: No
International Travel: No

Denys Byrchak
Email: denys.byrchak@temple.edu
Most Senior Project Role: Undergraduate Student
Nearest Person Month Worked: 2

Contribution to the Project: Developed machine learning models for segmentation of biofilm images.

Funding Support: None

International Collaboration: No
International Travel: No

Dennes Dennis
Email: dennes.dennis@lions.lincoln.edu
Most Senior Project Role: Undergraduate Student

Nearest Person Month Worked: 2

Contribution to the Project: Annotated 3D images to train and test machine learning algorithms for cell segmentation.

Funding Support: Temple University's Summer Scholars Program

International Collaboration: No
International Travel: No

Sylvan Drobny
Email: sylvan.drobny@student.montana.edu
Most Senior Project Role: Undergraduate Student
Nearest Person Month Worked: 1

Contribution to the Project: Annotated 3D images to train and test machine learning algorithms for cell segmentation.

Funding Support: Montana State University's Eco-Start Program

International Collaboration: No
International Travel: No

Eleena Suja John
Email: eleena.john@temple.edu
Most Senior Project Role: Undergraduate Student
Nearest Person Month Worked: 1

Contribution to the Project: Annotated 3D images to train and test machine learning algorithms for cell segmentation.

Funding Support: None

International Collaboration: No
International Travel: No

Sami Kazi
Email: sami.kazi@temple.edu
Most Senior Project Role: Undergraduate Student
Nearest Person Month Worked: 1

Contribution to the Project: Annotated 3D images to train and test machine learning algorithms for cell segmentation.

Funding Support: None

International Collaboration: No
International Travel: No

Georgia McNutt
Email: georgiamcnutt@montana.edu
Most Senior Project Role: Undergraduate Student
Nearest Person Month Worked: 1

Contribution to the Project: Annotated 3D images to train and test machine learning algorithms for cell segmentation.

Funding Support: Montana State University's Eco-start Program

International Collaboration: No
International Travel: No

Helisa Nunez
Email: helisanunez@gmail.com
Most Senior Project Role: Undergraduate Student
Nearest Person Month Worked: 2

Contribution to the Project: Annotated 3D images to train and test machine learning algorithms for cell segmentation.

Funding Support: Temple University's Summer Scholars Program

International Collaboration: No
International Travel: No

Aryan Pasyar
Email: aryan.pasyar@temple.edu
Most Senior Project Role: Undergraduate Student
Nearest Person Month Worked: 1

Contribution to the Project: Annotated 3D images to train and test machine learning algorithms for cell segmentation.

Funding Support: Temple University's Research Scholars Program

International Collaboration: No
International Travel: No

Tanishta Potluru
Email: tanishta.potluru@temple.edu
Most Senior Project Role: Undergraduate Student
Nearest Person Month Worked: 1

Contribution to the Project: Annotated 3D images to train and test machine learning algorithms for cell segmentation.

Funding Support: None

International Collaboration: No
International Travel: No

Erielle Zaina Roxas
Email: erielle.roxas@temple.edu
Most Senior Project Role: Undergraduate Student
Nearest Person Month Worked: 1

Contribution to the Project: Administered the computers and web server for project specific needs. Organized and curated the pilot databases being developed.

Funding Support: None

International Collaboration: No
International Travel: No

Ayesha Siddiq
Email: ayesha.siddiq@temple.edu
Most Senior Project Role: Undergraduate Student
Nearest Person Month Worked: 1

Contribution to the Project: Annotated 3D images to train and test machine learning algorithms for cell segmentation.

Funding Support: None

International Collaboration: No
International Travel: No

What other organizations have been involved as partners?

Name	Type of Partner Organization	Location
Eastern University	Academic Institution	St Davids, PA
University of Colorado	Academic Institution	Anschutz School of Medicine
Unversity of Florida	Academic Institution	College of Dentistry

Full details of organizations that have been involved as partners:

Eastern University

Organization Type: Academic Institution
Organization Location: St Davids, PA

Partner's Contribution to the Project:
In-Kind Support
Collaborative Research

More Detail on Partner and Contribution: We provided data sets for annotation as research opportunities for three undergraduate students supervised by Dr. Brandi Megonigal, an assistant professor of Data Science at Eastern University.

University of Colorado

Organization Type: Academic Institution
Organization Location: Anschutz School of Medicine

Partner's Contribution to the Project:
Collaborative Research

More Detail on Partner and Contribution: The lab of Dr. Kelly Duran, professor of Immunology & Microbiology, has deposited 3D image data of multi-domain biofilms into the Biofilm Image Library. We are collaborating with Dr Doran's lab to analyze these data using the Fungal Quantitation Tool. Dr. Buttaro is presenting a poster on this work at MBM

2026.

Unversity of Florida

Organization Type: Academic Institution
Organization Location: College of Dentistry

Partner's Contribution to the Project:
Collaborative Research

More Detail on Partner and Contribution: The lab of Dr. Jacqueline Abranches, associate professor of Oral Biology, has deposited 3D image data of multi-domain biofilms into the Biofilm Image Library. We are collaborating with Dr Abranches' lab to analyze these data using the Fungal Quantitation Tool and using the commercial software Dragonfly. Dr. Buttaro is presenting a poster on this work at MBM 2026.

Were other collaborators or contacts involved? If so, please provide details.

Dr. Gillian Queisser, Department of Mathematics at Temple University, and her student are developing the Fungal Quantitation Tool for 3D image data for use in the Biofilm Imaging Library.

Dr. Isaac Klapper, Department of Mathematics at Temple University, and his students have developed mathematical models of biofilms and would like to incorporate 3D spatial information to improve models and include in the Biofilm Imaging Library.

Impacts

What is the impact on the development of the principal discipline(s) of the project?

The project impacts the development of bioimaging and related disciplines by establishing integrated workflows that combine advanced microscopy with automated image analysis and computational tool development. By enabling more efficient and reproducible extraction of quantitative information from imaging datasets, the work addresses key bottlenecks in the field and supports the transition toward high-throughput, data-driven analysis. These contributions enhance methodological capabilities across disciplines that rely on imaging, including microbiology, environmental science, and biomedical research.

What is the impact on other disciplines?

The project impacts a range of disciplines by providing scalable and reproducible approaches for extracting quantitative information from imaging datasets. The integration of 3D image segmentation, annotation, and computational tool development is broadly applicable to fields including environmental science, biomedical engineering, and materials science. These advances facilitate the integration of machine learning/data science into different disciplines and will ultimately improve the overall understanding of complex spatially rooted data.

What is the impact on the development of human resources?

An undergraduate student introduced to machine learning applications in biofilm engineering may be interested in pursuing machine learning applications in the health sciences as a career and consequently pursue a masters degree in this area.

The Biofilm Image Library will routinely assist users, many of whom are entry-level graduate students, with technology-related problems and the associated machine learning software.

What was the impact on teaching and educational experiences?
Nothing to report.

What is the impact on physical resources that form infrastructure?
Nothing to report.

What is the impact on institutional resources that form infrastructure?
Nothing to report.

What is the impact on information resources that form infrastructure?
Nothing to report.

What is the impact on technology transfer?

The Biofilm Image Library web site (www.biofilmimagelibrary.org) is operational and has begun accepting subscribers. Users can sign a data sharing agreement to receive anonymous access to our software and data, or simply sign up to receive announcements. Data use agreements are archived as part of the subscription process.

What is the impact on society beyond science and technology?
Nothing to report.

What percentage of the award's budget was spent in a foreign country?

0%

Changes/Problems

Changes in approach and reason for change

Our award is a planning grant for a larger proposal to the CISE/CIRC program. Unfortunately, CIRC (NSF 23-589) is no longer active (www.nsf.gov/funding/opportunities/circ-community-infrastructure-research-computer-information/12810/nsf23-589). Dr Andy Duan, our current NSF Program Officer, suggested that CISE/IDSS may be an appropriate alternative focus for our planning grant (www.nsf.gov/funding/opportunities/idss-integrated-data-systems-services). However, Dr. Marlon Pierce Program Director, NSF CISE/OAC indicated that IDSS was not appropriate and instead suggested either CSSI (www.nsf.gov/funding/opportunities/cssi-cyberinfrastructure-sustained-scientific-innovation) or NSF BIO directorate's Division of Biological Infrastructure, https://www.nsf.gov/bio/dbi as possible foci for our planning grant. We contacted and met with Dr Katharina Dittmar, Section Head of Biological Infrastructure, and she suggested that we generte a proposal from our planning grant for NSF 23-580: Infrastructure Capacity for Biological Research (www.nsf.gov/funding/opportunities/capacity-infrastructure-capacity-biological-research/nsf23-580/solicitation) part of the Directorate for Biological Sciences' Division of Biological Infrastructure. Thus, our current plan is to generate a proposal for NSF 23-580.

Actual or Anticipated problems or delays and actions or plans to resolve them
Nothing to report.

Changes that have a significant impact on expenditures
Nothing to report.

Significant changes in use or care of human subjects
Nothing to report.

Significant changes in use or care of vertebrate animals
Nothing to report.

Significant changes in use or care of biohazards
Nothing to report.

Change in primary performance site location
Nothing to report.

Special Requirements

Responses to any special reporting requirements specified in the award terms and conditions, as well as any award specific reporting requirements.
Nothing to report.