

Brown Bag Seminars

SS/SC Brown Bag Seminar Series

The seminar should give staff scientists a platform to present and discuss their science. As SS/SC we are highly specialized and have greatly varying scientific interests, and we liked for the seminar to represent this; thus, the choice of topic and format will be speaker driven.

The seminar could be:

regular 45 min talk about your research, chalk talk, summary of cool new stuff you heard about at a conference you recently went to, talk you need feedback for, presentation of a manuscript you liked to get feedback on, talk about a project that just can't get off the ground and needs troubleshooting, presentation of a new technology/possible equipment purchases, presentations by several SSSC together or several shorter presentations.

We are also well aware that there is no time and location that fits all. We booked 37/2041 for the first Thursday of each month from 12(noon) to 1PM, however, if you wish to present a seminar at another time / location just find a room that suits you better and let us know.

If you would like to schedule your talk or have any questions, please contact:

Christina Stuelten (christu@mail.nih.gov), Yoshimi Greer (greery@mail.nih.gov) or Emily Tai (taic@mail.nih.gov)

2024 Spring Series – "Network and share your work "

Didn't have a chance to meet other SS / SC and talk science lately? - We invite you to share your work as a poster or a short talk with other SS/SC in a series Brown Bag Lunch Seminars.

Date and Time	Title	Speaker	Affiliation	WebEx Link/Sildes
3/1 (Fri) noon-1:30	TGF-beta regulated mRNA splicing	Christina Stuelten	LCMB	

2023 Summer Series – "Network and share your work "

Didn't have a chance to meet other SS / SC and talk science lately? - We invite you to share your work as a poster or a short talk with other SS/SC in a series Brown Bag Lunch Seminars.

Date and Time	Title	Speaker	Affiliation	WebEx Link/Sildes
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6/8 (Thu) noon-1:00	Empowering your research with services from the CCR Genomics Core	Madeline Wong	CCR Genomics Core	 20230608.SSSC.MadelineWong.pdf
8/17 (Thu) noon-2:00	Repurposing anti-viral vaccines for in situ cancer immunotherapy	Nicolas Cuburu	LCO	
	Thermal Proteome Profiling for Global Analysis of Drug Effects	Lisa Jenkins	LCB	
9/21 (Thu) noon-2:00	TumorMiner a new tool for precision medicine	Fathi Eloumi	DTB	
	Single Molecule Analysis of CENP-A Chromatin by High-Speed Atomic Force Microscopy	Daniël Melters	LRBGE	
	'Inside out', a novel CD47 signaling mediated via extracellular vesicles shed by immune and cancer cells	Sukhbir Kaur	Lab of Pathology	

10/19 (Thu) noon-2:00	Addressing transcriptomic spillover in NGS analysis of PDX models of metastasis	Brian Capaldo	Laboratory of Genitourinary Cancer Pathogenesis	https://cbiit.webex.com/cbiit/j.php?MTID=m12c0742ea9739c4c079bdf5ed59a8506
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2021 Fall/2022 Winter Series – "SS/SC Alumni - Where are they now?"

We are inviting our alumni who moved on to other positions in NCI, other ICs in NIH, FDA, academia or industry to share their experience with us.

Date and Time	Title	Speaker	Affiliation	WebEx Link/Sildes
9/13 (Mon) 11:30 -12:30	Staying at NIH BUT leaving the bench	Zack Howard	Center for Scientific Review, NIH	 SStoSRO2021.pdf
11/1 (Mon) noon-1:00	Outside of the lab BUT close to the science	Ana Roles	Office of Cancer Clinical Proteomics Research, DCTD, NCI	 SStoPO20211.pdf

1/26 (Wed) noon- 1:00	Research in a regulatory agency: the advantages of the researcher/assessor model at OPQ/CDER	Carole Sourbier	Office of Pharmaceutical Quality, Center for Drug Evaluation and Research, FDA	 20220126.FDA.CaroleSourbier.pdf
3/23 (Wed) noon- 1:00	Supporting Cancer Research through Planning and Analysis	Diane Palmieri	Center for Research Strategy, NCI	 Palmieri_NCI SCS...Bag_03252022.pdf
4/22 (Fri) noon- 1:00	Transition from Staff Scientist to Pharma	Eve Walsh Seng	AstraZeneca R&D Biologics Engineering	 SSSC_042222.SStoPharma.pdf

2021 Spring Series –

Understanding Tumor Heterogeneity and Plasticity through the Lens of Machine Learning and Mathematics

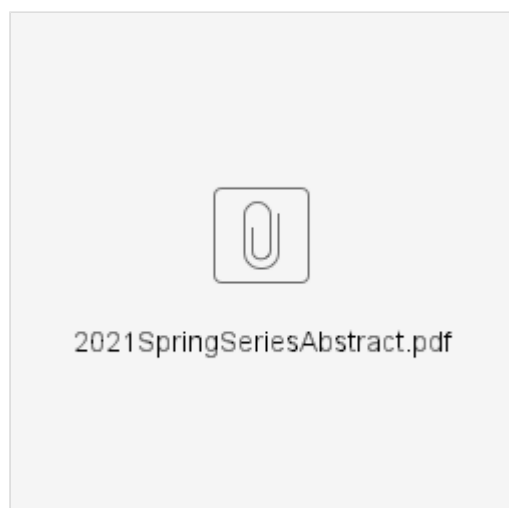
Maxwell Lee will review different approaches to understand tumor heterogeneity and plasticity. The topics includes using mixture models to deconvolute bulk RNA-seq data, clustering and classification of single cell RNA-seq to study tumor subtypes, and mathematic tools to predict cancer cell evolution. His talk abstract, outline, the topic of each week are listed below. Slides will be posted Monday morning before the talk and the video recording will be available afterwards.

Monday 10:00AM-11:00AM

WebEx Link: <https://cbit.webex.com/cbit/j.php?MTID=mc31fec457279698a34e0aa990172743e>

Meeting number: 157 260 1880 **Meeting Password:** UEuBV2P2Z\$3

Abstract and Outline:



Date	Title	Speaker	Affiliation	Slides	Video Recording Link
4 / 12	Cancer stem cell model and evolutionary dynamics	Maxwell Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR		Cancer stem cell model video

				 SSSC_MaxLee_04122021.pdf	link click here
4 / 26	Cell fate decision determined by Gene Regulatory Network (GRN)	Max well Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_04262021.pdf	Gene re gu lat or y ne tw or k vid eo lin k cli ck he re
5 / 10	Waddington's epigenetic landscape quantified with quasi-potential	Max well Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_05102021..pdf	W ad di ng to n's epi ge ne tic lan ds ca pe vid

					eo lin k cli ck he re
5 / 24	Network motifs and dynamics of cellular states	Max well Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_05242021.pdf	Ne tw or k m oti fs vid eo lin k cli ck he re
6 / 17	Network motifs for desensitization and history of the treatment exposure	Max well Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_06072021.pdf	Ne tw or k m oti fs for de se nsi tiza ti on vid eo lin k cli ck he re
6 / 21	Drug-tolerant persister (DTP) and cancer dynamics	Max well Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR		Dr ug -

				 SSSC_MaxLee_06212021.pdf	tolerant persister video link click here
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2020 Fall/Winter Series – Clustering Methods: from k-means to Gaussian mixture model and Louvain algorithm

Maxwell Lee will review some basic concepts of clustering analyses that are commonly used in cancer research, including 1) traditional methods of hierarchical clustering and k-means; 2) Gaussian mixture model (GMM) and latent Dirichlet allocation (LDA); 3) graph-based approaches, which are the state-of-the-art technologies used in the single cell data analysis. **Max will provide practical examples to illustrate how each method works, how to interpret the results of clustering analysis and explain the pros and cons of each method.** His talk abstract, outline, the topic of each week are listed below for your reference. Slides will be posted the weekend before the talk and the video recording will be available afterwards.

Monday 10:00AM-11:00AM

WebEx Link: <https://cbiit.webex.com/cbiit/j.php?MTID=m593aca29c65d0e9f7be43bfc2ad1b092>

Meeting number: 172 414 1612 **Meeting Password:** AmWdZgu*775

Abstract and Outline:

 abstract.MaxLee.20200831.pdf	 SSSC_ClusteringOutline.pdf
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	Title		Affiliation	Slides	Video
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Date		Speaker			Recording Link
9 / 21	Introduction and k-means clustering	Max well Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_09212020..pdf	K-means clustering video link click here
10 / 5	Gaussian mixture model (GMM) and Latent Dirichlet Allocation (LDA)	Max well Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_10052020.pdf	GMM and LDA video link click here
10 / 19	Non-negative matrix factorization (NMF) and its connection to k-means clustering	Max well Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_10192020.pdf	
	Hierarchical clustering		Laboratory of Cancer Biology and Genetics, NCI/CCR		Hierarc

1 1 /2		Max well Lee		 SSSC_MaxLee_11022020.pdf	hical Clustering video link click here
1 1 / 16	Spectral clustering and its connection to Laplacian Eigenmaps	Max well Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 Broken macro  SSSC_MaxLee_11162020.pdf	Spectral Clustering video link click here
1 2 / 21	Louvain clustering and its application to single cell RNAseq data analysis	Max well Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_12072020.pdf	Louvain Clustering video link click here
1 / 25	Latent Dirichlet Allocation (LDA) and its application to sequence motif analysis	Max well Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR		LDA video link

					 SSSC_MaxLee_01252021.pdf	click here
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2020 Spring/Summer Series

12:00 PM - 01:00 PM, Building 37, Room 2041 (second floor conference room) - please note the location and time may be different in some cases

Date	Title	Speaker(s)	Affiliation	Slides	WebEx Link, Video Recording Link and Abstract
04/16	Dimension Reduction Methods: from PCA to TSNE and UMAP - Part I	Maxwell Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_05222020.pdf	Recording link Principal Component Analysis (PCA) provides a foundation to understanding various dimension reduction methods. Principal components are the linear combinations of the original variables with the 1 st principal component captures the largest variance, followed by a descending order for the rest of the principal components and subject to the principal components being orthonormal. A geometric perspective of PCA is the rotation of coordinate system.
04/23	Dimension Reduction Methods: from PCA to TSNE and UMAP - Part II	Maxwell Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR		Recording link Multidimensional Scaling (MDS) provides an alternative strategy for dimension reduction. The data matrix is pairwise distance matrix. The distance matrix is converted to Gram matrix (similarity matrix). Eigen decomposition of Gram matrix generates eigen vectors and eigen values. The product of eigen vector matrix and square root of eigen value matrix is identical to principal component matrix.

				 SSSC_MaxLee_04232020.pdf	
04 /30	Dimension Reduction Methods: from PCA to TSNE and UMAP - Part III	Maxwell Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_04302020.pdf	Recording link Non-linear dimension reduction is essential for the analysis of data that lie in non-Euclidian space. Geodesic distance is better measurement for points on a curve or curved surface. Iso map is similar to MDS except that pairwise distance matrix uses geodesic distance instead of Euclidian distance.
05 /07	Dimension Reduction Methods: from PCA to TSNE and UMAP - Part IV	Maxwell Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_05072020.pdf	Recording link TSNE models data in high-dimension with Gaussian distribution and data in low-dimension with t-distribution. Covariance matrix adjusted distance matrix is converted to similarity matrix through Gaussian distribution. The cost function is KL divergence to minimize the two probability distributions. Seurat package was used to analyze RNAseq data. Effect of mitochondria gene percentage cutoff was analyzed.
05 /14	Dimension Reduction Methods: from PCA to TSNE and UMAP - Part V	Maxwell Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR		Recording link TSNE and UMAP were compared. UMAP uses k-nearest neighbor (KNN) and calculates weight matrix. The cost function is binary cross-entropy. It is much faster than TSNE and also achieves better separation between clusters.

				 SSSC_MaxLee_05142020.pdf	
05 /28	Dimension Reduction Methods: from PCA to TSNE and UMAP - Part VI	Maxwell Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_05282020.pdf	Recording link More detailed analyses of scRNAseq data with UMAP were performed. The effect of filtering out cells with high mitochondrial genes was discussed. Algorithm of UMAP was explained.
06 /04	Dimension Reduction Methods: from PCA to TSNE and UMAP - Part VII	Maxwell Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	 SSSC_MaxLee_06042020.pdf	Recording link Trajectory analysis was performed using Monocle 2 and 3 packages. Two datasets were analyzed, Human Skeletal Muscle Myoblasts (HSMM) and neural crest cells from Mouse Organogenesis Cell Atlas (MOCA). Monocle 2 uses minimal spanning tree model where Monocle 3 uses general graph and produces trajectory analysis for multiple subgraphs.
06 /18	Dimension Reduction Methods: from PCA to TSNE and UMAP - Part VIII and Q&A	Maxwell Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR		Webex Thursday, Jun 18, 12noon - 1pm https://cbit.webex.com/cbit/j.php?MTID=md38682248ab766611823beee46acab18 Meeting number (access code): 476 578 641 Meeting password: c3wEha9Y5h\$

				 SSSC_MaxLee_06182020.pdf	Summary of comparison between Monocle 2 and 3 analysis. Monocle 2 generates plot with coordinates resulted from the reversed graph embedding. Monocle 3 plot uses UMAP data and shows trajectory for multiple subgraphs. The objective function Monocle 2 has 3 parts: Pearson residuals in high-dimension, cost function for the minimal spanning tree, and k-means like clustering.
07/15	What Should Staff Scientists & Staff Clinicians (SSSCs) Know About Technology Transfer?	CCR SSSC Professional Development Committee Aida Cremesti Laura Prestia	Special Seminar from the CCR SSSC Professional Development Committee and NCI's Technology Transfer Center (TTC)	 SSSC Tech Transfe...binar 7.15.20.pdf	Webex Wed, July 15, 12noon - 1pm https://cbit.webex.com/cbit/j.php?MTID=m610dac8f56d3c290997f2bf6c97 The following topics will be covered in an interactive Webex: • Overview of the technology transfer process • Material Transfer Agreements (MTAs) • Cooperative Research and Development Agreements (CRADAs) • Technology transfer training /programs and discussion for future opportunities

2019 Series

12:00 PM - 01:00 PM, Building 37, Room 2041 (second floor conference room) - please note the location and time may be different in some cases

Date	Title	Speaker(s)	Affiliation	Slides	Location
01/04	Five reasons to pay attention to SAXS-assisted protein structure prediction	Susan Tsutakawa	Lawrence Berkeley National Laboratory, University of California at Berkeley		3-4 pm 374041

				 190104nih_tsutakawa_saxs.pdf  BrownBag_Flyer.pdf	
01/25	Principles of cancer modeling in mice	Chi-Ping Day	Laboratory of Cancer Biology and Genetics, NCI/CCR	 Day.pdf	1 2- 1 pm 3 7 /2 0 41
03/01	The Advanced Imaging & Microscopy Resource: a new trans-NIH resource for next generation microscopy	Harsh Vishwa srao	Director, Advanced Imaging and Microscopy Resource, NIH		1- 2 pm 3 7 /6 0 41
03/28	The Genome Modification Core at the Frederick National Lab for Cancer Research – a collaborative	Raj Chari	Director, Genome Modification Core, NCI		1 2-

resource for the NCI CCR	/FNLCR	1 pm 3 7 /2 0 41
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2018 Series

12:00 PM - 01:00 PM, Building 37, Room 2041 (second floor conference room)

D ate	Title	Speak er(s)	Affiliation	Slides
02 /15	Single Cell Genomics - CCR new initiative and practical tips	Liz Conner Mike Kelly	CCR Genomics Core Single Cell Analysis Facility	 Kelly.PDF
03 /01	Mass Spectrometry – How it works, what it does, and how it can help you	Lisa Jenkins	Mass Spectrometry Program, Laboratory of Cell Biology, NCI/CCR	 Jenkins.pdf
04 /27	Statistical analysis: concept, practice, and interpretation. Part I	Maxwell Lee	Laboratory of Cancer Biology and Genetics, NCI/CCR	

				 SSSC_MaxLee_04272018.pdf
05 /03	Statistical analysis: application to NGS data with DESeq2 and GSEA. Part II	Howard Yang	Laboratory of Cancer Biology and Genetics, NCI/CCR	
05 /31	High-Throughput Imaging for System Cell Biology	Gianluca Pegararo	Laboratory of Receptor Biology and Gene Expression, NCI/CCR	 Pegararo.pdf.pdf
09 /27	Cutting edge protein analysis technologies - advancing quantitative proteomic research, biomarker assessment, and molecular profiling	Jinjiu (Jessie) Chen Noemi Kedei	Collaborative Protein Technology Resource, NCI/CCR	 Chen_Kedei.pdf.pdf

2017 Series

12:00 PM - 01:00 PM, Building 37, Room 2041 (second floor conference room)

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Date	Title	Speaker(s)	Affiliation
04/06	Innovative Sequencing Resources in the CCR Sequencing Facility	Bao Tran	CCR, Sequencing Facility
05/18	ONC201 Kills Breast Cancer Cells by Inhibiting Mitochondrial Respiration	Yoshimi Endo Greer	Women's Malignancies Branch
06/01	Kicking Lymphoma When It's Down - How we can exploit the apoptotic threshold therapeutically in Diffuse Large B Cell Lymphoma	Art Schaffer	Lymphoid Malignancies Branch
07/06	Leukocyte adhesion deficiency in a cat due to a deletion in the CD18 gene	Thomas Bauer	Experimental Transplantation and Immunology Branch
12/01	Predicting targets of T cell responses in cancer: Evaluating algorithms and lessons learned from the Immune Epitope Database	Bjorn Peters	La Jolla Institute for Allergy and Immunology
12/07	CCR Collaborative Bioinformatics Resource: Our NGS Pipeline Tools (Introduction by Maggie Cam)	Justin Lack	CCR Collaborative Bioinformatics Resource (CCBR)