AGENDA as of 11/4/21

AMP 2021: Get AMPed!: Updates and Case Studies in Molecular Pathology
Thursday, January 13, 2022
VIRTUAL

TIME (Eastern)	SESSION	SPEAKER
10:00 am	**Welcome and Introductions**	**Nathanael G. Bailey, MD** Training and Education Chair *University of Pittsburgh*
10:05 am	**HOT TOPICS IN MOLECULAR PATHOLOGY:** • Updates on Molecular Testing and Practice Guidelines in Colorectal Cancer • Digital Spatial Transcriptional/Transcriptomics Profiling	**Antonia Sepulveda, MD, PhD** AMP President *George Washington University*
10:50 am	**From the Operating room to the Laboratory: Pre-analytic Considerations for Tissues** This session will cover best practices for molecular diagnostic testing on tissue with a focus on pre-analytic factors. The suitability of the tissue used for subsequent molecular testing is impacted by a variety of different factors that start in the operating room or radiology suite when the tissue is being obtained through processing in gross pathology, histology, and finally in the molecular diagnostic laboratory. We will cover important best practices that include specimen types, multi-disciplinary communication, tissue fixatives and processing, as well as specimen enrichment and adequacy requirements. **Learning Objectives:** • Troubleshoot tissue specimens that fail molecular diagnostics. • Implement best practices for pre-analytic processes.	**Lauren L. Ritterhouse, MD, PhD** *Massachusetts General Hospital, Center for Integrated Diagnostics*
11:15 am	**Q&A Session**	
11:20 am	**BREAK** (15 min)	
11:35 am	**Testing Modalities to Look at Genome Structure: Conventional Cytogenetics, FISH, and Chromosomal Microarray Analysis** This session will describe various testing modalities to assess structural and numerical variations that occur throughout the whole genome. **Learning Objectives:** • Demonstrate the clinical utility of identifying whole genome structural and numerical aberrations in disease workup. • Describe testing modalities that aid in the diagnosis of such genome aberrations. • List the advantages and disadvantages of each modality in the context of clinical case workup.	**Yassmine Akkari, PhD** *Legacy Health*
12:00 pm	**Q&A Session**	
12:05 pm	**Application of genomic technologies in clinical practice** The session will review the different genomic technologies used for molecular profiling of tumors in clinical practice with associated limitations and challenges. **Learning Objectives:** • Describe the fundamentals of the various genomic technologies. • Apply the knowledge gained to molecular profiling of tumors in clinical practice.	**Honey V Reddi, PhD, FACMG** *Medical College of Wisconsin*
12:30 pm	**Q&A Session**	
12:35 pm	**LUNCH (for Eastern Time) / EXTENDED BREAK (for Pacific Time)**	
1:05 pm	**Introduction to Bioinformatics Pipeline & Data Analysis** This session is an introduction to a comprehensive bioinformatics pipeline for DNA and RNA including tumor mutation burden assessment and detection of small variants, copy number variation, and fusion. It describes the major components in the pipeline, basic algorithms in the analyses, and summaries the considerations for the pipeline design.	**Weiwei Zhang, PhD** *University of Nebraska Medical Center*

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	Learning Objectives: • List the major components of a comprehensive bioinformatics pipeline. • Describe the approaches for the detection of small variants, TMB, copy number variation, and fusion. • Explain the basic algorithms involved in analyzing the NGS data.	
1:45 pm	**Q&A Session**	
1:50 pm	**Hot topics in SARS-CoV-2 and COVID-19** The speaker of this session will provide recent updates to the COVID-19 pandemic, with a particular focus on SARS-CoV-2 testing. Topics will include molecular diagnostic testing and technical aspects and applications of whole-genome sequencing of SARS-CoV-2. **Learning Objectives:** • Describe the importance of limiting cross-contamination in molecular SARS-CoV-2 testing. • Describe the most common platforms and workflows for SARS-CoV-2 whole-genome sequencing. • Explain the usefulness of whole-genome sequencing for lineage/variant typing, outbreak response, and other applications.	**Allen Bateman, PhD, MPH, D(ABMM)** *Wisconsin State Laboratory of Hygiene*
2:25 pm	**LUNCH (for Pacific Time) / EXTENDED BREAK (for Eastern Time)**	
2:55 pm	**Introduction to Interactive Case Sessions**	**Nathanael G. Bailey, MD**
3:00 pm	**Case Study Session: Solid Tumors** This is an interactive session that highlights the role of mutation signature analysis in the diagnosis and management of patients. This session describes a pediatric case of medulloblastoma in which the finding of an ultra-hypermutated brain tumor with a distinct mutational signature led to the identification of an unusual germline cancer predisposition syndrome. **Learning Objectives:** • Identify the likely underlying germline cancer predisposition syndrome based on the mutation signature analysis. • Distinguish between Constitutional Mismatch Repair Deficiency Syndrome (CMMRD) and POLE/POLD1 polymerase cancer syndrome	**Annie Garcia, MD** *Baylor College of Medicine* **Eduardo Castro-Echeverry, MD, MPH** *Baylor Scott and White Medical Center*
3:30 pm	**Case Study Session: Hematopathology** This session will review the important role of next-generation sequencing (NGS) testing in both risk stratification and therapy selection for patients with acute myeloid leukemia. We will present two illustrative cases, one which highlights how mutational ontogeny informs selection of measurable residual disease molecular markers and another which illustrates the importance of germline variants in predisposing some patients to myeloid malignancy. **Learning Objectives:** • Describe the importance of mutational ontogeny in defining preferred targets for disease monitoring • Identify potential germline variants identified in leukemia sequencing assays and select appropriate methods for distinguishing somatic versus germline origin	**Nathan D. Montgomery, MD, PhD** *University of North Carolina* **Amir Behdad, MD, MBA** *Northwestern University*
4:00 pm	**BREAK** (15 min)	
4:15 pm	**Case Study Session: Genetics** This interactive session will review cases demonstrating detection of multiple types of non-single nucleotide variant (SNV) genomic events, including copy number variants, fusions, and germline variant interpretation using next generation sequencing (NGS) data and confirmatory testing methods. **Learning Objectives:** • Interpret NGS findings for evaluation of copy number variants, gene fusions, and germline variants. • Describe some potential pitfalls in using NGS for detection of non-SNV variants. • List some of the common scenarios when NGS findings should be followed up with confirmatory testing.	**Ying Zou, MD, PhD, FACMG** *Johns Hopkins University* **Jeff Kleinberger, MD, PhD** *University of Pittsburgh Medical Center*

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4:45 pm	**Case Study Session: Infectious Disease** In this session, case-based examples will demonstrate how infectious disease molecular testing should be effectively used by ordering providers to improve patient care. Key concepts around interpretation of complex molecular infectious disease test results and stewardship to prevent inappropriate testing will be addressed. This includes issues around the sensitivity, specificity and cost of molecular testing and potential negative consequences to patients and facilities. **Learning Objectives:** • Illustrate the complexities of syndromic panel testing. • Propose a diagnostic stewardship algorithm for a molecular infectious disease test. • Estimate the patient care impacts of diagnostic stewardship approach to a molecular infectious disease test.	**Paige M.K. Larkin, PhD D(ABMM)** *NorthShore University HealthSystem and University of Chicago Pritzker School of Medicine* **Erin H. Graf, PhD, D(ABMM)** *Mayo Clinic Arizona*
5:15 pm	**Closing Remarks, and Evaluations**	**Nathanael G. Bailey, MD**
5:30 pm	**Adjourn**	