**Schedule**

**VISIT DATES FROM OCTOBER 18 – 26**

**SUNDAY, OCTOBER 18**

Fly from Seattle to San Diego, and traveling to SD to Ensenada by car (around 2 hours). Stop by at Puerto Nuevo to eat Red Lobster.

**MONDAY, OCTOBER 19**

* Visit CICESE to check out CICESE’s computer lab and facilities and make arrangements for the course (if you need something to installed software or other thing).

Course opening

* 40 min Seminars presentations

1. Brent Vadopalas *Tentative title:* “Challenges in shellfish aquaculture and omics based solutions”
2. Steven Roberts “Does DNA Methylation Facilitate Phenotypic Plasticity in Marine Invertebrates?”

**FROM TUESDAY 20 TO SATURDAY 24**

**Course name: “**Bioinformatics for Transcriptomic and Epigenomic Analyses**”**

20-24 October 2015

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Morning 9am - 1pm

Afternoon 3pm - 6pm

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Marine environments are continually changing in response to both natural processes and human activities, both having distinct impacts on marine organisms. Furthermore, shellfish aquaculture is increasingly faced with challenges that require a better understanding of basic biology. This course will focus on the computational tools to explore the surprising similarities and unique differences in the physiology of aquatic organisms. A core component of this course will be hands on tutorials examining high-throughput sequencing data. Specifically, transcriptome (RNA-seq) and epigenetic (BS-seq; MBD arrays) data will be analyzed. Bioinformatic instruction will include modules on gene annotation, differential gene expression, and DNA methylation analyses. In addition, we will introduce genome browsers as a tool to examine structural relationships among genomic features. There will be an emphasis on open science practices including the use of electronic lab notebooks.

This is a five-day course with hands-on bioinformatics analyses accompanied with discussions of fundamental physiological processes, specific case studies, and underlying laboratory techniques. The general objective of this course is to provide participants with core computing skills and experience with genomic datasets.

Participants will learn how to

1) Set-up computing environments for bioinformatics analysis and learn basic unix commands.

2) Use version control for effective documentation of analyses, backup, and collaboration.

3) Characterize and annotate novel transcriptomes

4) Identify differentially expressed genes and alternative splice products

5) Assess epigenetic variation in relation to genomic features

We will be using local (desktop) software including bash, blast, tophat, bedtools, IGV, tophat and jupyter (IPython) notebooks. Additionally, participants will learn how to use open, web-based platforms including iPlant Collaborative, SQLShare, and Galaxy.

**SUNDAY, OCTOBER 25**

Visit to Guadalupe’s Valley wineries (course closures) – event closing

**MONDAY, OCTOBER 26**

Traveling from Ensenada to SD by car (early morning)

Flying from SD to Seattle (afternoon).