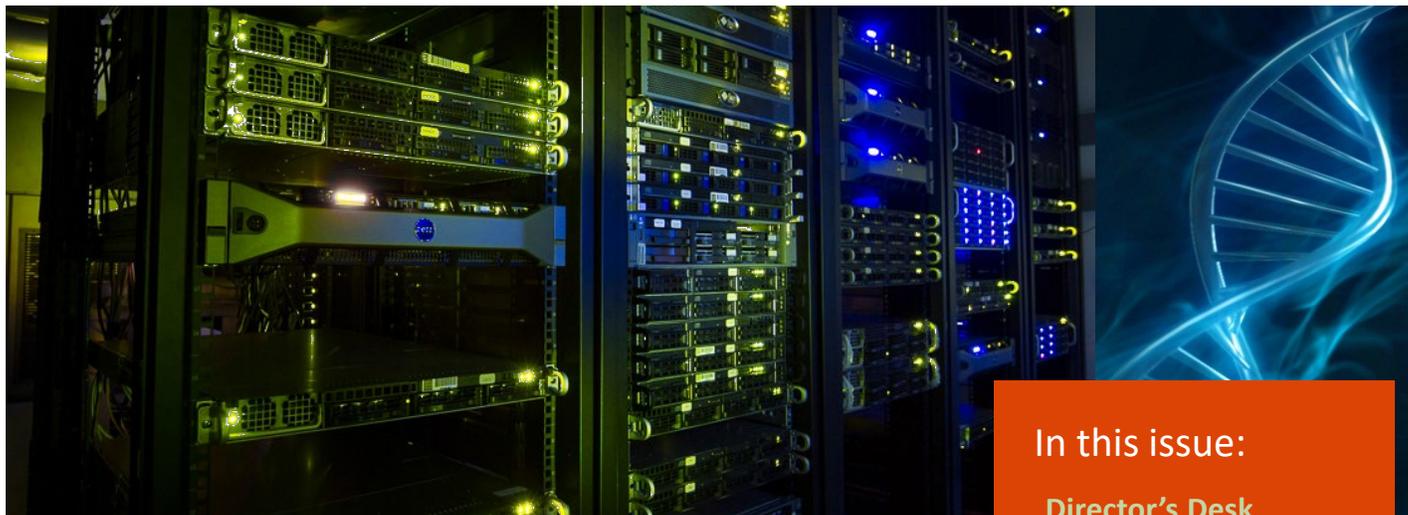


TRANSCRIPT *The Next Generation*



From the CGRB Director's Desk

Hello everybody! With this issue of CGRB's new newsletter, I would like share some fun facts about the CGRB that emerged from our recently completed five year self study (July 2013 to June 2018).

- Over the five years, we interacted with 2066 researchers and students, either because they used some of our services, took some of our training workshops, attended one of our conferences, or participated in a collaboration.
- We have interacted with 291 faculty from 37 different departments, schools, centers or other units from 10 colleges.
- Researchers we have collaborated with have published 496 peer-reviewed papers in which they cited the assistance of the CGRB.

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(Director's Desk continued)

- CGRB services have supported more than 225 extramurally funded projects worth an aggregate of \$208m
- The 11 faculty most closely associated with the center, including the six cluster hire faculty, brought in \$34.3m in extramural funding during the five years.
- 523 unique students and trainees participated in at least one of the 43 training workshops taught by the CGRB, 243 from the College of Science and 104 from the College of Agricultural Sciences.
- The CGRB's Advanced Cyberinfrastructure Teaching Facility has supported the teaching of 2087 students

All of us at the CGRB would like to express our appreciation for the diverse, stimulating, challenging, rewarding and fun interactions we've had with our broad community of life and environmental scientists as we've assisted them with their genome-enabled and data driven research.

- Brett Tyler

Thank you for attending the

SPRING
CONFERENCE!

BUG Spring Term 2019

May 15 Greg Goralogia (Steve Strauss Lab)
May 29 Felix Vaux (Kathleen O'Malley Lab)
June 12 Michael Nagle (Steve Strauss Lab)

<https://cgrb.oregonstate.edu/bug>

BUG is at noon in ALS 3005

No BUG this summer
See you in the fall



Bioinformatics User Group

FALL CONFERENCE

September 20, 2019

Our Fall Conference Speakers

Dr. Doris Taylor

Director,
Regenerative Medicine Research
Texas Heart Institute

Dr. Daniel Liefwalker

Research Assistant Professor,
Molecular & Medical Genetics
Oregon Health & Science University

Dr. Ed Kelly

Associate Professor,
Department of Pharmaceutics
University of Washington

Spotlight: Taal Levi Lab

Our lab has three main foci including (1) the ecology and conservation of carnivores, (2) the community ecology of disease, and (3) molecular methods for biodiversity monitoring. Illumina sequencing, bioinformatics, digital PCR, and qPCR services provided by CGRB have been instrumental to this research. For all of these research foci, we use DNA metabarcoding with highly multiplexed amplicon sequencing on the Illumina HiSeq 3000 to identify species in bulk DNA samples. We apply this extensively for animal diet analysis, including for projects with a myriad of carnivores, as well as bats, insectivorous birds, and ungulates. Understanding what these species eat has important implications for conservation and management. Additionally, we have used CGRB support and bioinformatics training to develop a new approach for amplicon sequencing of single nucleotide polymorphisms from carnivore feces in order to improve the success rate of genotyping carnivores from noninvasively collected scats. We also apply DNA metabarcoding to test the hypothesis that fragmented tropical forest changes vertebrate communities to increase the risk of contracting *Leishmania*, the sandfly transmitted protozoa that causes Leishmaniasis. To do so, we metabarcode pools of sand flies



Speedy the brown bear (Ursus arctos) feasting on Sockeye salmon (Oncorhynchus nerka) in the Chilkoot River, Haines, Alaska - Photo by Jennifer Allen

to determine which sandfly species are in each pool and which vertebrate hosts they fed on, which we then follow up with qPCR for pathogen detection. In addition, we extensively use the droplet digital PCR and qPCR machines provided by CGRB to detect and quantify fish based on the “environmental DNA” that they shed into water. The DNA collected from water filters is highly sensitive for species detection, and we have shown that the concentration of DNA *also* provides an index of abundance for anadromous fish such as salmon. To facilitate future biodiversity monitoring in Oregon, we have initiated the Oregon Biodiversity Genome Project in collaboration with other faculty and biologists in state

and federal agencies. Phase I, which is almost complete, includes the collection, vouchering, sequencing, and mitogenome assembly of all aquatic vertebrates in order to facilitate the next generation of freshwater environmental DNA surveys in Oregon. Future phases will include the creation of reference sequence databases for pollinators and benthic invertebrates as well as the development of tools for monitoring the diversity and relative abundance of species in a bulk invertebrate sample. These projects would not have been possible without the support of the CGRB’s core facility, bioinformatics training, and computational infrastructure.

Taal Levi,
Assistant Professor
Fisheries and Wildlife



Lab Highlight: Nanodrop

By Anne-Marie Girard, CGRB Core Lab Technician

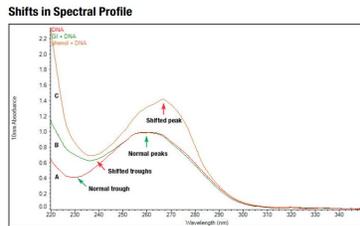


Figure 2: Spectra of purified DNA without contamination (A), and of the same DNA sample contaminated with guanidine (B) and phenol (C)

There are several different methods available to QC your RNA and DNA samples. They assess different qualities but all provide useful data. Some are better for quality, others for quantity, and others for sizing. Qubit, Nanodrop, Bioanalyzer and TapeStation are a few instruments we use to help determine the quality of samples before proceeding with sample preparation for our services. Here are a few tidbits about Nanodrop and spectrophotometer readings, which are better for assessing contaminants, but less accurate in quantitating if contaminants are present.

When light shines through a DNA or RNA sample, a certain amount is absorbed by the sample itself. Spectrophotometric or absorbance readings assess this loss of light at wavelengths of interest. Quantity of DNA and RNA and free nucleic acids in solution are measured at 260nm, but are not differentiated. You can access the presence of contaminants by absorption readings over the full spectrum. Readings at A280, A230 and A320 can give an indication of what contaminants may be present. The contaminants can also contribute to the absorbance at 260nm, so the quantity of RNA or DNA will be inaccurate if contaminants are present.

A260 – Besides DNA, RNA and free nucleotides, guanidine isothiocyanate, used for RNA isolations will also absorb at 260nm

A280 – Proteins, TRIzol® reagent (270nm) and phenol absorb more at this wavelength.

A low A260/A280 ratio can indicate contaminants such as protein. Pure DNA will have an A260/A280 ratio of 1.8 and pure RNA a ratio of 2.0. DNA with a ratio over 2 may indicate RNA contamination.

A230 – higher absorbance at this wavelength can indicate the presence of Urea, EDTA, carbohydrates, phenolate ions, TRIzol® reagent, and Guanidine HCL, which is used in the extraction of DNA.

Expected A260/A230 values are commonly in the range of 1.8-2.2. Low A260/A230 ratio indicates more salts.

A320 - You can adjust for turbidity of the solution by subtracting the absorbance at 320nm.

pH of the solution can also affect the A260/A280 ratio, with acidic solutions having a lower ratio and alkaline solutions having an increased ratio of up to 0.2–0.3. Water from different vendors or purification systems may have different pH. A low salt solution such as 10mM Tris or TE can buffer so the DNA/RNA readings are more consistent.

The accuracy of the value is affected by the proportions of nucleic acid bases. AGCT each have a different absorbance and an average is assumed in calculations. The five nucleotides that comprise DNA and RNA exhibit widely varying 260/280 ratios. 1.15-4.5

Out of the Past

CGRB was split between Cordley and Weniger halls originally. It consolidated into Agriculture and Life Science Building during the summer of 1992. Russel Meints was director at the time. Our name changed in 2005

transcript

Oregon State University

July 1992

NEWSLETTER OF THE CENTER FOR GENE RESEARCH AND BIOTECHNOLOGY

FROM THE DIRECTORS OFFICE

The move of the Center for Gene Research and Biotechnology office to the new Agriculture and Life Sciences (ALS) Building is now complete. The space provides for quite efficient and very pleasant new quarters located on the third floor on the east side of the building, near the elevator (Room 3021). For the present, we are also home for the administrative aspects of the Molecular/Cellular Biology

CENTRAL SERVICES LABORATORY

While the Central Services Laboratory has not yet moved, it will begin the process by moving the big instruments on or around July 6. As you can guess this will lead inevitably to some down-time in providing services to you. We hope to have ongoing oligonucleotide service by leaving one machine operable in Weniger Hall until the other is working in ALS.

techtips

A Table Makeover with DT in R

by Dana Gibbon, Bioinformatics Analyst

R's default print function for data frames and matrices is not an effective way to display the contents, especially in a report. RStudio created a R package, [DT](#), that is an interface to the JavaScript library DataTable. DT allows users to have interactive tables that includes searching, sorting, filtering and exporting! I routinely use these tables in my analysis reports.

Example Table:

Install the DT package through cran with `install.packages("DT")`. Let's make a table with the preloaded iris data that's in a data.frame. The basic call is `DT::datatable(iris)` but in our example I've added the filter option to the top of the table, and limited the number of entries to 5 per table. See code and table features below:

```
DT::datatable(iris,  
  filter = "top",  
  options = list(pageLength = 5))
```

Number of entries to display:

Show **5** entries

10
25
50
100

Filtering:

- Filter numeric columns with a slider
- Filter columns of class factor with a drop down

Sort column:

Sepal.Width ▲
Sepal.Width ▼

Search Bar:

Search:

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
All	All	All	All	All
1	5.1	3.5	1.4	0.2 setosa
2	4.9	3	1.4	0.2 setosa
3	4.7	3.2	1.3	0.2 setosa
4	4.6	3.1	1.5	0.2 setosa
5	5	3.6	1.4	0.2 setosa

Showing 1 to 5 of 150 entries Previous 1 2 3 4 5 ... 30 Next

Export Data:

Another useful aspect of the datatable function is the "Buttons" extension. This enables users to copy the table, save as a csv, excel or PDF file, or print the table. The table "remembers" what you've—so if you sort by Sepal Length, filter pedal width to > 1 and select species "versicolor" the copied/saved table will have these same restrictions.

```
DT::datatable(iris,  
  extensions = 'Buttons',  
  options = list(dom = 'Bfrrtip',  
    buttons = c('copy', 'csv', 'excel', 'pdf', 'print')))
```

Copy CSV Excel PDF Print

Sepal.Length

Sepal.Width