

Thursday, August 31

- meeting w/ mentor next week (Thursday or Friday)

Things to discuss:

- UCID

- research proposal

- possible experiments - readings?

- future meeting dates

in-class discussed paperpile use

↳ adding pubmed articles to paperpile

↳ adding & changing citations in google docs

↳ organization within paperpile

worked with RStudio to create occurrence maps of species

↳ persild's byrum & slender mouse-ear-cress

↳ wouldn't work (-didn't work -did work error

> sprnames ← c('slender mouse-ear-cress')

> out ← spocc :: occ(query=sprnames, from='gbif',

gbifopts=list(hasCoordinate=T, country='CA'), limit=1000)

> res ← spocc :: occ2df(out)

> res ← a.tibble: 0x0

> Precatcoords ← res[, c(2,3)]

> Precatcoords ← data.frame(Precatcoords)

> Canada ← rnaturalearth :: ne_countries(scale='medium',
returnclass='sf', country='Canada')

> Canada ← terra :: vect(Canada)

> plot(Canada) > terra :: points(Precatcoords)

error in as.double(y):

cannot coerce type 'sf' to vector of type 'double'

meeting w/ Dr. Garcia on Friday

Thursday, September 7

meeting w/ mentor

what was discussed:

- looking into UCID

- write papers w/ APA

- look for readings

↳ plants of interest

↳ advancements in the field

- possible issues w/ experimenting

on an endangered species

- send research proposal as its

written

- more research based

↳ talks to Dr. Garcia about designer gene

- is there a genetic diff. between

endangered & non-endangered?

- what would happen if gm a plant?

- future meetings mostly online

- try diff species in R

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To Do:

- ☑ find papers on diff. plant species
- ☑ find papers on discoveries in the field
- ☑ talk to Dr. Garcia about genetic modification
- ☑ send R code
- ☑ send next weeks schedule
- ☑ continue practicing using Rstudio

meeting w/ Dr. Garcia tomorrow

Friday, September 8

idea: lots of research into protecting agricultural species & genetically modifying them, not enough in other species for biodiversity

meeting w/ Dr. Garcia:

- talk w/ Nick
- good shape
- ↳ paper sites
- discussed meeting w/ Nick
- ↳ long term & short-term
- what project will look like
- ↳ methods
- narrowing down question

look up species on gbif

↳ white-bark pine (find articles)

found articles & added to paperpile

↳ ☐ read 1 from each folder by next Friday

checked research proposal guidelines

↳ variables?

Engineering Climate-Change Resilient Crops: New Tools & Approaches

Fahimeh Shahinnia

↳ drought & nutrient limitation r major issues

↳ transgenic / chemical approaches previously used

Cyanobacterial proteins regulate cell behaviour & gene expression in response to changes in the external environment

↳ poor plant conditions cause oxidative stress

Oxidative stress is caused by an imbalance between production and accumulation of oxygen

↳ osmotic stress can also be caused by a decrease in water availability

↳ selective breeding may have caused decrease in stress tolerance

↳ ↑ tolerance mainly done by overexpressing certain genes

endogenous is a process that results in a change of state or activity as a result of a stimulus ✓

↳ lots of work on strengthening these responses

↳ these manipulations often don't translate well to field conditions

↳ caused alternative explorations (cell wall metabolism, phytohormone levels)

phytohormone levels are naturally occurring molecules that play a role in regulating plant physiology, development, etc. due to environmental stimuli

↳ nutrient status is very important as improving those pathways

(especially of chloroplasts) increases tolerance to many stressors

↳ plant-microbe interactions can influence abiotic stress tolerance

↳ photosynthesis very sensitive to stress, but chloroplasts are important to adaptation as centers of key metabolic processes

↳ starch important to abiotic stress b/c the energy aids survival

↳ amino acids, NADPH, and ATP also help w/ stress tolerance

↳ CBC is very sensitive to drought which declines PETC

photosynthetic electron transport chain (PETC) generates a proton gradient across the thylakoid which drives ATP synthesis

↳ oxygen used for ROS which leads to oxidative damage

ROS are oxygen containing radicals that can exist w/ 1+ unpaired electron

↳ under short-term stress chloroplasts activate photoprotective mechanisms ✓

↳ prolonged stress = ↓ PS proteins, carotenoids as antioxidants

↳ AET & dissipative systems minimize misrouting of energy

↳ protective systems offer chance for genetic intervention

↳ protective system to dissipate light energy is based on NPA

nonphotochemical quenching (NPA) is a process in which excess absorbed light energy is dissipated into heat

↳ genes associated w/ ROS scavenging are induced under stress

↳ introgression of alleles via breeding are limited by regulatory systems

↳ can be overcome by synthetic promoters/stress-inducible

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- ↳ promise in encoding electron carrier proteins not found in plants
- ↳ cyanobacteria provide many genes for genetic engineering
- ↳ most mechanisms involved in regulation of gene expression due to endosymbiosis
- ↳ **endosymbiosis** is a type of symbiosis in which one organism lives inside the other usually acting as a single organism
- ↳ Ferredoxin (Fd) present in cb & is essential for distributing low-potential reducing equivalents to energy-demanding metabolic steps (gas assim., reg. paths, amino acid synth. etc)
- ↳ cyanobacteria induces Fld under stress to compensate for Fd decrease
- ↳ net outcome is augmented tolerance to stressors in cyanobacteria
- ↳ plastid-directed cb greatly increased stress tolerance & metabolite content
- ↳ **transgenic lines** are a lineage of organisms that have been genetically modified to contain a gene from another species
- ↳ Flavodoxin (Fld) created compensated for loss in Fd
- ↳ proven to work in multiple species (tobacco, potato, bentgrass etc.)
- ↳ metabolic profiling under drought showed ↑ soluble sugars, amino acids and a shift of sucrose into starch similar to drought resistant genotypes
- ↳ Flv2/Flv4 complex acted as additional electron sink despite differences
- ↳ FDPs not present in angiosperms
- ↳ Flv2/Flv4 can operate as electron sink @ PSI but Flv1/Flv3 are reduced
- ↳ associated w/ cb stress response & loss due to as = ↑ in photorespiration
- ↳ **synechocystis** is a genus of unicellular, freshwater cyanobacteria
- ↳ **Flv** is photosynthetic flavodiiron
- ↳ Flv1/Flv3 increased biomass & showed imp. of sugar & amino acids in drought
- ↳ nutrient supplementation can help avoid deficiency due to droughts
- ↳ application of potassium and zinc decreased effects of drought & ↑ yield
- ↳ nanocoated micro/macro nutrients resulted in better performance
- ↳ overexpression of N23 reduced production & length of root hairs
- ↳ enlarging root systems increased tolerance to long-term drought
- ↳ exposure to volatile compounds also displays promise
- ↳ urgent need to develop and utilize existing plant protection resources
- ↳ reasonable to expect successful outcomes for plant development

~~Sept 12~~ Task List:

- ☑ finish article 1
- ☑ start article 2
- ☑ work on R (talk to Nick)
- ☐ plan research proposal
- ☑ add definitions
- ☐ open intro for research proposal
 - ↳ Monday?
- ☑ finish article 2
 - ↳ Tuesday

(September 13)
code (still not fully working)
w @ 2:30

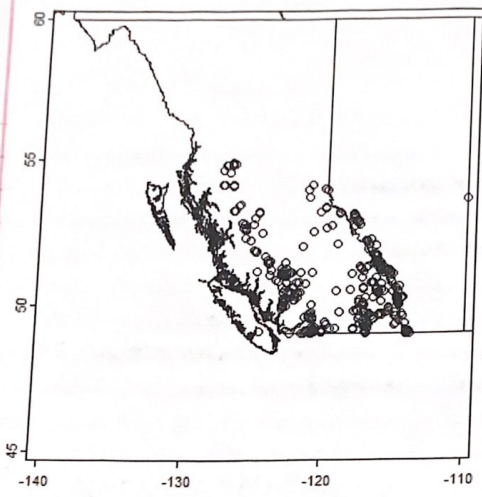
- ✓ - findings in reading ✓
 - ✓ - narrowing down question ✓
 - data ✓ - summary emails
- er 13

Discussed:

- fixed R code (see pg. 2)
- habitat suitability maps
- comparison between gene #
- difference between threat + non
- due dates for research proposal
- endangered vs. non-
 - ↳ use distribution models
 - ↳ predictive habitats
 - ↳ literature review

Due Dates:
Intro Draft/Outline - next meeting
Intro Due - week after
↳ group w/ objective 1/2 variables
Methods/Significance - week of
October 11

Question: What are the genetic differences between an endangered species and a non endangered species?
↳ find non-endangered species
↳ endangered: whitebark pine (Pinus albicoulis)
made map in R of whitebark pine occurrences in Canada
↳ add details
googled how to add provinces
downloaded shapefile of Canada from GADM
↳ extracted into ASP/Provinces



Map of White Pine Occurrences
 - most occurrences in the rocky mountain
 - many closer to the west coast
 look into precipitation #
 look into soil quality
 look into carbon emissions

Sept. 14 To do list:
 write intro draft (next meet)
 finish article 2 (tuesday)
 email mentor abt next meet
 further explore r mapping
 find 2nd plant

next meeting
 after
 variables
 - week of

Thursday, September 14

analyzed above graph
 variables may not be needed for research
 what type of project? →
 actual due date: October 6th?

Plant Carbon Metabolism and Climate Change

danielle a. way
 I.

- CO₂ concentrations rising from 280 → 410 ppm since 18 (0.8°C ↑ globally)
- ↳ emissions will continue to rise (550-1000 ppm) (1-3.7°C ↑ globally)
- ↳ only minor changes depending on regions (weather, plant/soil activity)
- ↳ certain regions will experience greater warming (high latitudes & tropics)
- higher temps will alter thermal environments & ↑ dryness
- higher CO₂ will increase photosynthesis (BUT depends on temp & water)
- plants very important for regulating CO₂ levels
- due to elevated CO₂ plants could slow climate change
- ↳ only if in recalcitrant pools & ocean not in rapid carbon fluxes
- Carbon Flux** is the amount of carbon exchanged between carbon stocks over time
- if plant net CO₂ is reduced world could warm faster than expected

V.

many impacts of rising CO_2 offset by rising temperatures
high CO_2 increases thermal assimilation $\frac{1}{2}$ can \uparrow heat tolerance in C_3 plants

lower g_s reduce A_{net} but also warms leaves via \downarrow latent heat loss

trees in elevated CO_2 shed more leaves and would \uparrow in high leaf temp.

net effect on change in carbon dynamics depends on plant responses

rising CO_2 lowers photorespiration

\hookrightarrow eliminating photorespiration could \uparrow photosynthesis (12-55%)

elevated CO_2 can alter plants exposed to heat stress

\hookrightarrow + legumes but - C_4 plants

carbon flux responses may be more imp. than responses to CO_2

different levels of CO_2 $\frac{1}{2}$ A_{net} affected diff. plants differently

high CO_2 may stimulate A_{net} but plants may still have \downarrow carbon uptake

effects of temp $\frac{1}{2}$ CO_2 on respiration were independent

\hookrightarrow warming reduced respiration $\frac{1}{2}$ CO_2 had no effect

some studies found similar responses of carbon dynamics to warm $\frac{1}{2}$ CO_2

\hookrightarrow but large variation in response to climate treatment

\hookrightarrow Scots pine $\frac{1}{2}$ norway spruce had varied responses (why?)

important to also look at extreme responses

VI.

when water $\frac{1}{2}$ nutrients low lower positive responses to rising CO_2

\hookrightarrow impacts on photosynthesis $\frac{1}{2}$ respiration erased in drought

effects of elevated CO_2 on photosynthesis differed in dry conditions (why?)

high CO_2 affects plant response to drought (C_i declined faster)

leaf and canopy structure affect transpiration, growth in drought

water stress enhances impact of warming on plant carbon metabolism

\hookrightarrow warm + dry = early budburst but soil moisture \downarrow faster b/c of early leaf development

water stress can also create photosynthetic heat stress tolerance

\hookrightarrow alters chloroplast membrane $\frac{1}{2}$ may underlie drought mods of temp response

nitrogen availability could also impact response (\downarrow nitrogen = \leftarrow responses)

growth responses to CO_2 due to nitrogen availability differed greatly

few studies on how nitrogen supply alters effects of warming on plant carbon metabolism

Research Proposal Planning

Working Title:

Plant Responses to Climate Change & the differences

Introduction:

1. Climate Change (4, 6)
2. Climate Change on Biodiversity ^(driving other factors) (5,
3. Importance of Biodiversity (3)
4. Plant reactions to Climate Change (2, 1, 6)
5. Differences in reactions (2, 1, 3, 7)
6. Importance of knowing these differences ^{how we can study it} (7,

Notes:

- keep citations consistent
- make point of impact on humanity (w/ biodiversity)
- define functional traits (other vocab) ✓
- ↳ sent definition & what's behind the services ✓
- losses in ecosystem services (biodiversity)
- w/ plant reactions connect better w/ biodiversity ✓ ✓
- include carbon capture
- start w/ the end (it's stronger) ✓ } plant reactions

Question:

- include distribution aspect
- ↳ how genetic differences may impact plant reaction to climate change

Methods:

- find method to actually compare the genetic differences
- retrieve occurrence data from global biodiversity facilitation
- retrieve climate data for current & future
- reading model output (habitat suitability)
- R basics & packages
- comparative biology (surface level differences)
- find paper w/ basic outline

Monday, September 18

Working Title: concise, specific

Abstract (not marked): optional

Introduction: background info

↳ studies, sources, interpretation

Question / Hypothesis: direct

Goals (Short & Long): read literature

Variables: ask mentor, clearly labelled

Methods: not marked heavily, what?, why?, general explanation

Significance: summarize, contributions, larger implications

References: lots of sources, stick with a style use paperpile

made research proposal intro outline (Fig. 9)

oral presentation based on content, flow, presentation, graphics

unable to finish article 2 (talked about research proposal)

↳ nevermind: a lot of info on differences in responses

non-endangered plant: lodgepole pine (*Pinus contorta*)

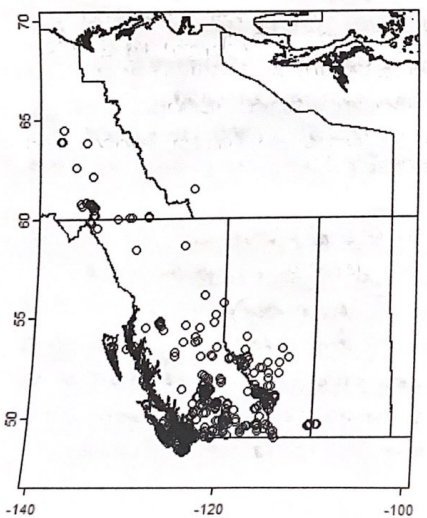
↳ plot occurrences like w/ whitebark

mentor meeting Wednesday @ 12:30

can change order 4 E/B/W

Sept. 18 To Do List:

- check in w/ mentor w/ email
- start article 3 - finish Friday
- make plot occurrence for lodge
- find articles abt lodge
- correspond articles into
- make working title



Map of Lodgepole Occurrences

- visibly more than whitebark
- many more in Alberta
- many along southern border
- some in the Yukon
- wider range of habitats
- look into climate
- look into CO₂ levels
- look into soil quality

Biodiver

- ▷ 20 yrs
- ↳ many n
- ① cool
- ② many e
- ③ new co
- ↳ create
- ↳ Con
- ① biodive
- ↳ decom
- ↳ the eff
- ↳ general
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- ② biodiver
- ↳ no rea
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- ↳ saturat
- ④ diver
- ↳ cont
- ↳ both
- ↳ com
- ⑤ loss
- ↳ trc
- ↳ los

Biodiversity Loss and its Impact on Humanity

20 yrs of Research

- ↳ many milestones crossed since 2000
- ① coalesced around key findings & themes
- ② many early debates subsided b/c of ↑ in data
- ③ new consensus on questions & how to answer them
- ↳ create opportunity to re-evaluate conclusions & identify trends

6 Consensus Statements

- ① biodiversity loss reduces efficiency of resource collection, biomass production, & decomposition/recycling of nutrients
 - ↳ the effects on decomposition/recycling are weaker
 - ↳ general consistency among organism, trophic levels, & ecosystems
 - ↳ suggests underlying reason for the influence of organization on ecosystems
- ② biodiversity increases the stability of ecosystems
 - ↳ no reason that biodiversity enhances all forms of stability
 - ↳ greater temporal stability of community property w/ ↑ biodiversity
 - ↳ diversity confers stability via overyielding, stat avg, & compensatory dynamics
 - ↳ stat avg occurs when random variation reduces variability of aggregate ecosystem variables
 - ↳ comp dynamics driven by competition / diff responses to fluctuations
 - ↳ haven't quantified importance of the mechanisms & their conditions
- ③ impact of biodiversity on ecosystems is non-linear & saturating
 - ↳ initial loss has small impacts, but ↑ loss accelerates change
 - ↳ questioning of saturating curves b/c of factors that ↓ opp for express of niche diff
 - ↳ biodiversity-ecosystem function in natural eco differs from saturating curves
 - ↳ saturating curves are
- ④ diverse communities more productive (key species / diff in functional traits)
 - ↳ controversy over if diversity effects driven by 1 very prod species or 'complementary'
 - ↳ both identity & diversity control functioning of ecosystems
 - ↳ complementary may rep niche partitioning but contributions unconfirmed
- ⑤ loss of diversity across trophic levels could have ↑ impact than loss within trophic levels
 - ↳ transformation of diverse plant assemblage can reduce biomass
 - ↳ loss of consumers can alter veg structure, fire freq, & disease epidemics

- ⑥ Functional traits impact magnitude of ecosystem functions ∴ create many plausible impacts of extinction on ecosystem function
 - ↳ depending on traits lost there can be vast diff in impact on eco functions
 - ↳ results that show this questioned b/c of experiment duration
 - ↳ to know consequences of extinction scenarios need to know extinction risk & how they influence function (expanding area of research)
 - ↳ Emerging Trends
- ⑦ Impacts of diversity loss may rival other drivers of climate change
 - ↳ exact relationship depends on mag. of div loss & other changes
- ⑧ diversity effects increase over time & may ↑ at larger spatial scales
 - ↳ small scale, short term exp. underestimate impacts
- ⑨ current research may have underestimated min levels of biodiversity
 - ↳ maintaining many ecosystem processes in many places needs ↑ biodiversity
 - ↳ organisms that control processes in 1 place & year differ from ones in other places & years
- ⑩ consequences of biodiversity loss predicted by evolutionary history
 - ↳ genetic variation that affects organisms eroded by common ancestry
 - ↳ phylogenetic distances explain biomass var. better than taxonomic diversity
- ⑪ Phylogenetic distances are a measure of genetic divergence
- ⑫ Balance of Evidence
 - ↳ lots of evidence is mixed or opposes expectations & may be insufficient
 - ↳ test of article mainly discusses policies & changes that need to be made to make predictions more accurate

- Tuesday, September 19
meeting tomorrow at 12:30
- Discussed:
- intro outline ✓
 - graphs ✓
 - readings ✓
 - sending readings? ✓
 - Wednesday, September 20
 - meeting w/ mentor (moved Garcia meeting)
- Discussed:
- shifted due date
 - ledge pole
 - send articles
 - sending articles
 - look at more writing this week
 - online resources
 - details about research proposal
 - began reading article 3
 - Garcia Meeting:
 - generally in good shape
 - Friday, September 22
 - worked on finishing article 3 → finished
 - added mentor papers into paper pile
 - installed ^{small} spreadsheet package into R
 - E: Exploratory Data Analysis Lesson
 - sent email with papers I found
 - modern global climate change - article 4
 - improving forecast for biodiversity under climate change
 - writing to stand still - article 6 & 7
 - predicting global change impacts - article 7 & 8
 - completed EDA lesson 1
 - making graphs accurate, reading different graphs, content is 'ring'
- changed due date → expectations ✓
- type of experiment ✓
- non-endangered species ✓
- only 2 techniques need to learn ✓
- there will be variables
- ↳ not really a control
- ↳ find studies that have done comparative
- space, response plots, comparative
- R practice (spread package)
- ↳ requires you know it works
- Sept 22 To Do List:
- ↳ finish Monday
 - ↳ article 4 → finish Monday
 - ↳ R practice w/ spreadsheet
 - ↳ start writing intro
 - ↳ have good amount by next week
 - ↳ ask Garcia about extension
 - ↳ work on significance
 - ↳ Monday

Modern Global Climate Change

Thomas R. Karl & Kevin E. Trenberth

- ↳ main source of climate change: human-induced changes in atmos. composition
- ↳ uncertainty over rates of change but will be shown in physical ways
- ↳ anthropogenic climate change will continue
- ↳ anthropogenic climate change is climate changed that is caused by human activity
- ↳ unknown w/ climate & impacts could be very disruptive
- ↳ air over one location 1/2 way around world later = global issue
- ↳ natural greenhouse effect (60% water, 25% CO₂, 8% ozone)
- ↳ clouds reflect energy from sun back (test absorbed/reflected)
- ↳ human activity primary force for climate change
- ↳ changes in atmospheric composition due to anthropogenic emissions
- ↳ fossil fuels, methane, nitrous oxide have long lifetimes ∴ accumulate
- ↳ carbon dioxide has increased 31% (1/2 since the 60s)
- ↳ fossil fuels result in oxidized gases that are highly reflective
- ↳ typically removed fast via hydrological cycle & dry decomposition
- ↳ depending on reflect, absorb, etc. net-cool or net-heat
- ↳ sulfate aerosols affect climate directly by reflect solar radiation
- ↳ humans also impact land-surface (urbanization & agriculture)
- ↳ 'tropical jungles' result in urban heat islands
- ↳ both greenhouse gas emissions & concentration of aerosols increasing
- ↳ radiative forcing > net cooling ∴ global warming
- ↳ global temperature increase only one consequence
- ↳ surface moisture helps to cool by evap. instead of heat
- ↳ another consequence is speed up land-surface drying & ↑ water vapour
- ↳ increases droughts & risk of heavy precipitation
- ↳ length, size, & onset the effects of anthropogenic climate change is largely unknown
- ↳ magnitude of anthropogenic change > natural changes
- ↳ w/ no interreference qo: choice temp will increase from 1.7° - 4.9° from 1990 - 2100 (alternative source)

- ↳ uncertainties b/c of future emissions & climate models
- ↳ likely outcome is more droughts, heatwaves, & extreme precipitation
- ↳ human induced climate change much faster than naturally
- ↳ thresholds that if crossed could irreversibly switch climate
- ↳ ocean temp ↑ and ice sheet melting will cause ↑ sea levels
- ↳ substantial further climate change guaranteed
- ↳ can't be stopped now but can be slowed
- ↳ b/c of accumulation of greenhouse gases it would take decades for changed emissions to take effect
- ↳ there is unrealized warming & oceans will see even w/ stabilization
- ↳ understand of climate system compl. by water feedback
- ↳ temp ↑ water holding capacity of atmosphere ↑
- ↳ contributed radiative effect 1-2x anthropogenic greenhouse gases
- ↳ precipitation runoff feedback: occurs b/c of intense rain & warming of soil moisture
- ↳ cloud storage feedback: includes water vapor, heat, and radiative via currents
- ↳ cloud feedback: occurs b/c clouds reflect solar radiation, causing cooling & warming
- ↳ changes in clouds largest source of uncertainty (temp. in changes in greenhouse gases)
- ↳ clouds & precipitation can't be resolved in climate models & will continue
- ↳ albedo feedback: occurs as warming reduces snow & ice cover = decrease in radiation = ↑ melt
- ↳ decreased snow cover has led to early onset spring
- ↳ primary tool for prediction is global climate models but there are issues
- ↳ satellite observations & analysis of surface, upper air, & ocean temp. indicates effects of sulfate aerosols on clouds may be high
- ↳ human behaviour, arrangements, & pop. growth also affect emissions & predictions
- ↳ regional predictions are needed for improvement
- ↳ atmospheric-ocean system preferred behaviour is El Niño and others is NAO
- ↳ El Niño & NAO unusual behaviour linked to global warming
- ↳ El Niño has large regional effects around the world
- ↳ North Atlantic Oscillation (NAO) effect severity of winter temp. precip. in Europe & most NA
- ↳ prediction in uncertainty driven by simulations of past climates
- ↳ climate change unlikely to be adequately addressed w/out improved cooperation

Sunday, September 21

worked on introductions

had trouble using paper

Went to class for extra

from due the next day

Tuesday, September 24

Errol Nick will read and

figured out paper to be

off at end of sentence

read 1/2 of article 4

to make change

will be able to write

Be aware of sources

Meeting will Nick tomorrow

Discuss:

introduction ✓

moved due date ✓

upcoming commitments ✓

work with Smith ✓

Wednesday, September 25

meeting with Nick at 12:30

discussed:

corrections for intro

looking into comparative game

will ask others at uni

specifics for methodology

wrote rough draft of meth

applied some of the intro

can be seen on page 9

logbook due tomorrow

tomorrow's tasks:

finish article 4, start article 5, 6

Improving forecast for biodiversity under climate change

- ↳ new biological models incorp realistic process but need more info
- ↳ need to collect mechanistic data (biochemical gene expression etc.)
- ↳ need to predict how climate change affect biodiversity to stop damage to biosphere
- ↳ models to understand impacts but biological responses difficult to predict
- ↳ but many models ignore demographic shifts, interactions, evolution
- ↳ don't rely on tools based on the past (species article 4)
- ↳ mechanistic models essential to mediating responses to climate change
- ↳ mechanistic models can include processes that are currently hidden
- ↳ needs high-quality data on species biology (gen response to climate)
- ↳ mechanisms that determine biological response to climate change
- ↳ physiology, demography, evolution, pop differentiation, interactions, dispersal, (responses)
- ↳ **Physiology**: mediates how climate conditions (temp, water, evapotranspiration) will influence survival, growth, development, and reproduction
- ↳ **Demography**: critical in climate change responses (long term veg. pat's survival)
- ↳ density dependence & gen length affect extinction risk

~~Self~~

Great work on literature review!
Good organization with Task lists —
Calendar should have these tasks and due dates

↳ more ASP tasks on each class on the calendar / less other activities / classes

↳ do this figure out how to do this better - in our next meeting.

Date?

- ↳ **evolution**: growing amount of genetic variation is imp for knowing future responses b/c it could allow pops to adapt to climate change
- ↳ may not shift if they become isolated
- ↳ more information needed to generalize adaptive rates
- ↳ **interactions**: underlie unexpected responses to climate change
- ↳ local extinctions due to climate change have involved diff species interactions
- ↳ **dispersal**: species usually track good climates via dispersal to combine
- ↳ depends on interplay between behaviour, fitness, habitat, & landscape
- ↳ **responses**: depend on sensitivities per species to climate & habitat variation
- ↳ conservation focuses on overall biodiversity
- ↳ focus on top-consumers can indirect effect's throughout foodwebs
- ↳ global coordination critical as well as regional
- ↳ IPCC's climate change predictions can guide template for biodiversity
- ↳ need to be broad when planning for climate change which will help protect biodiversity
- ↳ knowing how nature works will benefit everyone
- ↳ **Environmental Change, Changing Biodiversity**
- ↳ Part II: Meena & Vivekanand Dha
- ↳ direct & accelerating connection between climate change and biodiversity loss
- ↳ rising global temperatures threaten biodiversity
- ↳ anthropogenic climate change is primary & results in biodiversity collapse
- ↳ climate change and biodiversity have a bidirectional relationship
- ↳ **bidirectional relationship** is a mutual interaction where one variable affects the other (owning & inverse side)
- ↳ ecosystems exposed to unprecedented conditions => loss of local populations
- ↳ 3 important climatic factors on biodiversity loss
- ↳ frequency of natural disasters, temperature, & precipitation
- ↳ beach / increase in frequency causes loss from 0.2-1H, normal to 0.5-2H plants
- ↳ 11 higher biodiversity loss with temperature
- ↳ 3rd most important cause of bio loss after land-use & exploitation

- ↳ Will become main driver of biodiversity loss in coming years
 - ↳ biodiversity loss also accelerates climate change
 - ↳ limits ecosystems ability to regulate green-house gasses
 - ↳ also limits ability to maintain soil nutrients & water quality
 - ↳ creates a vicious cycle
 - ↳ loss of plant diversity threatens food diversity & security
- Monday, October 2
- evidence of work on research proposal (print / summary)
- include daily tasks in calendar
 - be specific w/ tasks (due dates)
 - only have applied science in calendar (some exceptions)
- Work on reading article 5 & Garcia meeting today discussed:
- logbook Feedback
 - monitor evolution (not complete)
 - Oct 16th due date
 - Garcia feedback at least 5 day after started reading article 6
 - ↳ Finished: only read summary & line between of biodiversity
- Wednesday, October 4
- meeting w/ Nick
- Discussed:
- Work on research proposal:
 - TP due date
 - three genome database (use alignment if there is -> will send link)
 - need to find gene control (schroeder in Ro much & many)
 - look into difference between species (significance) - terminated at level
 - not a lot of shift for pine bleb of genome size - Thursday @ 10
 - occurrence / adaptation is most used
 - to create habitat programs w/ climate models (genome shift)
 - send paper w/ why its helpful (significance)

To Do List:

- Finish intro (Friday)
- Read effects on ppi (Friday)
- Complete 2 shift (Monday)
- Method draft (Saturday)
- Goals & variable complete (Sunday)
- Significance draft (Monday)
- fill draft done (Tuesday)

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 ↳ Ms
 ↳ little
 ↳ Flor
 ↳ will

Biodiversity and Health in the Urban Environment

Hellsea, R. Marselle

- ↳ loss of biodiversity could threaten quality of life for all people
- ↳ urban forests are harmful (higher road emission & storage)
- ↳ WHO working w/ CBD & see potential of aligning health, climate, & biodiversity goals
- ↳ benefits for health not only b/c of quantity of blue & green space but quality
- ↳ direct mechanism for role of biodiversity on health related to microbiome
- ↳ symbiotic microbes beneficial for immune & digestive system
- ↳ less biodiversity = less exposure
- ↳ mitigate severity of urban stressors: environmental noise
- ↳ excessive exposure impacts cardiovascular, respiratory, metabolic, etc.
- ↳ structural components of vegetation buffer noise (clats = noise barrier)
- ↳ vegetation reduce effects of heat islands (evapotranspiration & shading)
- ↳ contact w/ nature can increase social interaction & cohesion
- ↳ biodiverse environments should be foundation for public health

Thursday, October 12

meeting w/ Nick

discussed:

- come to meeting w/ more questions
- oral presentation
- science fair deadline
- science fair deadline
- have habitat modelling done end of november
- oral paper
- genetic parts after matings into february
- bonuses due
- genetic comparison is between presence & absence of genes
- find papers about white bark & lodgepole
- control genes to make sure program is working
- MSA package in R: finds best match for gene you're looking for
- look into more features
- labialpine: a fairly common pine species (reference gene)
- add citations to document
- significance is good
- author date: 1900s - current
- next meeting: two tables w/ latitude & longitude
- weekend: 1 or 2 diff. between species (basic)
- wednesday @ 2

Friday, October 13

added mentor corrections to rp
copied to november calendar
meeting w/ Dr. Garcia

discussed:

- check citation format
- get to biodiversity sooner
- oral presentation Oct. 31
- start planning ahead
- science fair between march 1 - 8 (p
- school science fair & c. score: nuphize
- march 15 - city science fair online portal
- need to submit ethics form
- school provides info

be done around mid-february
added tasks to oct & nov calendar

research proposal w/ non-intro edits sent to Dr. Garcia

made account w/ biorender

Tuesday, October 17

made tables?

look about specifics (how to do it)

differences:

white bark ~

- needles in bunches of 5, 3-9cm, slightly curved, ends of branches

- 5-20m tall, rounded or irregularly spreading crown shape

lodgepole ~

- branches of 2, twisted in a spiral, sharp points

- usually > 30m tall, sparse/variable crown, spreading branches

needle shape for water retention

meeting w/ Nick tomorrow

look about tree site, info for articles, reports make tables.

next steps, time-line, tellack & info found

October 13 "look left":
- send list
- add mentor corrections
- add mentor corrections into
- get to biodiversity sooner
- make 1st table - wednesday
- find basic diff's - wednesday
- find articles for oral presentation
- get up slides for oral presentation
- thursday
- add Garcia edits - thursday

Wednesday, October 18

meeting w/ Nick

- increase limit for maps
 - changed names for res
 - 'unique' in R
 - ↳ only two species
 - next part: selecting area
 - ↳ behind area to look at
 - ↳ what values show up
 - ↳ then able to make full models
 - include measure of precipitation
 - ↳ look at core record of large pole
 - ↳ time limit to 1900
 - ↳ worked on how to do this
 - filter out N/A
 - Monday @ 10: if Wednesday doesn't work
 - find out for next text meet if in person moves (email)
- Thursday, October 19
- received price corrections and applied
 - ↳ re-wrote methodology to be more understandable
 - ↳ raised introduction
 - ↳ added citations
 - ↳ reviewed question, goals, & variables
 - ask for one last look through then hand in
 - emailed mentor about next meeting date
- Monday, October 23
- rewrote methodology w/ more specific corrections
 - ↳ sent to Dr Garcia to review
 - oral presentation Oct. 31
 - ↳ 10 minutes long
 - ↳ start w/ punchline (less than a minute brief description)
 - ↳ methodology → flow diagram
 - ↳ end w/ significance
 - ↳ graphics and visuals over text (large font)

pick out a few variables? look for in

↳ most limiting

↳ uses for justification

↳ maybe meet in person?

↳ then able to make full models

↳ look at core record of large pole

↳ time limit to 1900

↳ worked on how to do this

if Wednesday doesn't work

find out for next text meet if in person moves (email)

received price corrections and applied

re-wrote methodology to be more understandable

raised introduction

added citations

reviewed question, goals, & variables

ask for one last look through then hand in

emailed mentor about next meeting date

rewrote methodology w/ more specific corrections

sent to Dr Garcia to review

oral presentation Oct. 31

10 minutes long

start w/ punchline (less than a minute brief description)

methodology → flow diagram



meeting w/ Nick on Wednesday will interfere with Garcia meeting

↳ email Garcia about it

begin work on introduction slides

Wednesday, October 25

- next week meeting ✓
- november look ✓
- increased groups ✓
- next work ✓
- things looked into about species ✓
- punchline ✓
- oral presentation ✓
- next steps ✓
- send code file
- ↳ trimmed environmental data
- cooling w/ environmental variables
- ↳ see if able to go to campus
- need to identify specific genes
- associated w/ resistance
- meet on Wednesday?
- tasks for November
- increase sample number (7000)
- make table w/ species attributes
- Garcia meeting
- ↳ more specific tasks, oral presentation
- ↳ submit permission form for science
- added final edits to RP => submitted
- worked on adding diagrams to presentation
- Monday, October 30
- reviewed oral presentation w/ Dr. Garcia
- ↳ read background & make images
- ↳ split 3 re-word goals
- ↳ add new methodology & re-do
- ↳ talk about w/ Nick on Wednesday

To Do:

- ▷ detect difference error → Med
- ▷ find more articles → Med
- ▷ see if in person possible → Sun
- ▷ add intro to oral → Fri
- ▷ add method to oral → Fri
- ▷ cite image in oral → Fri
- ▷ look @ slide site → Wed
- ▷ make cards for oral → Fri
- ▷ new oral date
- ▷ November

Tuesday, October 31

Oral presentations (Cooper & Jessica)

Jessica:

- about knocking out polymids for autism-risk genes
- autism becoming increasingly common
- using CRISPR as a knockout tool
- homologous recombination or T4-ligase
- ↳ what's the difference? asked & answered
- ↳ why autism? asked & answered

Cooper:

- about effects of concussions on protein levels
- concussions could lead to neurodegenerative diseases
- complement proteins play a role in synaptic pruning
- synaptic pruning
- ↳ what does the motor cortex do? asked & answered
- work on table for meeting tomorrow
- ↳ added differences in cones & blooming season

Wednesday, November 1

meeting w/ Nick at university

- ↳ created code for lodgepole pine current habitat
- ↳ learned how the code works
- ↳ prepared code for comparison later
- ↳ prof'd method
- ↳ ISA ~ takes the given gene sequence and finds best match in given species' gene code
- control ~ genes? what they do identified
- ↳ see what the similar gene code in other species does
- ↳ find genetic genes to test if program is working
- ↳ print off phenotype chart & graphs made w/ R
- ↳ create code for whitebark
- ↳ print off graphs made
- ↳ decide date for meeting next week

Thursday, November 2

Introduction - Dec 15th (literature review)

- ↳ background research from proposal
- ↳ w/ greta edit's & feedback added
- Methodology - early February
- Results - end of February / beginning of March
- Analysis - April
- Full Paper - may / newest reigned
- add edit's to slides
- ↳ Methodology } tomorrow
- ↳ goals
- ↳ introduction } tomorrow
- begin practicing presentation (meet w/ Greta tomorrow)
- created whitebark current habitat modelling
- ↳ evaluate & compare results (Wednesday)

11/15

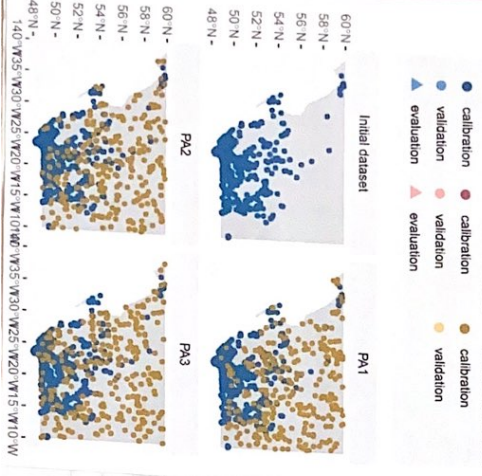
Great nuts for Oct, Bryna ✓
Your calendar / tasks are also well done!

- Monday, November 6
- completed code for whitebark
- ↳ absence chart
- ↳ current habitat model
- ↳ accuracy of results
- ↳ environmental factors
- rehearsed oral presentation
- Wednesday, November 8
- printed off charts → ? where are these?
- rehearsed oral presentation

Thursday, November 9
 increased accuracy (whiteboard):

?

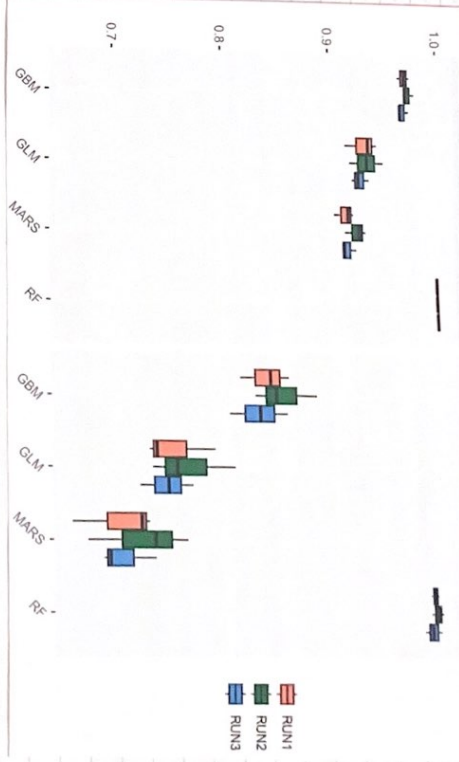
absense plot (whiteboard):



analysis:

✓

accuracy of models (whiteboard):

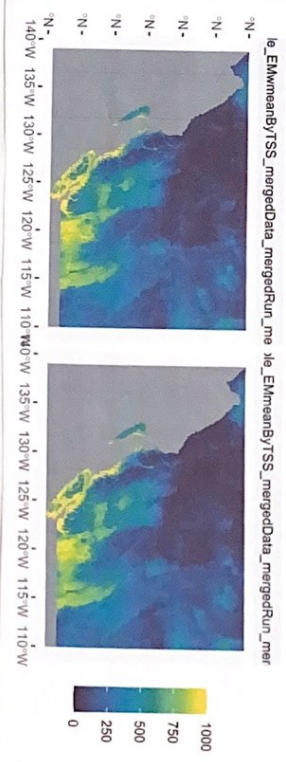


analysis:

- all models are fairly accurate
- above 0.9
- above 0.7
- all runs are fairly similar for each

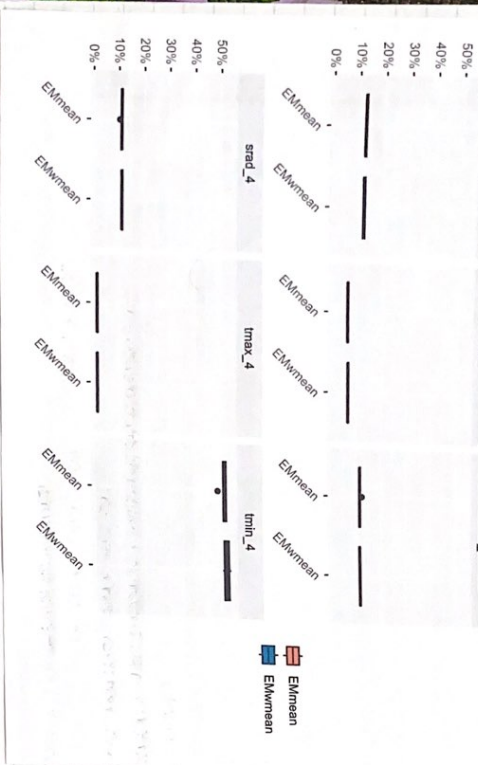
✓

Current habitat model (whiteboard):



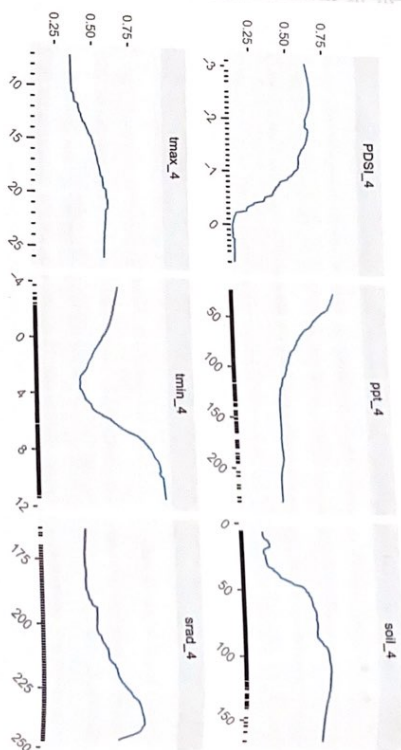
- analysis:
- both maps fairly similar
 - really prevalent on coast lines
 - mostly in lower BC

max of data set (white box):



- analysis:
- temperature minimum is the highest factor
 - not much difference between weighted mean & normal mean

environmental factors (whiteboard):



- analysis:
- doesn't like medium minimum temperature
 - likes warmer temperatures
 - does better w/ higher solar radiation until ≈ 2.50
 - prefers drier conditions

Wednesday, November 15

Day of oral presentation

- ZZ & Toin Oral Presentation:
- Project is an effects of ketamine on the brain
- looking at hippocampus
- Why both ketamine & CBD? asked for overview reflection:

- take more time for methodology (focus on main points)
 add more wide project description at very beginning

Friday, November 17
 meeting w/ Nick discussed:

- ☑️ reconfirm local plots 06 pmg
- ☑️ add comparisons to acc
- ☑️ complete comparisons Nov 22
- ☑️ expected 1% results Nov 22
- ☑️ look for elevation file Nov 22
- ☑️ store accs & code tomorrow
- ☑️ store lodge predicted model Nov 22
- ☑️ look at how to use Rbbest Nov 22
- ☑️ remove gregoriuski but issues
- ☑️ look at IP corrections Nov 22
- ☑️ fill in ethics & future care read fr

- first Nov: more comparisons
- last Dec set up alignment & trouble shooting
- Garcia Meeting:
 - methodology done Feb 1, results error of reb, discussion error of qpr1
 - switching to Rbbest (more helpful)
 - plan for December
- signed into CUSF portal
- allied in basic project info

- research proposal
- ↳ literature review & corrections
- change HSA to Rbbest
- ↳ Rbbest: 1 file is data other is searching
- ↳ HSA not as helpful
- look up basic local alignment search tool
- ↳ review Rbbest
- genes related to stressors - when paper will start + ?
- go over future projections next meet

reviewed research proposal corrections to apply

- ☑️ file too vague
- ☑️ further explain greenhouse effect
- ☑️ why is physiology compared w/ dispersal
- ☑️ add a couple sentences leading up to research question
- ☑️ add specificity } question
- ☑️ remove sentence
- ☑️ add specificity } Goals
- ↳ three genomes & habitat models
- ↳ reward final goal

- ☑️ explain what kind of stressor
- ☑️ change how HSA will be used to Rbbest } Methodology
- ☑️ explain what we're looking for
- ☑️ dynamical errors } General
- ☑️ rewarding certain areas
- complete intro corrections by monday

Tuesday, November 21

- completed ethics due core for CUSF portal
- ↳ look Nick if they work under ethics
- possible elevation file: geografts.gc.ca

Comparative Genomics (David Kheeler & Heetha Bhagwat)

- Basic Local Alignment Search Tool (BLAST)
- ↳ finds regions of similarity between protein/nucleotide sequences
- ↳ compares sequences to sequence in database & calculates start sig of matches
- generated alignments: queries sequences in a database: subject
- query sentences are character strings of single letter codes then definition lines
- alignment consists of a pair of sequences (aligned or gapped)
- search begun by matching all character strings within the query
- versions for matches between 'words' and strings in sequences
- ↳ extends from the match to form an alignment
- ↳ will continue until alignment score drops off due to mismatches

To Do:
 Complete ethics form care
 Find omics and free genomes
 Describe tree db site
 Briefest specifics
 Expect ed vs. results
 Inform mentor our holdings
 How do breaks align

assigned on 'Expect Value'
 alignment better than BLAST would occur by chance
 1000001 to resist known alignments to high quality
 annotation of BLAST to complete genomic sequences
 ing to implement access to BLAST tools
 use comparison chart
 see main stressors
 next does to complete assessments
 narrow

work under ethics?
 Expect ed vs. result
 prepared model models
 final paper due dates
 next meeting time

Wednesday, November 22
 meeting w/ Nick @ 2:00

discussed:
 error in comparison code
 fixed (run each port indiv)
 orange - lodge only
 green - white bark only
 gray both
 blue how much more lodge
 election can be used for all models - same code for past current
 only need predicted done
 meeting, Wednesday @ 12:30

Thursday, November 23
 completed ethics form care
 include brief summary of project
 created future plots for lodgepole

Monday, November 27

completed 2 increase prediction model
 completed 4 increase prediction model
 error w/ current 3 predicted comparison code
 range diff 2w = B10110D - Range size (prog. future =)
 error: external pointer is not valid
 Dec 15 - final paper introduction section

reading in december for understanding
 Main Focus: data collection, deep understanding of methodology

Where are sequences from? expression of genes?
 how will this be measured? how does it answer the research question?

logbook due November 30th
 checked CHSF portal

ethics form care approved
 midterms: January 12 - January 22

March 4th: oral science fair
 worked on fixing error

have to run plot (ain - project) that is in range diff beforehand
 white bark 2w range diff looks weird
 up Oak Nick

lodgepole 21 range diff looks as expected
 white bark 4w range diff looks weird
 code error?

lodgepole 4w range diff looks weird
 significant nek form 2B complete
 made introduction corrections

Wednesday, November 29

send Nick email w/ updates & questions
 February 26th - Oral Presentation
 15 minutes, 4 MUST have minute summary at beginning, no flexibility
 possible poster options for science fair

Nov 15/15 Excellent work! Biggie!

Start thinking about poster format

only science fair, more is judging 'level' (gold, silver, bronze, etc.)

Extensive Variation in Drought-Induced Gene Expression Changes Between

Locally Pine Genotypes - Virginia L. & Jason B. West

Seedlings exposed to drought show expression changes in genes encoding S-adenosylmethionine synthetase, transcription factors (TFs)

↳ donor of methyl, 2nd most used cofactor after ATP

↳ transferred to hormones, neurotransmitters, lipids, proteins, & nucleic acids

↳ rate regulates gene expression & signalling, also imp for metabolic processes

changing activity of genes encoding stress-response proteins

q-tics: epoxycarotenoid dioxygenase, zeatin O-glucosyltransferase, & ABA-responsive

in drought response

action of abscisic acid (ABA)

lived in plant growth, development, & stress response

at & shoot development

genes either over or under expressed in drought conditions

processes activated by drought stress

use to drought found in roots

logbook extension (deceMBER calendar)

not comparison to document

completed initial changes to introduction section

↳ ask Dr Garcia for corrections

sent introduction section for feedback

Northern Forest Tree Populations are Physiologically Maladapted to

Drought (Corrected) - Minom, Isaac-Renton, David Moritz, & Andreas Hamann

no increased primary production in climate change bic drought

↳ produce fewer tracheids w/ low stomatal response

↳ characteristics of drought tolerance

optimism of benefits due to climate change decreasing w/ trees

even w/ high probability trees still struggling to adapt to drought

↳ vascular damage, depletion of carbon reserves

xylem morphology & stomatal response affect drought behaviour

drought avoidance: closure of stomata in dry conditions to maintain

xylem potential preventing cavitation risk which leads to hydraulic failure

↳ air blockages that stop water flow

more tracheids = resistant xylem = stomata open = maintained carbon reserves

large pore pine really good for studying effects of climate change &

extremes & assisted gene flow

↳ tracheid thickness due to temp & growing season

↳ water use efficiency due to climate & seed origin

↳ south & trailing edge produced fewer tracheids

Tuesday, December 5

meeting w/ Nick

discuss:

↳ future models

↳ papers

↳ winter break

discussed:

- articles read

- genes & proteins found

↳ find viral codes for it

- depends how big genomes are

- his break 20-2

↳ no need to meet

- fix warning models

↳ find more literature

find genome & reference genes - next week Tuesday 10:00

find sequences for proteins found in article 9 > December 12

find what codes for amount of tracheids

find what codes for amount of tracheids

figure out RAST issues - December 12

check modelling ID for predicted models - Friday

hand in logbook to Dr. Garcia

To Do:
- Read moleculacion to drought
- Upload & results up to database
- Read non-gprots to doc - 10min
- Compare current & 2' - 15min
- Compare current & 4' - 15min
- Compare 2' & 4' - 15min
- Report on gaps into section - 20min
- Expect connecting genome - 10min
- Use to drought found in roots
- More on question into section 20min

Thursday, December 7

- science fair large plan → dec. 11
 - ↳ steps to complete project
 - ↳ big & small tasks
 - ↳ include in-class presentation date
 - reviewed Georgia corrections to introduction
 - ↳ remove unnecessary paragraphs
 - ↳ add more about genetics
 - ↳ add more about synthetic biology
 - ↳ remove repetitive areas
 - ↳ remove/work goals
 - (look at oral presentation)
 - *Spent 30 minutes studying for bio*
 - Checked chief portal → no new messages
- Monday, December 11
- Georgia meeting:
- add ranges to long-term plan
 - discuss what can be scrapped
 - methodology due mid-February
 - finished adding corrections to introduction
 - ↳ review for form & additional material
 - Dec. 15
 - add ranges to long-term plan
 - found gene sequencing for whitebark & lodgepole
 - found gene sequencing for thraexids in locally
 - found sequencing for 9-cis

Tuesday, December 12

- meeting w/ Nick @ 10
- discussed:
- gene sequencing that was found
- ↳ send to Nick
- ↳ keep table for protein
- BLAST downloaded

Friday, December 15

- worst case: lots of detail w/ models might be enough
 - CH1F: modelling ID = text (make sure text is different)
 - ? : shows where, name ⇒ nucleotide
 - shared lodgepole genome parts that code for proteins
 - ↳ protein is more stuff changes
 - tried to do stuff w/ lodgepole (r being weird)
 - ↳ code will be sent to make the work
 - try to make database - keep looking for genes meet during exam break
- Wednesday, December 13
- recognized OS database
 - ↳ blastn wont install (emailed nick)
 - changed modeling IDs
 - ↳ re-18 sets of code
 - ↳ future model comparisons fixed
 - completed final edits to intro section
 - ↳ look at significance
 - added ranges to long-term plan
 - handed in intro section
 - emailed final sequences & genomes
- Friday, December 15
- received code to help download blast
 - ↳ iron: worked
 - ↳ deebie ← blast ("filename", type = "blastn")
 - ↳ wont work ~ "blastn not found"
 - tried to get blastn to work/download
 - ↳ GOT BLASTN TO DOWNLOAD!!!
 - new error: problem trying to execute blastcmd
 - emailed Nick w/ progress & new variables
 - # of genes so far is good
 - ↳ add more later if needed
 - replaced 4 degree comparison charts in doc

Tuesday, December 19

- email Nick about issues (follow up)
- remove comparison models for predicted (2 degree)
- issues w/ making alignment databases
 - pre-evaluate what can get done
 - How do models help w/ question?
- response curves
 - ↳ diff enviro preferences
 - ↳ there has to be something causing these differences
 - ↳ look at diff's more closely
 - ↳ if alignment is done use to explain diff's
- use future comparison to show necessity of study
 - ↳ combine w/ diff of niches
 - ↳ characteristics of those areas
 - ↳ what do these changes mean?
- complete analysis: December 21
- mode database
 - ↳ if local have to use makebase function
 - ↳ next steps?
- review criteria for procedures section
- update Nick in new email
- got recd from ShmugSet to work w/ my foeta file
- Tuesday, January 8
- sent email to Nick w/ updates from the break
- sent email w/ questions on what to do
- maybe completed one alignment?
 - ↳ foeta locally
- [1] seqid seqid pident length mismatch gapped gstart ...
- [1] evolve bitcore
- < 0 rows > (or 0-length row/names)
- tried to add another database -> not working
- ↳ database not found

updated R to try? fix issue without database issues & assuming correctness time for each alignment: 5-10 minutes

- learn how to analyze predictions
- send email tomorrow about setting up earlier meeting
- work on analyzing climate graphs
- work on case book

start procedures work for climate

Wednesday, January 10

- received email about meeting to work on alignment
- wanted to meet today: didn't see until now
- beholed book that we can still meet / give alternate dates
- downloaded new notebook for alignments

fixed database issue: must use notepad

- ↳ had foeta alignment w/ laptop: maybe worked
- > FASTA-Reader: Ignoring invalid residues at positions: on line 2: 2-11,15,19,23, 24, 32, 33, 35, 36, 38, 40, 42, 43
- with current methods no similarities
- sent email with updates on progress
- estimated time for alignment: 5-10 minutes
- time for analysis: unknown
- * Check email every day

Monday, January 15

- spent last 1/2 hour studying
- meeting w/ Nick at 1:30

discussSeq:

- code looks right
- don't worry about bit score
- lower evaluate better alignment
- can make threshold
- mismatch = how many times don't
- line up
- opt+Hpend = where alignment happens
- gapped = how many letters are the same
- seqid = question
- seqid = sample
- length = how many nucleotides
- gapped % code missing for by amount

- put a lot of genes in one file (try to get something)
- @10, fasta: lodgepole pine (all identified stuff)
- make entire thing for each species
- methodology (what terminology?)
- in a good place for scientist
- meet next week @ 10

Wednesday, January 24

- uploaded relevant files to new computer
- downloaded R (looks weird)
- code that worked on other computer not working
- ↳ fight schedule to complete comparison & analysis
- meeting w/ Dr. Garcia
- ↳ in an ok spot

worked on methods
↳ how does libdilly work?

↳ finish this week for Garcia & Nick feedback

Thursday, January 25

meeting w/ Nick @ 1

- discussed:
- download R studio
- use NCB as another option
- when looking at genome try to find what it does
- pick out 10 interesting genes
- ↳ put in a table
- ↳ look at number of matches
- ↳ copy numbers?
- then compare graphs
- think of whole story
- text meeting: Tuesday @ 10
- find papers about not a lot done w/ pine

- ideally use libdilly to align scaffold genome to determine function
- ↳ hopefully gives good results
- sorting alignment will be most of the work
- send methodology by the end of the week
- send genomes
- ↳ figure out best method
- find papers about sequence alignment

Friday, January 26

- logbook due January 31
- finished methods rough draft
- ↳ issues with paperpile ask Gori
- emailed Nick w/ genomes found
- draft of research proposal
- * will spit up analyzing task later *

Sent Dr. Garcia procedures section for feedback

downloaded R studio onto new computer

↳ check if code still works

old issue of 'unable to find function "makeblastdb"'

Tuesday, January 30

meeting w/ Nick tomorrow @ 10

ask Gori about space (probably good)

↳ Cysf screenshot (Monday)

↳ explanation of figure BEFORE figure

↳ NEED to reference figure

↳ NEED figure legend

(for table title & legend at top)

comparison of general genome similarity (lodgepole & whitebark)

analysis:

- large overall similarity between nucleotides

- 2d-100% similarity

- relatively low e-value

- 85 percent has many mismatch & gopen

↳ gstart/legend: 92-405, start/legend: 163-470

- most lengths in the 100s but large variety

↳ find ident average (Friday)

↳ find areas of gseq/id & sseq/id with > similarity

trifold: 152cm, 86cm, 82cm

↳ good graphics, large headers, large font, good flow

To Do:

- ↳ Fix code (Monday)
- ↳ download R studio (Monday)
- ↳ add citations (Monday)
- ↳ send Nick methodology (Friday)
- ↳ send generic methodology (Friday)
- ↳ align sequences to libdilly (Friday)
- ↳ align sequences to whitebark (Friday)
- ↳ align to libdilly (Friday)
- ↳ methods final (Feb 3)
- ↳ analyze alignments (Feb 3)

more important for results

run lodgepole & lobiolly trackaid code
 ↳ giving some as whiteboard/lodgepole alignment
 ask Nick (fixed?)
 plotting:
 create summary data table (w/ taxonomic names)
 ↳ bind blast hits w/ table
 ↳ ggplot for top hits
 ↳ compare alignment length
 can create subsets to include/exclude/select variables
 create plot comparing patent
 (BLAST: Prof Harbert & Jordan Callahan)
 seq now giving right one
 ↳ prediction - out still looks the same
 ↳ still ask Nick

Thursday, February 1
 meeting w/ Nick
 discussed:
 ↳ protein - as long as its
 ↳ work done - similarity
 ↳ methods - added almost
 ↳ issue - send code
 ↳ three genes & cdna file
 ↳ lodgepole & lobiolly
 ↳ open CDNA then chr
 ↳ filter through
 ↳ compare via # of matches → estimate for copies
 ↳ do CDNA first / in place
 ↳ lobiolly: q lodgepole
 ↳ sent CDNA
 ↳ read sent code
 ↳ comment's for methods next week
 ↳ direct pathing function - next: Thursday @ 10

add options to methods
 (#Feb-5)
 work on CDNA code for
 lodge (Saturday)
 work on protein code
 (Feb-8)
 work on protein (white)
 (Feb-2)
 organize lodge (Feb-7)
 organize white (Feb-12)
 compare analysis (Feb-14)
 HOW DOES IT ANSWER Q?

Science Fair schedule:
 8:15-8:45 - Set-up Posters } (missing morning classes
 9:00 - judging (5) 30 mins } (email teachers)
 11:30 - done
 made schedules for Jun & Feb
 ask about methods
 submitted prots of approved project info
 set date for practice presentation w/ Garcia
 Feb 23 (12:30-1:00)
 run lodgepole CDNA vs. lobiolly CDNA
 (very high similarity)
 length of heat shock matches: 21
 length of drought matches: 12

Dec 15/15
 Jan 15/15

Monday, February 5

- got Garcia methodology corrections back
 - ↳ add more procedural details □
 - ↳ specify the why □
 - ↳ add analysis explanation □
 - ⇒ Background (less time)
 - ⇒ RA / Goals
 - ⇒ Methods (slightly longer)
 - ⇒ Results (most time) ↳ can intermingle
 - ⇒ Analysis / Conclusions
 - ↳ C has to answer the question
 - ↳ what went wrong/how to fix ↳ what's next
 - Whitebark v. Loblolly Analysis
 - fairly high over all similarity
 - 75-91% similarity
 - low e-value
 - lengths in 100s w/ high variety
 - 75% similarity, 34 gap open & 98 mismatch
 - eg: 24408-24954 s: 13195-130653
 - no matches for loblolly genes that didn't match
 - length of 12 match for expressed under drought
 - very few matches > 95%
 - Lodge v. Loblolly Tracheid
 - ↳ no matches
 - ↳ White v. Loblolly Tracheid } *fruits not proven?*
 - ↳ no matches
 - ↳ print tables (Friday)
 - not much success aligning genomes w/ individual proteins
- Garcia meeting:
- Graphics for analysis meeting w/ Nick

Work on poster & presentation design

- explained results
 - explained what was done
 - create table w/ results (Thursday)
- ## Tuesday, February 7
- add corrections to first 3 sections of methods
 - ↳ 30 minutes
 - send email to make sure JB is not needed
 - ↳ don't use apod email
 - ↳ march 15 @ 9am portal closes
 - let teachers know morning of the 4th will be missed □
 - CDNA ~ synthetic DNA that has been transcribed from a specific mRNA through a reaction using the enzyme
 - ↳ ask Nick why □
 - completed correcting first 3 sections of methods w/ Garcia feedback
 - ↳ specific changes made shown on printed copy
- ## Comparison notes:
- not a lot of success when trying to align proteins w/ whole genome
 - ↳ unable to find nucleotide sequences for proteins from the trees studied (something for future?)
 - Whitebark & lodgepole comparison:
 - only 5 alignments (highest 91)
 - to find matches for specific gene sequences in loblolly > 95% used
 - ↳ ask Nick why
 - ↳ ask if possible to see the write & lodge sections that match w/ loblolly → sequence align visual
 - cysteine protease ~ essential for plant growth & development
- ## Role of Cystein Proteases in Plant Development
- ↳ Huijun Liu

- function in seed germination, abiotic stress & immunity
 - present in programmed cell death - also good for disease
 - highly expressed in drought & salt stress
 - important to enhance plant stress tolerance
 - getting some results now for matones
 - ask nick why
 - prediction sorted are diff
 - look at poster examples (Friday)
 - found 10 gene sequences to align for in labrally
- Thursday, February 8
 - meeting w/ Nick @ 10
 - discuss:
 - look about code issues
 - talk about results
 - how to show results
 - why using cDNA
 - see white & lodge sections
 - discussed:
 - length is # of columns in table (wrong)
 - need to add & -> moves number of genes copy #
 - genomes in wrong column
 - make squid squid
 - mention that we're trying to find copy number
 - occurrence data (points in space at lat. & long)
 - citations (he will give links)
 - similar # copies = obser generically
 - good to find other
 - hasn't really been done yet (harder to study)
 - most couraus cutoff 95% or 90%
 - general standard
 - cDNA has annotations & interested w/ stuff that encodes for phenotype
 - just nucleotides that encode for something



- align display possible
 - will try to find code
 - yes interested in judging
- Friday, February 9
 - do not need to fill out significant nick 2B
 - finished adding Garcia corrections to methods
 - finished methods corrections
 - work on adding 2 citations
 - found kagepole gene copy sequences for 10 interesting
 - look into dehydration and temperature
 - found white bark gene copy # for 10 interest
 - print off draft (Monday)
 - worked on analysis of copy #
 - look at cold induced
- Tuesday, February 13
 - methodology due today
 - handed in on turn it in and google classroom
 - Garcia meeting:
 - don't have to use rp formula for pres
 - split methods
 - lots of explanation for methods
 - images (ask Nick)
 - visual results:
 - habitat model comparison graphs
 - sequence comparison
 - graph comparing avg pident
 - don't show whitebark results b/c there aren't any
 - ask Nick
 - response curves for each plant
 - how to add axis titles and titles in general & legend
 - ask Nick
 - return habitat comparison code to get graphs



- To Do:
- Create p-ident graphs (Friday)
 - Remake habitat graphs (Friday)
 - Try to find good sequence alignment of lodgepole visually (Friday)
 - Make groups clearer (Friday)
 - Adjust matrix of slides (Friday)
 - Images for presentation (Friday)
 - Discussed:
 - gave code to visualize alignment
 - ↳ have to change numbers to match genes
 - global is entire thing
 - local picks similar fragments
 - ↳ good is long w/ lots of consensus
 - histogram of p-idents
 - type of graph after? then adjust as wanted
 - ↳ comparison models might be easier to pose over
 - error w/ old code
 - ↳ might have to run earlier code
 - visual for what goes in and out
 - ↳ don't just show code
 - will take a look at pres & ask if more gaps needed
 - next meet Thursday @ 10
 - * Practice slide sections as they are added
 - Wednesday, February 14
 - med sequence visuals for:
 - pins
 - chap
 - drought induced
 - drapin
 - draic
 - drastnock
 - temperature
 - draic
 - ↳ heat & drought are longest but have mismatch
 - ↳ temp is next w/ no mismatch
 - ↳ drask Nick which are good
 - adjusting intro slide
 - ↳ got rid of climate on bio (add all the info enviro on plant)

□ Add results to slides (Wednesday)

□ Good conclusions to slides (Thursday)

□ Print off charts & graphs (Friday)

□ Done work on poster (Saturday)

- Improve graphic for stress on plants
- ↳ climate change & bio added to quick overview
- methods adjustments:
- ↳ most of it doesn't make sense
- habitat modelling
- ↳ bio render input & output - use?
- ↳ rewrite 'script'
- genome comparison
- ↳ rewrite flow chart
- ↳ rewrite 'script'
- found lodgepole object
- ↳ now able to remake graphs
- Saturday, February 17
- remade response curve graphs
- remade current comparison graphs
- avg. p-ident between white & locally: 82.4%
- avg. p-ident between lodge & locally: 95.6%
- ↳ created histogram
- added graphs & results to presentation
- added conclusions to presentation
- ↳ add adjustments section
- Tuesday, February 20
- email Nick w/ visualized alignments
- ↳ are they usable
- references need URL -> check OML Purdue
- take screenshots of alignment & add to doc
- ↳ print off & add to loopbook
- ↳ ask Nick about Graph files & axes
- edited Graphs of Results
- finished 'script' for habitat comparison results
- base Nick what soil things measured

write 'script' for alignment results
begin conclusions 'script'

↳ add errors

↳ add future

Thursday, February 22

meeting w/ Nick @ 10

discussed:

- gave longer smy alignment
- slide 7: y-axis: suitability (now favourable)
- maps that u are more likely to see species
- ↳ temp & axis: °C, precip & axis: mm, soil & axis: mm (soil moisture)
- ↳ how deep soil is: moist
- slide 9: green lodge, red: white bark, yellow: overlap
- ↳ more graphy one may not be as helpful
- some results and areas for further research
- methodology explanation
- ↳ include plot of climate variables (may be useful)
- ↳ individual projection maps (for in & out)
- ↳ how did you determine copy number?
- ↳ how many unique matches were found
- ↳ copy number shows advantage
- (higher copies confers greater advantage)
- ↳ possibility lodge is genetically closer in time to job
- don't need to add U of C logo
- one sent is neat snack
- ↳ add to table (already there)
- ↳ just showing genes are similar
- made map combining points on R occurrence w/ conclusions
- ↳ some kind of thing as response curves
- ↳ meet next Thursday @ 10
- add alignment visual to presentation
- add axes and legend titles

checked individual habitat models

↳ practice presentation (at least twice)

↳ tomorrow practice w/ Dr. Garcia @ 12:30

↳ make poster plan (Friday)

↳ review judging score sheet (Monday)

↳ review in class next (Friday)

Friday, February 23

practice presentation w/ Garcia

notes:

- work on beginning plan
- goals is kind of crowded
- ↳ separate long term goals
- ↳ unclear explanation (too general)
- ↳ cut out determining possibility
- ↳ move title up
- ↳ add long term goals to significance
- ↳ variables only connect to 2nd part
- ↳ too fast
- add title to habitat (sections of methods)
- ↳ don't need two boxes just take more time
- ↳ say preferred (slow down more)
- add titles to slides
- how do maps work? what they
- try to superimpose graphs
- there may be other factors (pests)
- ↳ more cohesive
- show what results look like
- add units to axis (show disparity of scales)
- try to just find them in general
- ↳ similarity is excluding them
- replicate: in terms of genes whose functions could potentially be
- remind of endangered area
- non
- speculating
- include stuff that isn't
- talk slower and give time to process
- ↳ double check w/ Nick
- ↳ if able to lower similarity
- reinforce appl.
- synthetic biology
- some stuff on processes
- emphasize as raw data

Saturday, February 24

emailed Nick w/ questions

tried searching for copy # of whiteboard for matches XO

↳ there were none

↳ more conclusive that they do not have these genes added corrections to presentation slides

Monday, February 26

listened to presentation

besaica:

- finding which knockout method is more effective

- 2 extra restriction sites needed to perform mutagenesis

↳ how could this be applied to cancer?

↳ answered ↳ following logic flow

Owen:

- identifying heart disease w/ machine learning

- error w/ small sample size

↳ how could you fix the 'fuzziness'?

↳ add a filter to make spectrogram more clear

meet w/ Dr. Garcia about presentation corrections

↳ tomorrow during spare

Cooper:

- investigating how concussions affect amounts of proteins

- compliment proteins in blood may have been washed out

↳ why are there more SH1H1 mice than Rmthb1?

↳ more efficient & cost effective

improve punchline □

try to make presentation more 'loose'

↳ don't need to worry about time for poster

have conclusions before significance (poster)

make sure to add reference section

Tuesday, February 27

Garcia presentation notes:

- look at what makes a plant better able to handle stress

↳ mainly genetic differences (punchline)

- use genetic differences as title

- images need a purpose and title

- some genes haven't been assigned a function (whiteboard)

- what if it's completed

discuss time to go over poster

↳ will email

Wednesday, February 28

listened to presentations

Vincent:

- effectiveness of bacterial proteges in municipal waters

- the proteges could be a potential solution

↳ do you know the statistical significance/results?

↳ repeated several times / killed 73111's strains

finished adding borders to graphs

↳ print words papers □

board borders to word papers □

↳ finish lettering □

Thursday, February 29

meeting w/ Nick @ 10

discuss:

▷ whiteboard verification

▷ presentation

▷ Emeet every 2 weeks?

discussed:

▷ suitability = probability

▷ whiteboard verification

▷ hard to know much

▷ hasn't been segmented

▷ still have to write paper

- Wednesday @ 12:30 next meet

▷ what's next

▷ best of paper

▷ Enext meeting

- more don't reproduce

↳ difficult to consider w/ a model

↳ didn't look into bic interspecies is harder

↳ outside of the scope of the project

meet every other week

15/15
Th.

Thursday, March 7

- mention March break to Nick
- results due March 19 (5 classes left)
- results:
- figures and tables
 - ↳ look at orientation to see standards for APA
 - ↳ explain figure prior (description)
 - ↳ for graph: comparison, legend
 - ↳ colour, standard deviation
 - ↳ mention numbers, trends, narrative
- ↳ little mention to methods
- ↳ description should be concise
- ↳ multiple: make sure to label
- ↳ no conclusions/why?
- ↳ don't show raw data
- ↳ length doesn't matter
- ↳ minimal citations
- ↳ comments on science fair review/reflection
- ↳ sent Nick science fair results
- ↳ added problem to CHSF platform
- ↳ Garcia meeting:
 - make goal of study clear
 - gone research (some chapters in textbook)
 - research = background (intro)
 - data (where it comes from)
 - acrn. (Garcia, UoC, member)
 - added citations & acknowledgement to CHSF
 - ↳ added research

Monday, March 11

- need reflections (March logbook)
 - ↳ main thing
 - log book (March) will be w/ April logbook (April 30th)
 - Final Oral Presentation - June 4th (50%) (15% of total grade)
 - Final Paper (15% total grade) } formal
 - Discussion (6% total grade)
 - city science fair is extracurricular
 - added methods & conclusions to portal
 - APA tables & figures:
 - tables numbered w/ arabic numerals
 - title in Italics (blank between number & title)
 - leave blank if no data (add dash if expansion needed)
 - 3 types of notes
 - ↳ General: explain table as a whole (double spaced)
 - ↳ Specific: explains a specific column (superscript)
 - only have borders that help w/ clarity
 - figure title under number (double spaced)
 - signs serif font within figures
 - legend within or underneath
 - notes the same as tables
 - added Figure 1 to results
 - ↳ not a comparison map
 - ↳ ask Garcia if response curves should be split up.
 - ↳ write narrative but waiting to complete
- Wednesday, March 13
- meeting w/ Nick today
 - discussed:
 - genes translated into amino acids then proteins
 - increased copy # means they wanted to keep it
 - split response curves into smaller graphs
 - how many times it was run (# pseudo * # of runs)

- add this map captures western canada
- style of writing is good
- could talk about the trends
 - ↳ people like quantitative results
- maybe look into cDNA
 - ↳ issue w/ description
- look for papers similar to project
 - ↳ diff in gene copy number (within or between)
(relates to survival $\frac{1}{2}$ # of proteins created)
 - ↳ comparative studies
 - ↳ endangered vs. non-endangered
- science fair is similar to school one
- spring break
 - ↳ meet after but before city science fair
- might send a couple of papers for discussion
- scan logbook pages
- record video
- choose header, presentation, and picture
- made header image (on slideshow)
- split up response curves image (4 figures each)
- look at bio textbook for gene info
- send email to Nick w/ April availabilities

Mon

Tues

Wed
Med

Thurs

Fri

4 SCIENCE FAIR

5 email Nick
write in log

6

7 email Nick
write in log

8

1 work on poster
uploading images
email Nick

11 email Nick

write in log
acid methods
& conclusions
to portal
look at APN
format for figures

scan logbook
upload to portal
work on habitat
models figures

13 email Nick

write in log
take photos
film presentation
work on response
curves figures

14

meeting w/ mentor
upload photos
& presentation
to portal
check figures w/ Nick

15

email Nick
write in log
portal complete
General alignment
figures
(Gene copy table
over weekend)

18 double check
results

19 email Nick
write in log
results due

20

21 email Nick
write in log

22

23

26

27

28 spring break

29



Monday

Tuesday

Wednesday

Thursday

Friday

FEBRUARY

5 analyze lodge
CDNA
Finish protein
(lodge)
email mentor
Garcia meeting
post abt design

6 work on CDNA
(white)
work on protein
(white)
analyze lodge
protein ✓

7 email mentor
work on CDNA
(white)
work on protein
white ✓

8 mentor meeting
@ 10
Finish CDNA (white)
work on protein
(white)
correct methods

9 email mentor
analyze CDNA (white)
Finish protein (white)
correct methods

12 analyze white
protein
compare data
correct methods

13 methods due
email mentor
create data table
(begin making
graphs)
Garcia meeting

14 work on graphs
take home poster
begin planning
pres (make slides)

15 work on poster
fast make
slides
Long
Weekend →

16 work on poster
finish slides

19 work on poster
begin practice

20 email mentor
ask Garcia abt
slides
practice pres ✓

21 practice pres

22 email mentor
practice pres ✓

23 practice in
front of Garcia
12:30 - 1:00

what section
of poster?

26 In-class
presentation

27 work on poster
adjust presentation

28 email mentor
work on poster
(attend these
presentations)
adjust present.

29 work on
poster
present in front
of Garcia?

1 work on poster
email mentor
practice
pres.

what
sections of
poster on each day?



JANUARY

Monday

Tuesday

Wednesday

Thursday

Friday

1

8 Email Nick
Exam
Break

2

9

3

10

4

11

5

12

15 Meeting
w/ Nick

16

17

18

19

22

→

23 work on
methods

24 Email Nick
Garcia meeting
Mentor Meeting
work on methods

what part?

25 Finish methods
rough draft
(send to Garcia &
Nick)

26 Email Nick
work on lodge
vs. white code

29 work on
lodge vs. white
code

30 Email Nick
finish lodge
vs. white code

31 Analyze new data
work on protein
code (lodge)

1 Mentor Meeting
work on CDNA
code (lodge poles)
work on protein code
(lodge)

2 Finish
lodgepole CDNA
work on protein
code (lodge)

20

DECEMBER

Monday

Tuesday

Wednesday

Thursday

Friday

4

5 ASP
email mentor
write in logbook
meeting w/ mentor
@ 10:00

6 finish reading
article 10

7 ASP
email mentor
write in logbook
start reading article
||
||
find sequences for
proteins

8 download Blast?

11 ASP

email mentor
write in logbook
finish reading
article 11
And genomes

12 mentor meetings
@ 10:00
find candidate genes

13 ASP
email mentor
write in logbook
fix warning models

14 start poster
board planning

15 ASP
email mentor
write in logbook
introduction due
begin aligning process

18 split genomes
into smaller
sections

19 ASP
email mentor
write in logbook
align genes in
whiteboard
lablily

20 begin aligning
whiteboard

*no meetings
during break
WINTER BREAK →

60

NOVEMBER 2023

SUN	MON	TUE	WED	THU	FRI	SAT
	29	30	31			
	5	6	7	8	9	10
	12	13	14	15	16	17
	19	20	21	22	23	24
26	27	28	29	30	1	2

OCTOBER 2023

SUN	MON	TUE	WED	THU	FRI	SAT
Soccer inputs 1	ASP (1) intro- template no test 2	methods complete 3	ASP (2) meeting w/ Nick @ 10 4	Orientation? 5	ASP (3) read article 7	methods draft 7
goals ignore complete 2 swirl 8	significance complete 9	rp draft done 10	ASP (1) send drafts to gercia 11	mentor meeting @ 10 have rp done 12	ASP (2) add RP edits 13	add RP edits 14
add RP edits work on table 15	research proposal done work on table 16	ASP (3) hand in rp 17	meeting w/ Nick @ 2 table due 18	ASP (1) write in logbook 19	add variables to pres 20	21
22	ASP (2) write in logbook 23	24	ASP (3) Gerica meeting 25	26	ASP (1) write in logbook 27	practice oral 28
practice oral 29	practice oral review oral slides 30	ASP (2) write in logbook 31	meeting w/ Nick @ 12:30 discuss methods 1	ASP (3) write in logbook 2	3	4

Holidays and Observances: 9: Columbus Day, 31: Halloween

Genermade
GIFTS MADE EASY

SEPTEMBER 2023

SUN	MON	TUE	WED	THU	FRI	SAT
27	28	29	30	31	1	2
3	4	5	6	7	8	9
10	11	12	13	14	15	16
17	18	19	20	21	22	23
24	25	26	27	28	29	30

Holidays and Observances: 4: Labor Day

Generade
GIFTS MADE EASY