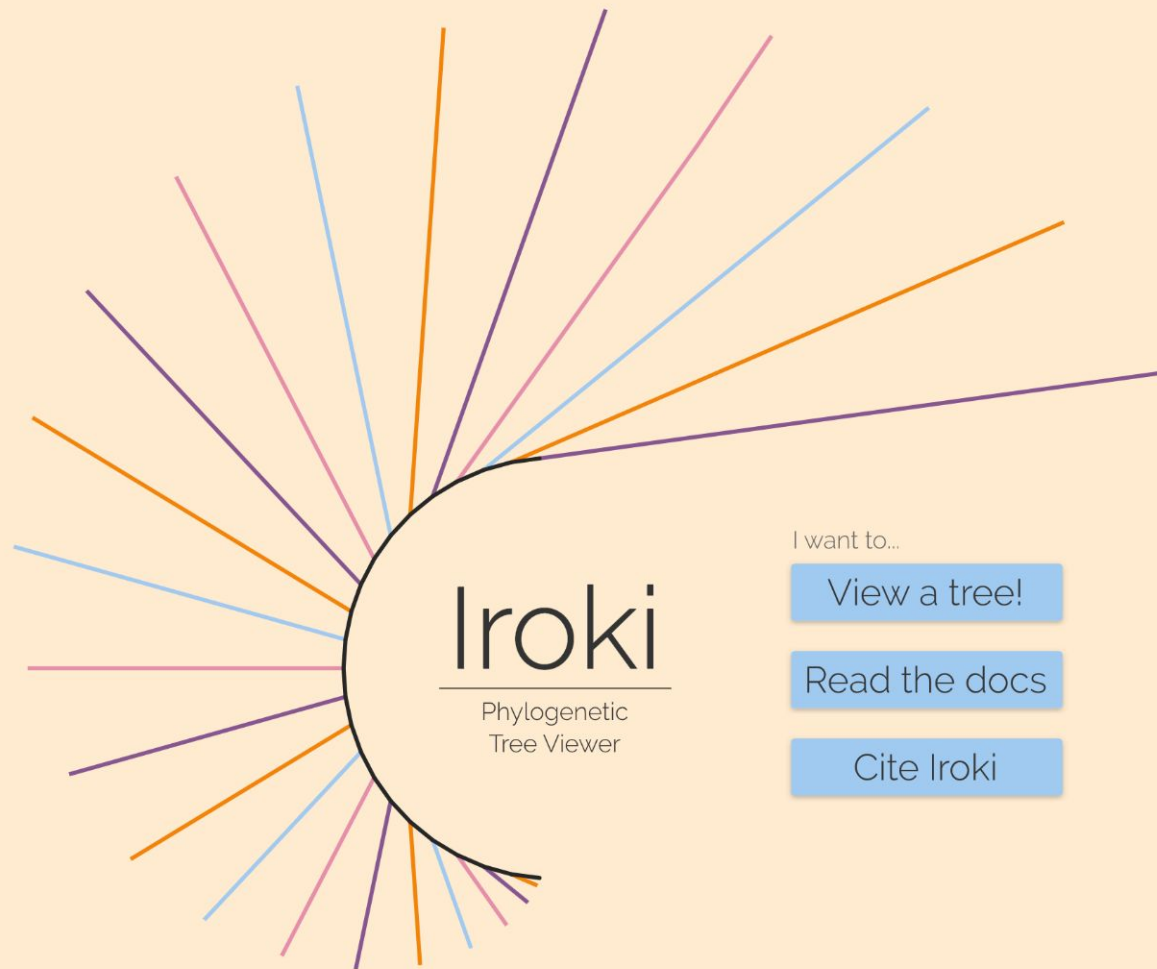# Iroki: Automatic Customization of Trees

Amelia Harrison

FAIR Data Practices for Omics Analysis
Presented: April 22, 2022

About Iroki

- Created by Ryan Moore, a PhD candidate at UD
- Web app for viewing and customizing trees
- Very easy to use
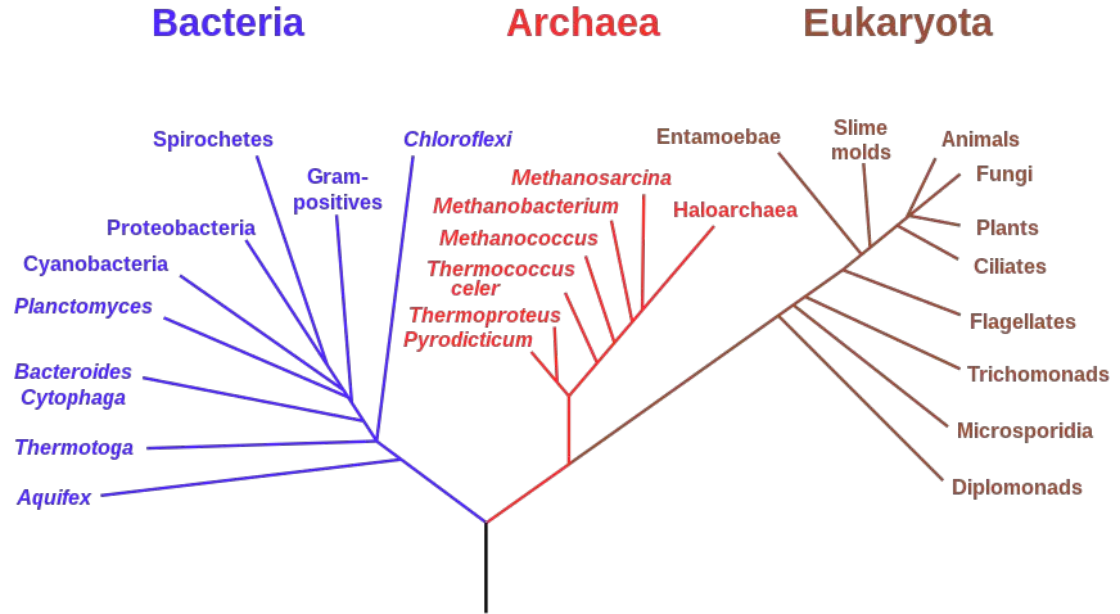- [Website](#)
- [Publication](#)
- [Documentation](#)

Iroki

Phylogenetic
Tree Viewer

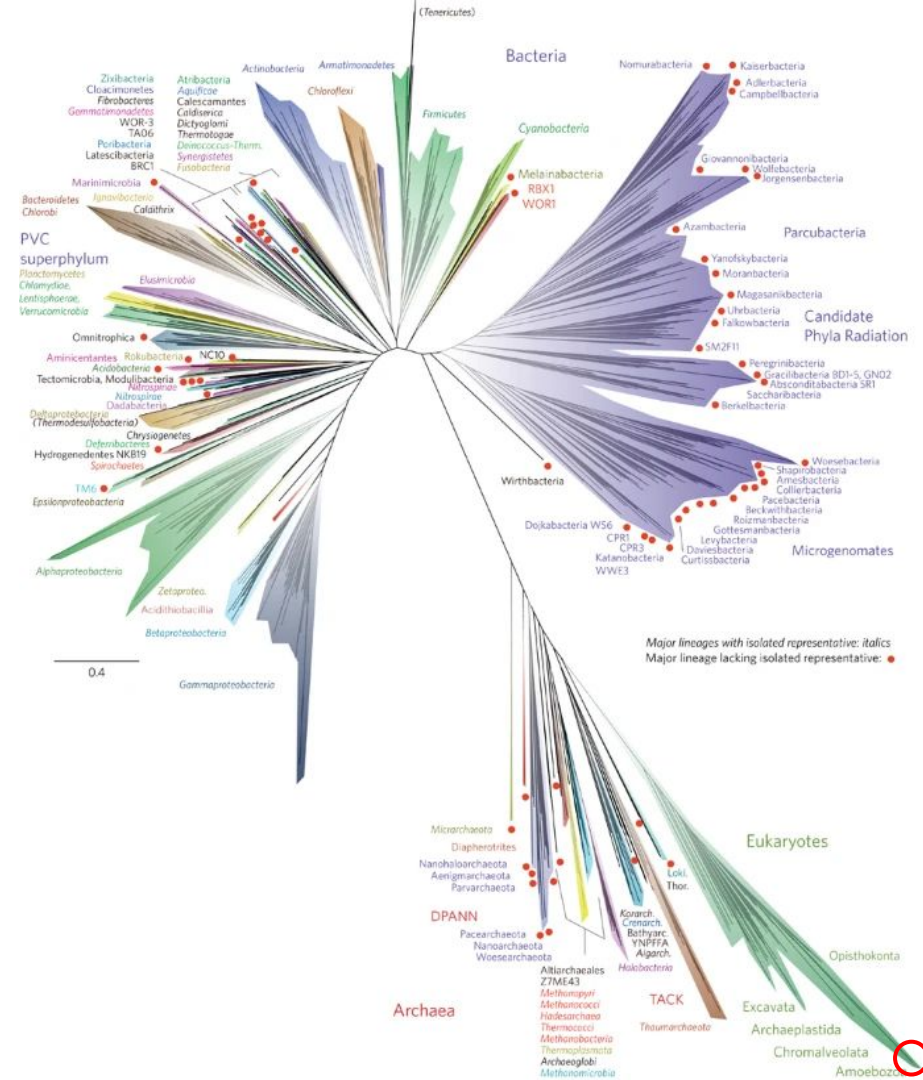I want to...

View a tree!

Read the docs

Cite Iroki

Phylogenetic tree

- Represents evolutionary relationships among organisms (and viruses)
- Now, they are usually made from molecular and sequencing data, but can be constructed from other types of data
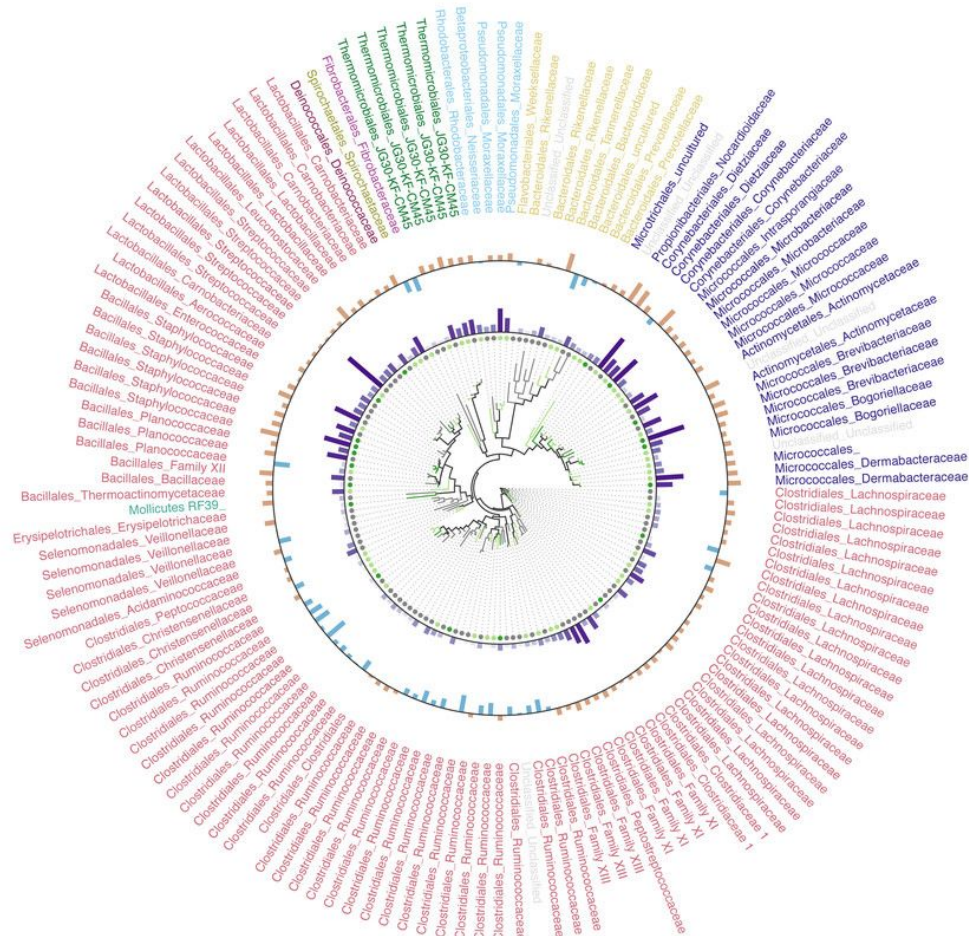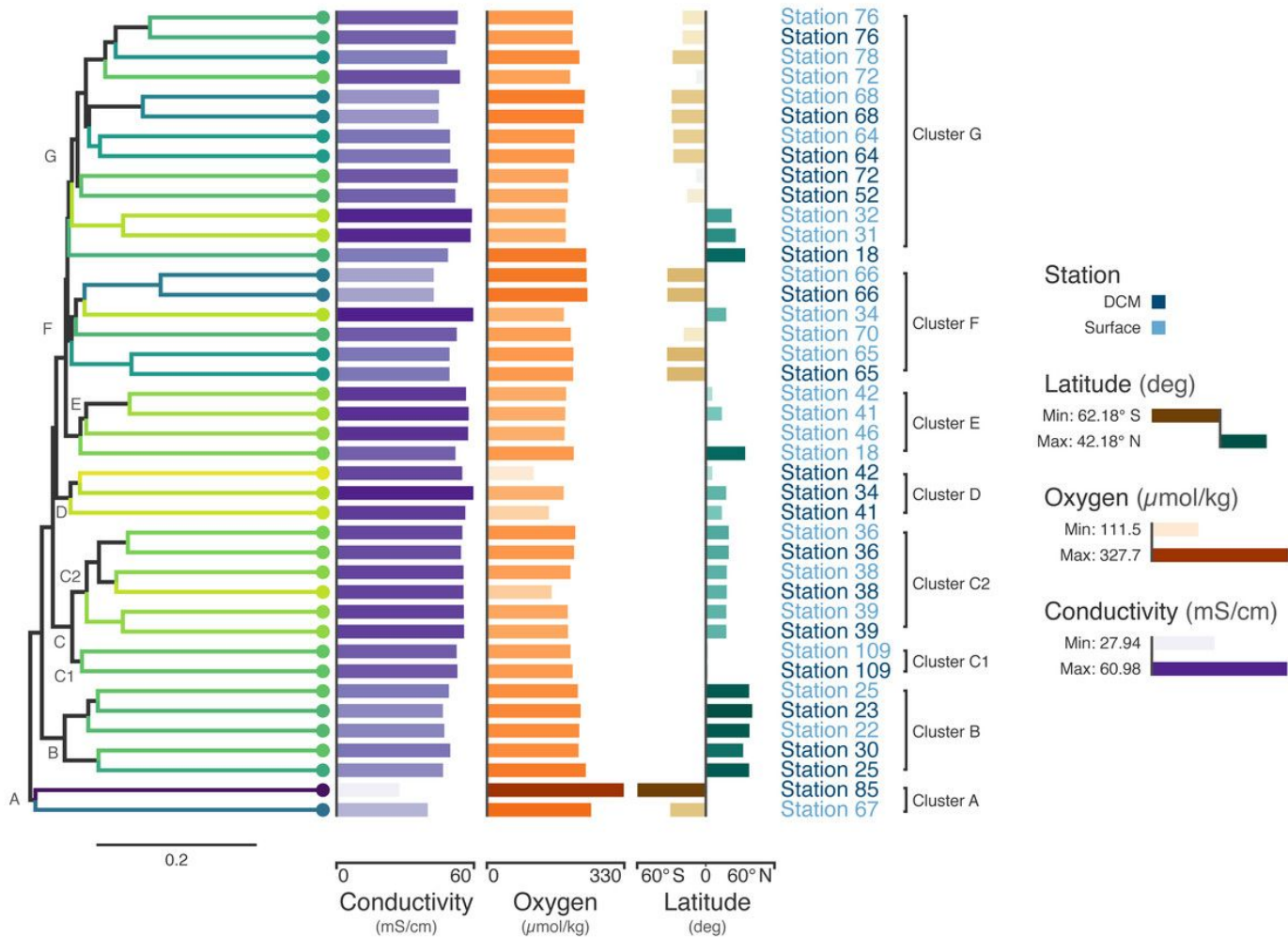 - E.g., morphological

The real [tree of life](#)

- Created in 2016 from a concatenated ribosomal protein alignment
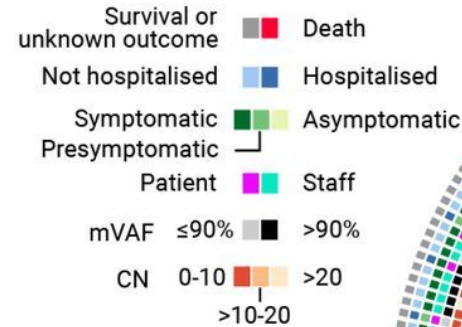- Red circle indicates organisms visible to the naked eye

Station	Cluster
Station 76	Cluster G
Station 76	
Station 78	
Station 72	
Station 68	
Station 68	
Station 64	
Station 64	
Station 72	
Station 52	
Station 32	
Station 31	
Station 18	
Station 66	Cluster F
Station 66	
Station 34	
Station 70	
Station 65	
Station 65	
Station 42	Cluster E
Station 41	
Station 46	
Station 18	
Station 42	Cluster D
Station 34	
Station 41	
Station 36	Cluster C2
Station 36	
Station 38	
Station 38	
Station 39	
Station 39	
Station 109	Cluster C1
Station 109	
Station 25	Cluster B
Station 23	
Station 22	
Station 30	
Station 25	
Station 85	Cluster A
Station 67	

Station
DCM
Surface

Latitude (deg)
Min: 62.18° S
Max: 42.18° N

Oxygen (μmol/kg)
Min: 111.5
Max: 327.7

Conductivity (mS/cm)
Min: 27.94
Max: 60.98

0.2

Conductivity (mS/cm)   0   60
Oxygen (μmol/kg)   0   330
Latitude (deg)   60° S   0   60° N

Clinical features

Survival or unknown outcome — Death
Not hospitalised — Hospitalised
Symptomatic — Asymptomatic
Presymptomatic
Patient — Staff
mVAF ≤90% — >90%
CN 0-10 | >10-20 | >20

Genomic data

Pangolin lineage
- B
- B.1
- B.1.128
- B.1.147
- B.1.281
- B.1.350
- B.1.36
- B.48

Haplotype group
- I
- IIb ○ IIa
- III
- VIII
- IX
- other

20 ⌐ Verdun Hospital

Wuhan-Hu-1

Haplotype group
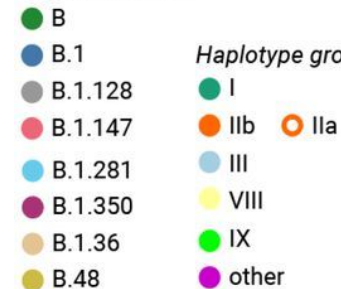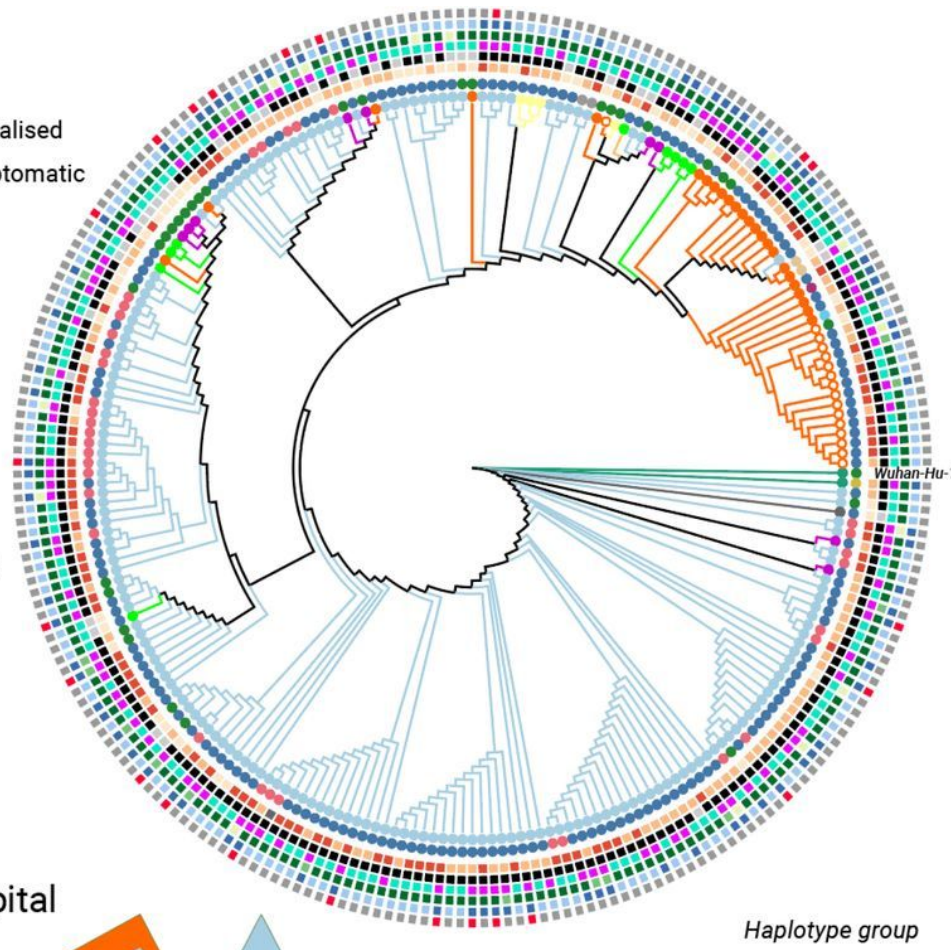
Maximum likelihood phylogenetic tree reconstruction of de novo assembled genomes spanning at least 80% of the SARS-CoV-2 reference genome (*Wuhan-Hu-1*) covered by ≥20 reads and annotated with clinical features of interest. The phylogeny was calculated from a multiple sequence alignment generated with MAFFT [6] using MEGA [7] and visualised with Iroki [8]. Lineage classification performed with Pangolin 2.1.10 [5] (outer circles) and haplotype assignment was performed based on the 20 most common variants in GISAID [4] from the first wave of the pandemic (inner circles)

https://www.medrxiv.org/content/10.1101/2021.05.29.21257760v1.full-text

Cyano SP RNR clade
A large clade of RNRs exclusively from cyanosipho- and cyanopodoviruses. These RNRs have diverged significantly from other RNRs and are proposed to constitute a novel subclass[3].

Cyano SP RNRs
- likely use an Fe/Fe cofactor (hypothesized)
- do not have ATP cones
- do not use the tyrosine radical nor conserve the residue

Branch color : Class I Subclass
Class I subclasses are divided based on radical generation method, which depends on cofactor identity, oxidant used, and the presence of a stable protein radical.

- Ia
- Ib
- Ic
- Id
- Ie
- Cyano SP (If)
- Class II

Want to learn more?
Just scan this QR code to be directed to our publication!

Ring 1: Metal cofactor
Excepting one metal-free subclass[7,8], Class I RNRs require a metal cofactor made up of two metal atoms for radical generation.

- Fe/Fe
- Mn/Mn
- Fe/Mn
- None
- Class II

Cyano M RNR clade
A large clade of RNRs exclusively from cyanomyoviruses. These RNRs are closely related to other RNRs from T4-like phage[2].

Cyano M RNRs
- use an Fe/Fe cofactor,
- have ATP cones in the α subunit
- use the tyrosine residue for radical storage

Ring 2: ATP Cones
ATP cones are evolutionarily mobile regulatory domains that serve essentially as on/off switches[9]. They are found in almost all Class I RNRs and switch the enzyme "off" when enough dNTPs have been produced.

- ATP cone in α subunit
- ATP cone in β subunit
- No ATP cone
- Class II

Ring 3: Tyrosine radical
All RNRs must produce a radical for catalysis. Most Class I RNRs store this radical on a tyrosine residue in the β subunit. A common method of RNR inhibition is to destroy this protein radical. Thus, some Class I RNRs have stopped utilizing the tyrosine residue for radical storage[10].

- Tyrosine radical
- Tyrosine residue only (no protein radical)
- No residue or protein radical
- Class II

Fig 2. Approximately maximum-likelihood tree of RNR Class I α subunits clustered at 70% and rooted with Class II sequences. Branch colors and rings around the tree represent different traits of Class I RNRs.

Color palettes

- Iroki comes equipped with several color palettes

    - Color-blind friendly

        - Kelly's 22 colors for maximum contrast and Paul Tol's palettes

    - Others

        - R colors, Color Brewer palettes

- Try to use color-blind friendly palettes when you can

- Iroki also allows the use of hex codes to create any other color you want!

    - Black: #00000