Assignment 4

Reading

[**mays** - **mexicana** introgression](#)

[ABBA-BABA example in butterflies](#)

Homework

Use the `Abbababa` and `Admixture` modules of ANGSD-WRAPPER to create an admixture plot and D-statistics for the three subspecies **mays**, **parviglumis**, **mexicana**.

The table below offers some information on the samples. For more detail, see [here](#).

Sample	Subspecies	Name	Location
BKN009	mays	Chullpi	Huanta, Peru
BKN011	mays	Pollo	Tiribita, Colombia
BKN014	mays	Assiniboine	Bismark ND, USA
BKN015	mays	Havasupai	Supai AZ, USA
BKN019	mays	Cateto	La Paz, Bolivia
BKN022	mays	Reventador	Las Penitas NAY, Mexico
BKN025	mays	Tuxpeño	Ursulo Galvan VER , Mexcio
BKN026	mays	Pisankalla	Tarija, Boliva
BKN027	mays	Cristalino Norteño	Cautin, Chile
BKN033	mays	Chapalote	Culiacan SIN, Mexico
BKN035	mays	Tabloncillo	Santa Ana, Mexico
TIL01	parviglumis		Tzitzio MICH, Mexico
TIL03	parviglumis		Toliman JAL, Mexico
TIL04	parviglumis		Teloloapan GUE, Mexico
TIL07	parviglumis		Tierra Colorada GUE, Mexico
TIL09	parviglumis		Tejupiclo MEX, Mexico
TIL11	parviglumis		Amatlan de Cana NAY, Mexico
TIL15	parviglumis		Palo Blanco GUE, Mexico
TIL16	parviglumis		Palo Blanco GUE, Mexico
TIL17	parviglumis		Teloloapan GUE, Mexico
TIL08	mexicana		Tepoztlan MOR, Mexico
TIL25	mexicana		Degollado JAL, Mexico

Questions

- How and why do your results differ from Hufford et al. 2013?

- Do the D statistics jive with the admixture plot? Why might these two methods give different answers?

Challenge

This one's a lot of work and I will likely not do. But if you're gung-ho, take a look at Martins 2014 and their "fd" statistic. Can you figure out a way to use ANGSD-WRAPPER to implement this window-based admixture statistic, in order to identify where along the sequence admixture has occurred?

Hint: Yes, this is doable. But it involves a bit of coding and understanding the popgen and the math. Not for the faint of heart.