

# AFLP

- Amplified Fragment Length Polymorphism
- Genome-wide survey (many loci)
- Does not require primer development
- Dominant data
- Utilize to evaluate subspecies and population relationships
- References
  - Ulrich G. Mueller and L. LaReesa Wolfenbarger. 1999. “AFLP genotyping and fingerprinting” *REVIEW ARTICLE* Trends in Ecology and Evolution. 14(10): 389-394. [DOI](#)
  - Bensch, S., and M. Akesson. 2005. Ten years of AFLP in ecology and evolution: why so few animals? *Molecular Ecology* 14(10):2899-2914. [DOI](#)



# What binary data look like

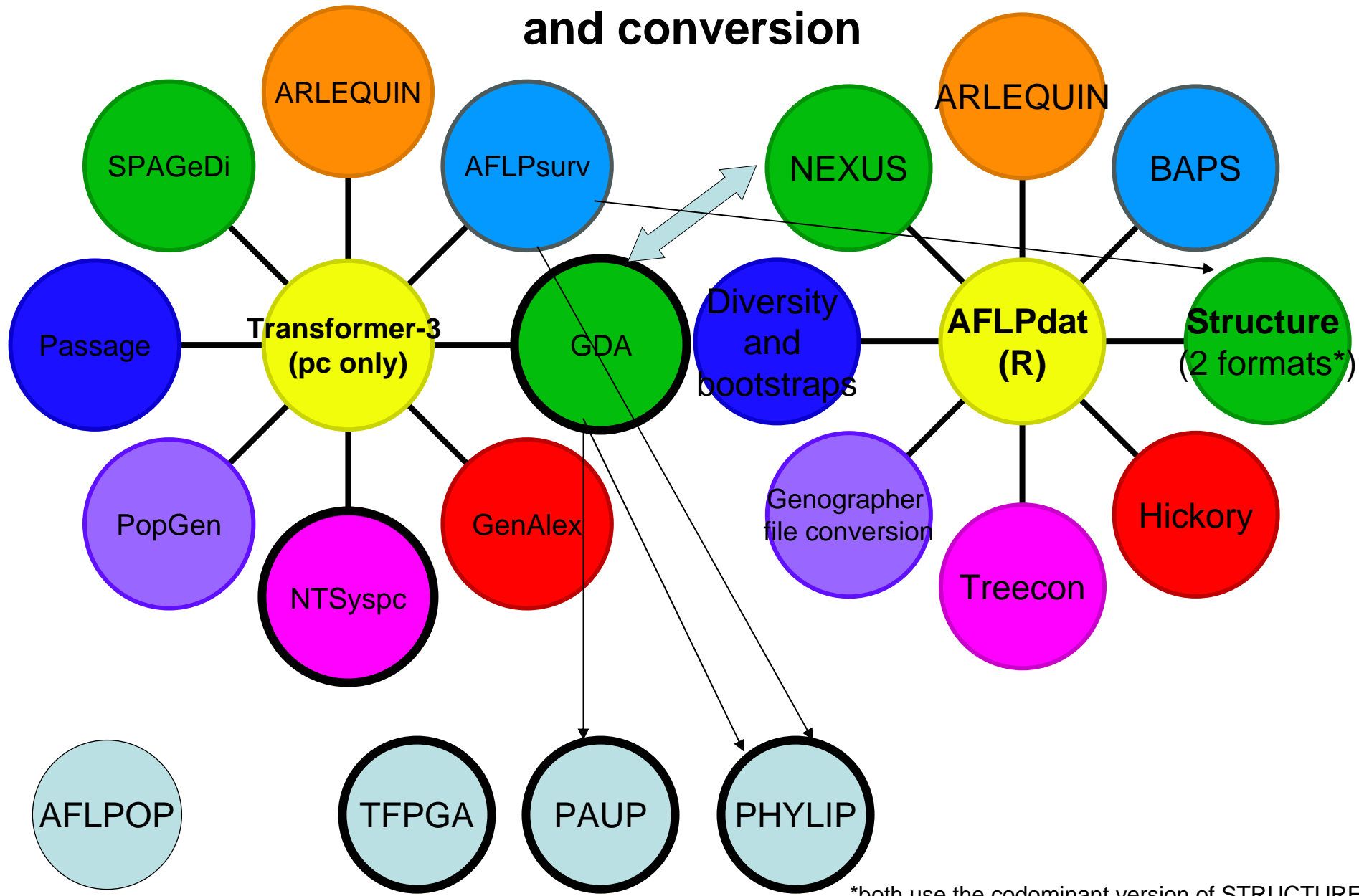
N	Species	Code	eACTmCGG1	eACTmCGG2b	eACTmCGG3	eACTmCGG4	eACTmCGG5	eACTmCGG6	eACTmCGG7	eACTmCGG8	eACTmCGG9	eACTmCGG10	eACTmCGG11	eACTmCGG12	eACTmCGG15	eACTmCGG16	eACTmCCG1	eACTmCCG2	eACTmCCG3	eACTmCCG4
1	Paiute	NFCC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1
2	Paiute	NFCC	0	0	0	0	1	1	1	0	0	0	0	0	0	0	1	0	1	1
3	Paiute	NFCC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1
4	Paiute	NFCC	0	0	0	0	1	1	1	0	0	0	0	0	0	0	1	0	1	1
5	Paiute	NFCC	0	0	0	0	1	1	1	0	0	0	0	0	0	0	1	0	1	1
6	Paiute	NFCC	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	1
7	Paiute	NFCC	0	0	0	0	1	1	1	0	0	0	0	0	0	0	1	0	1	1
8	Paiute	NFCC	0	0	0	0	1	1	1	0	0	0	0	0	0	0	1	0	1	1
9	Redband	SHP	1	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1
10	Redband	SHP	1	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1
11	Redband	SHP	1	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1
12	Redband	SHP	1	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1
13	Redband	SHP	1	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1
14	Redband	SHP	1	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1
15	Redband	SHP	1	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1
16	Redband	SHP	1	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1
17	Redband	SHP	1	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1
75	Cagolden	VC	0	0	0	1	0	0	0	1	1	1	0	0	1	0	0	0	0	1
76	Cagolden	VC	0	0	0	1	0	0	0	1	1	1	0	1	1	0	0	0	0	1
77	Cagolden	VC	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	0	1
78	Cagolden	VC	0	0	0	0	0	0	0	0	1	1	1	0	1	0	0	0	0	1
79	Cagolden	VC	0	0	0	1	0	0	0	0	1	1	1	0	1	1	0	0	0	1
80	Cagolden	VC	0	0	0	1	0	0	0	0	1	1	1	1	1	0	0	0	0	1
81	Cagolden	VC	0	0	0	1	0	0	0	0	1	1	0	0	1	0	0	0	0	1

**Analyzing AFLP data** – do most of the same things as you would with codominant data, but with fewer software options

1. Visualize data in 3D space (ordination, PCA)
2. Calculate basic statistics (Percent poly. Loci, Na, Fst, He, etc.)
3. Make dendrograms and bootstrap tree
4. Identify groups (structure)
5. Define statistical support for groupings (AMOVA; e.g. Arlequin)
6. Assign individuals, mixture, admixture analysis (structure, AFLPop, BAPS, other)

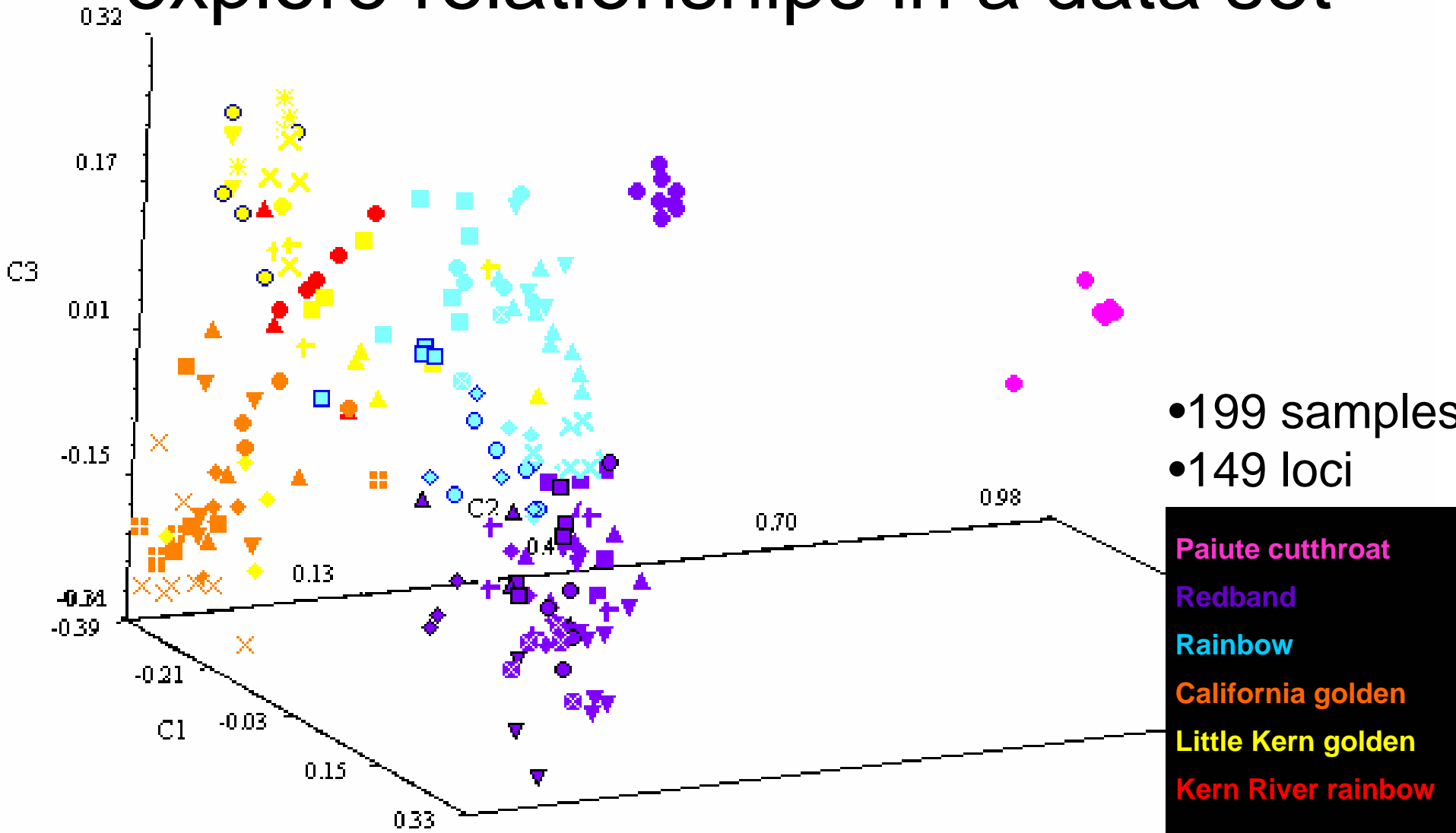
*Getting the data infile...*

# Recent programs allow easy data file composition and conversion

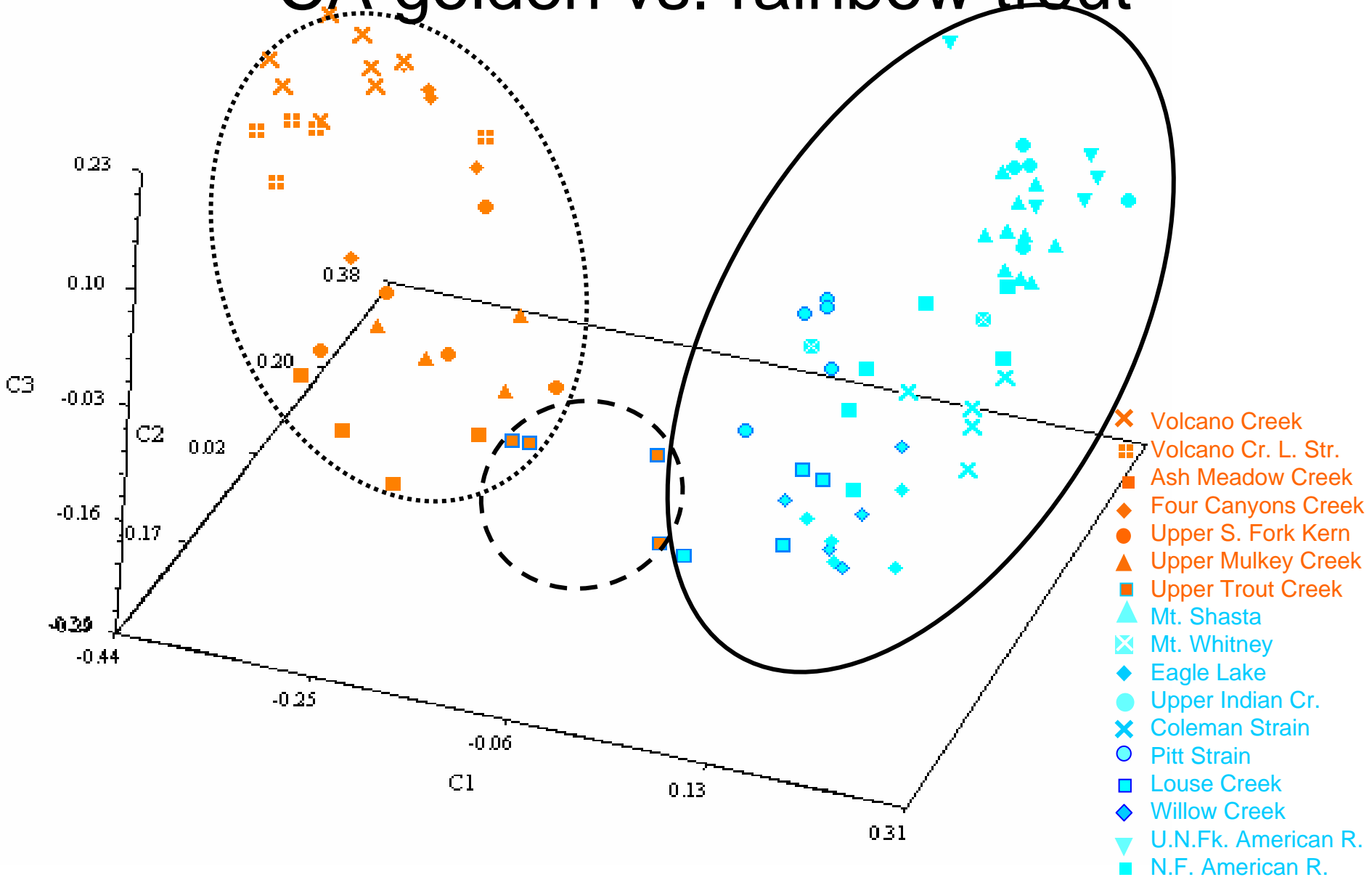


\*both use the codominant version of STRUCTURE; a new dominant-adapted version of STRUCTURE (2.2) will be available soon

# AFLP ordination examples – explore relationships in a data set



# AFLP – detecting clusters and hybrids: CA golden vs. rainbow trout



# Using Transformer-3 to make Data Files

- Make an NTSys-pc data file:
  - Open file “T3\_Datainputforclass.xls” – enable macros!
  - Select “Transformer” from the menu tabs
  - Select “Configure Data”
  - Select the “Dominant” radio button
  - Select “NTSys-pc” from the “Choose file” pull-down options
  - Select “Create File” and name it T3\_TEST
- Make a GDA file called T3\_GDA using the same method (we will be using this file)

# Make a PCA plot

- See handout instructions on how to use NTSys to make a plot using dominant data set “NTSYSclass.xls”

# Creating Trees in GDA

- How to use GDA to make a tree and display in TreeView:
- File – Open (your GDA file you just made)
- “Dist” – “Options” – pull down all of the menus to examine your options, but use the defaults and select “Estimate”
- “Dist” – “Invoke TreeView” – this should pull up your tree in a more user-friendly format
- You can bootstrap trees in other programs like Phylip, PAUP\*, and TFPGA (TFPGA does UPGMA trees only)