**Methods:**

*Datasets:* We collected datasets from several other in prep and previously published studies. To demonstrate the capability of t-SNE depict within and between population differences as well as family structure based on different types of genomic data, we used 1) microsatellite pedigree, 2) SNP pedigree, 3) microsatellite population structure, and 4) SNP population structure datasets. These datasets consist of: sibling assignments (from SOLOMON, Christie et al., 2013) and genotypes at 11 microsatellite for 2,077 juvenile Chinook salmon (*Oncorhynchus tshawytscha*) collected in 2011 by Sard et al. (2015); 11,588 SNP genotypes and sibling assignments (from breeding records) of 1,302 Chinook salmon collected by Pepping et al. (*in prep*); genotypes at 13 microsatellite loci from 1,574 steelhead salmon (*Oncorhynchus mykiss*) from Hemstrom et al. (2017); and 238,915 SNP genotypes from 289 monarch butterflies collected by Freedman et al (*in prep*), respectively. In addition, we used 8923 SNP genotypes for 420 three-spined stickleback (*Gasterosteus aculeatus*) collected by Hemstrom et al. (*in prep*) in order to evaluate the efficacy of t-SNE and PCA with multiple nested datasets (all chromosomes, all chromosomes sans the sex chromosome, and all divergent SNPs from the chromosomal inversion described by the authors). Lastly, we used 13 microsatellite genotypes for 250 white sturgeon (*Acipenser transmontanus*) collected by X and X to show the efficacy of t-SNE to visualize population structuring and family relationships in a polyploid organism, respectively.

To gauge the viability of t-SNE and PCA to visualize genetic datasets other than simple called genotypes, we generated several other datasets from the raw data for the SNP pedigree dataset (Pepping et al. *in prep*). We first used the ANGSD software package to estimate the posterior probabilities that each individual had each possible genotype at every putative SNP (SNP *p*-value <= 1x10-12) with a minor allele frequency above 0.05 (Korneliussen et al., 2014). We used mapping and base quality filters of 20, the SAMtools genotype likelihood model, and a uniform allele prior. We also used the ANGSD package to sample single bases at each putative SNP (SNP *p*-value <= 1x10-12) in each sample using the same filters (the Identity By State, or IBS, approach). Since this does not require calling genotypes or even estimating genotype likelihoods, this method tends to create larger datasets with less missing data.

*Data filtering and formatting:*

In order to have a consistent methodology across all of our datasets, we re-formatted all of the datasets into a “presence-absence” format, in which each possible allele at each locus is noted as a 1 if present or a 0 if absent. We used this approach rather than translating each genotype to a 0, 1, or 2 (for the minor homozygote, heterozygote, or major homozygote, respectively) since this format does not work for poly-allelic markers such as microsatellites. For the call genotype posterior probabilities, however, we instead calculated the expected count of each allele at each site according to the formula , where *E­i* is the expected count of allele *i*, *p­ii* is the posterior probability of the homozygote *i* genotype, and *pij* is the posterior probability of the *ij* heterozgote genotype using custom R scripts. For all basic SNP and microsatellite datasets we used the snpR package to reformat genotypes (Hemstrom et al. *in prep*). We used custom R scripts to reformat the polyploid, IBS, and posterior genotype probability datasets.

Prior to further analysis, we filtered each of these datasets to remove poorly sequenced individuals and loci and interpolated any missing genotypes which remained. Since neither PCA nor t-SNE allow for missing data, it is necessary to interpolate missing genotypes prior to analysis. To reduce the need for interpolation, we removed first all loci sequenced at less than 50% of individuals in each of our data sets, then all individuals sequenced at less than 50% of the remaining loci. For the posterior genotype probability dataset, individuals were determined to have missing data at a site if all three genotype probabilities were equal to the specified prior genotype distribution (1/3 for each genotype). For each data set other than the genotype posterior dataset, any remaining missing allele presence-absence calls were interpolated with the mean value of the presence-absence call for that allele. We used the snpR package to filter the SNP datasets and custom R scripts for everything else.

*PCA and t-SNE*: We created both PCA and t-SNE plots from each of the above datasets. PCA plots were created using the “prcomp” function in R, t-SNE plots were created using the Rtsne R package (Krijthe, 2015). Briefly, t-SNE uses a random-walk approach to minimize the Kullback-Leibler divergence between a multi and two or three-dimensional distance space (such as that contained across many principal components in a PCA) (Maaten & Hinton, 2008). The Rtsne R package, in particular, uses the Barnes-Hut implementation of t-SNE to minimize the search space the t-SNE algorithm must traverse by using a user-provided number (“perplexity”) of nearest neighbors to consider when embedding points into the two or three-dimensional matrix and by approximating to a user defined degree (θ) across nearby areas of the search space using “quadtrees” over which results are summarized based (Van Der Maaten, 2014). These functions are now wrapped for easy plotting of presence-absence data in the snpR package. Since our datasets were not prohibitively large, we used a θ of 0 (for a full, non-summarized search) for each t-SNE run. We estimated the perplexity value to use during t-SNE as described by van der Maaten and Hinton (2012) via the “hbeta” function as implemented in the mmtsne R package and used the default values for all other parameters.

To show how t-SNE results change as the number of initial dimensions or perplexity change, we created several plots using the first 500 individuals from the Chinook microsatellite pedigree data. To do so, we first calculated a baseline perplexity as above and number of initial dimensions from the number of unique observed mother-father combinations. We plotted every combination of these baselines multiplied by 0.10, 0.55, 1.00, 1.45, and 1.90.

Lastly, we attempted to determine if the clusters observed via t-SNE based on the divergent SNPs from chromosomal inversion described by Hemstrom *et al* (in prep) are likely to be statistical artifacts. To do so, we first re-ran the t-SNE multiple times under similar conditions and determined if the clusters were similar between runs. Following this, we created four bootstrapped datasets in order to determine if the clusters were likely due to chance concurrences of variance at a handful of alleles.

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