

# Code for Aguirre, Blasi & Sanchez 2020

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Load libraries and set options

## Loading and visualizing data

```
pan<-read.csv("/Users/damian/Desktop/Projects/Pan flutes/Final version/SuppFile2.csv",sep="," ,
stringsAsFactors = F,header=T,skip=1)
str(pan)
```

```
## 'data.frame': 401 obs. of 26 variables:
## $ Collection.code : chr "Elegant_Chiaohsiao_Tangdynasty" "Elegant_Shaol
## $ Ethnological.group : chr "China_Tang" "China_Tang" "Timor indet" "Timor
## $ Area_fine : chr "China" "China" "SE_Asia" "SE_Asia" ...
## $ Area_coarse : chr "Asia" "Asia" "Asia" "Asia" ...
## $ Area_coarse_time : chr "Asia" "Asia" "Asia" "Asia" ...
## $ Dated..archaeological..ethnological..modern.: chr "618?907" "618?907" "1888" "1888" ...
## $ Size : int 1 1 1 1 1 1 1 1 1 1 ...
## $ Wider.than.high : chr "1" "1" "0" "0" ...
## $ Material : int 2 2 2 2 2 2 2 2 2 ...
## $ Raft.or.bundle : int 0 0 0 0 0 0 0 0 0 ...
## $ One.or.two.rows : int 0 0 0 0 0 0 1 1 0 1 ...
## $ Parts : int 0 0 0 0 0 0 0 0 0 0 ...
## $ No.pipes.S1 : chr "24" "12" "10" "9" ...
## $ Stopped.or.open : int 0 0 0 0 0 0 0 0 0 0 ...
## $ Seriation.of.pipes : chr "0" "0" "0" "0" ...
## $ Ligature.material : chr "4" "4" "3" "3" ...
## $ Thread.ligature.knot : chr "-" "-" "0" "0" ...
## $ Splint.arrangement : chr "4" "4" "4" "4" ...
## $ Tubes.cut.below.node : chr "0" "0" "0" "0" ...
## $ Indentation.at.distal.end : chr "0" "0" "2" "2" ...
## $ Indentation.proximal.end : chr "0" "0" "3" "3" ...
## $ Distal.profile : chr "0" "0" "1" "1" ...
## $ cubical.tubes : chr "0" "0" "0" "0" ...
## $ painting : chr "0" "0" "0" "0" ...
## $ carving.model : int 0 0 0 0 0 0 0 0 0 ...
## $ textile : int 0 0 0 0 0 0 2 0 0 ...
```

```
table(pan$Area_fine)
```

```
##
##      Andes      China      Congo      Europe      NewGuinea      Papuans
##      225       12       5       14       20       3
## SA_notAndes  SE_Asia  Solomons      Tonga      Vanuatu
##      31       10       72       2       7
```

```
table(pan$Area_coarse)
```

```
##
##      Africa      Andes      Asia      Europe      Melanesia  SA_notAndes
##      5       225       22       14       104       31
```

Normalize NAs

```
pan<-as.data.frame(mapply(function(x)
  ifelse(x %in% c("?", "-"), NA, x), pan))
```

We recode number of pipes to coincide with its four quartiles

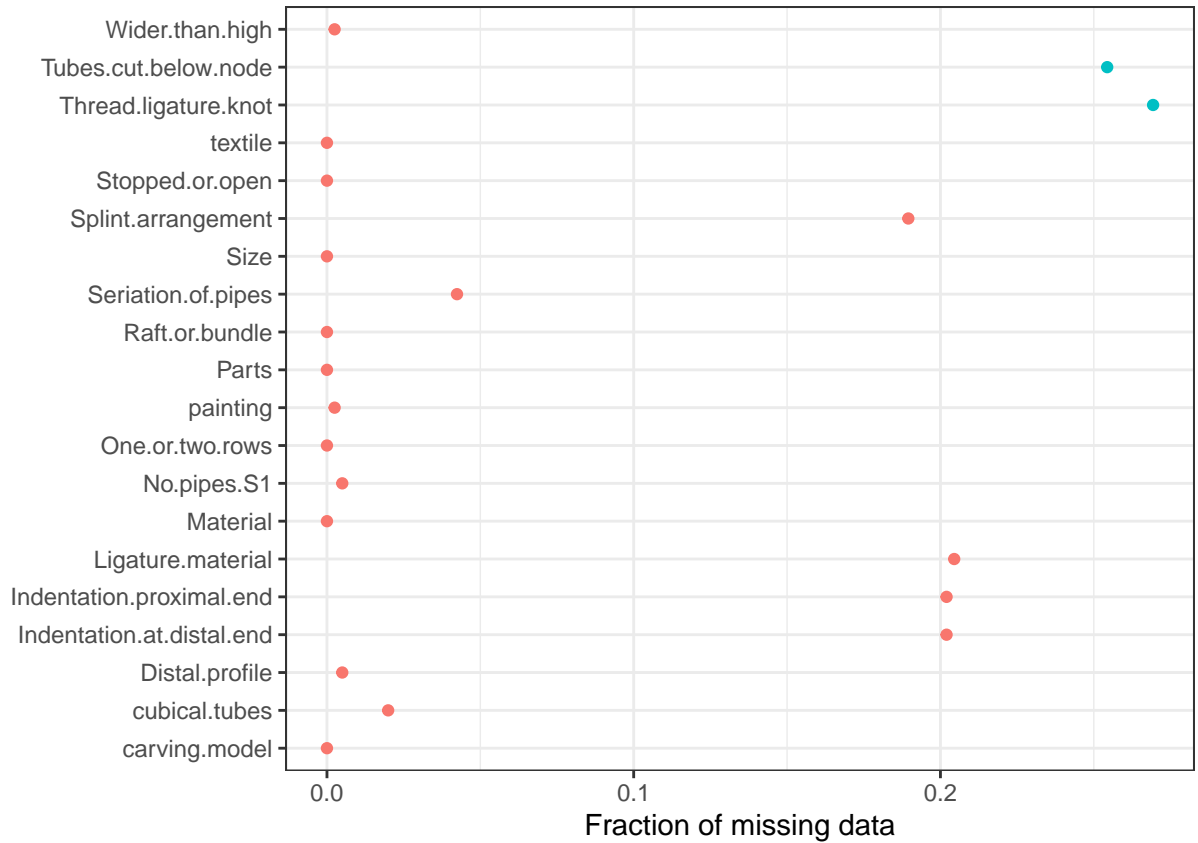
```
pan[["No.pipes.S1"]]<-sapply(as.numeric(pan[["No.pipes.S1"]]),function(x)
  ifelse(is.na(x),NA,
        ifelse(x<=12,0,
              ifelse(x<=26,1,
                    ifelse(x<=28,2,
                          3))))))
```

Check overall missingness

```
nas<-apply(pan[,c(7:ncol(pan))],2,function(x) sum(is.na(x))/length(x))
fmax<-apply(pan[,c(7:ncol(pan))],2,function(x) max(table(x))/length(x[!is.na(x)]))
```

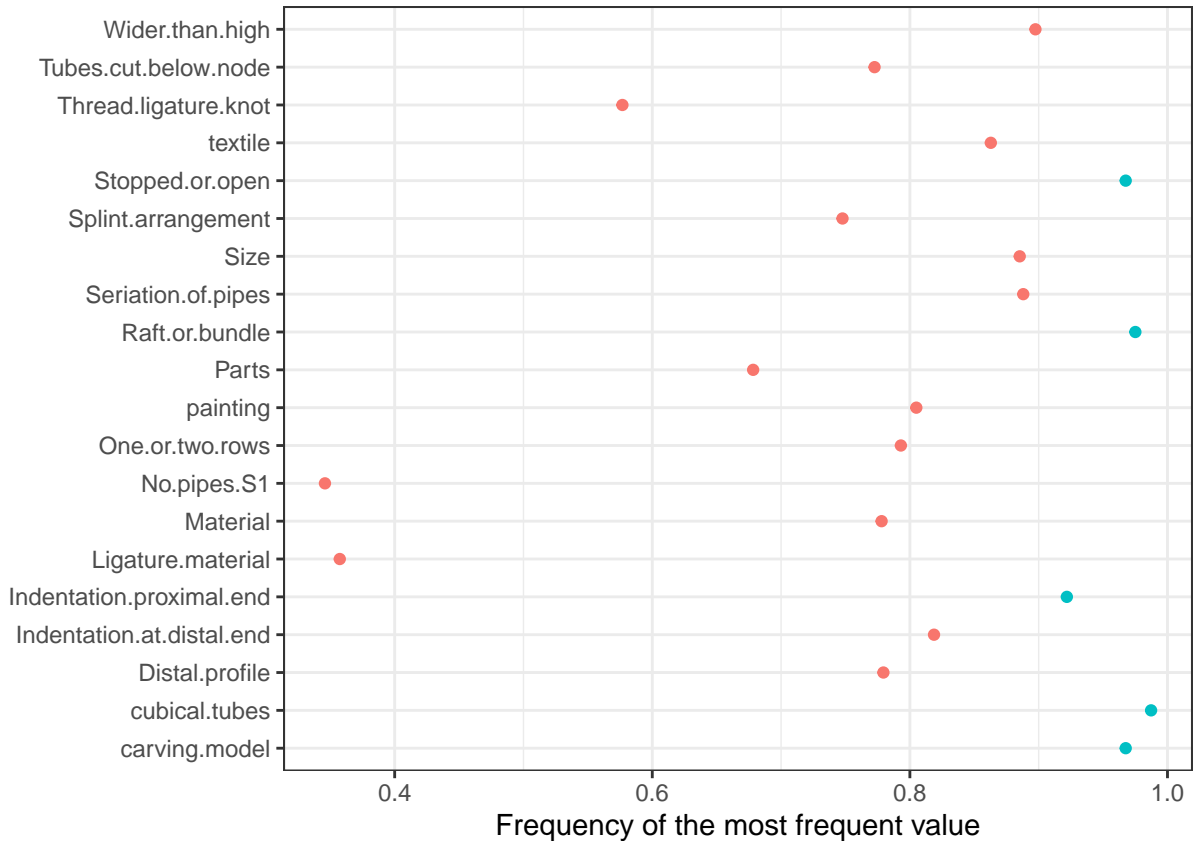
Plot fraction of missing data per feature

```
ggplot(data.frame(missing=nas,
                  id=sapply(names(nas),function(x) x),
                  threshold=sapply(nas,function(x) x>0.25)),
       aes(x=id,y=missing,color=threshold))+
  geom_point()+
  xlab("")+
  ylab("Fraction of missing data")+
  coord_flip()+
  theme(legend.position = "null")
```



Plot frequency of most frequent level per feature

```
ggplot(data.frame(freqmax=fmax,
                  id=apply(names(fmax),function(x) x),
                  threshold=apply(fmax,function(x) x>0.9)),
       aes(x=id,y=freqmax,color=threshold))+
  geom_point()+
  xlab("")+
  ylab("Frequency of the most frequent value")+
  coord_flip()+
  theme(legend.position = "null")
```



There are some features with a strong tendency of having the same coded value.

Plot nominal associations to assess the colinearity between traits

```
pan_gk<-GKtauDataframe(pan[,c(7:ncol(pan))])
assoc_feat<-(adply(pan_gk,1:2,function(x) ifelse(x>0.5,x,0)) %>% subset((V1>0)&(X1!=X2)))
print(assoc_feat)
```

##	X1	X2	V1
## 50	Ligature.material	Material	0.818
## 51	Thread.ligature.knot	Material	0.563
## 52	Splint.arrangement	Material	0.826
## 53	Tubes.cut.below.node	Material	0.702
## 54	Indentation.at.distal.end	Material	0.827
## 55	Indentation.proximal.end	Material	0.826
## 56	Distal.profile	Material	0.748
## 58	painting	Material	0.741
## 68	Stopped.or.open	Raft.or.bundle	0.614
## 144	Raft.or.bundle	Stopped.or.open	0.614
## 210	Ligature.material	Thread.ligature.knot	0.501
## 230	Ligature.material	Splint.arrangement	0.743
## 263	Material	Indentation.at.distal.end	0.529
## 270	Ligature.material	Indentation.at.distal.end	0.545
## 272	Splint.arrangement	Indentation.at.distal.end	0.533
## 275	Indentation.proximal.end	Indentation.at.distal.end	0.540
## 283	Material	Indentation.proximal.end	0.717

```

## 290      Ligature.material  Indentation.proximal.end 0.759
## 291      Thread.ligature.knot Indentation.proximal.end 0.504
## 292      Splint.arrangement  Indentation.proximal.end 0.664
## 293      Tubes.cut.below.node Indentation.proximal.end 0.522
## 294 Indentation.at.distal.end Indentation.proximal.end 0.724
## 296      Distal.profile      Indentation.proximal.end 0.571
## 298      painting           Indentation.proximal.end 0.603
## 303      Material           Distal.profile 0.712
## 310      Ligature.material   Distal.profile 0.691
## 311      Thread.ligature.knot Distal.profile 0.529
## 312      Splint.arrangement  Distal.profile 0.669
## 313      Tubes.cut.below.node Distal.profile 0.512
## 314 Indentation.at.distal.end Distal.profile 0.637
## 315 Indentation.proximal.end  Distal.profile 0.636
## 318      painting           Distal.profile 0.693
## 323      Material           cubical.tubes 0.749
## 343      Material           painting 0.694
## 350      Ligature.material   painting 0.681
## 352      Splint.arrangement  painting 0.694
## 354 Indentation.at.distal.end painting 0.640
## 355 Indentation.proximal.end painting 0.641
## 356      Distal.profile      painting 0.671

```

There are 39 dependencies where one variable predicts the other with a precision of over 50%, covering 12 unique variables. This entails that colinearity will play an important role in our results.

## Overall structure in panpipe data

We attempt at determining the provenance group where a flute comes from based on its morphological features. We consider how unique trait combinations are

```

pan_traits<-colnames(pan[,c(7:ncol(pan))])
unique_pan<-ddply(pan[,c("Ethnological.group",pan_traits)],pan_traits,
                 function(x) data.frame(l=length(unique(x$Ethnological.group)),
                                         e=paste0(unique(x$Ethnological.group),collapse = "|")))

```

There are 192 instruments that are found only within one provenance. The rest have the following distribution of provenances:

```

unique_pan$e[unique_pan$l>1]

## [1] Kwai0|Papua
## [2] Kwai0|Areare
## [3] Ecuador|Peru
## [4] Ecuador|Peru
## [5] Peru|Paracas
## [6] English|Peru|Yaguas
## [7] Lombards|English
## [8] Peru|Aymara
## [9] Peru|Bolivia|Aymara
## [10] Bolivia|Aymara
## [11] Ashaninka_Campa|Solomons

```

```
## [12] Wayana-Roucouyenne|Tupi|Nambikwara|Waura (Wauja)|Wayampi
## [13] Aymara|Peru
## [14] Nasioi|Papua
## [15] Colombia|Peru
## [16] Tupi|Yaguas
## [17] Waura (Wauja)|Ikpeng_Txikao
## [18] Urus|Aymara
## [19] Urus|Bolivia
## [20] Urus|Bolivia
## [21] Peru|Bolivia
## 66 Levels: China_Tang Timor indet Paracas Quechua Peru Pachacamac ... Karen
```

We compare this against 500 randomized versions of the pan flutes

```
nsim=500

baseline_unique<-function(DATA) {
  DATA<-as.data.frame(lapply(DATA,function(x) sample(x)))
  DATA$Ethnological.group<-DATA$Ethnological.group
  unique_rand<-ddply(DATA[,c("Ethnological.group",pan_traits)],pan_traits,
                    function(x) data.frame(l=length(unique(x$Ethnological.group)),
                                            e=paste0(unique(x$Ethnological.group),collapse = "|")))
  return(sum(unique_rand$l==1))}

comparison_unique<-rdply(nsim,function(x) baseline_unique(pan[,c("Ethnological.group",pan_traits)]))
```

Most randomizations (0.19) yield 401 distinct instruments. Now we move to compare the distribution of Gower dissimilarities between instruments - both in the actual dataset and the randomized control.

```
nsim=500

baseline_comp<-function(DATA) {
  D<-as.data.frame(lapply(DATA,function(x) sample(x)))
  D$Ethnological.group<-DATA$Ethnological.group
  unique_rand<-ddply(D[,c("Ethnological.group",pan_traits)],pan_traits,
                    function(x) data.frame(l=length(unique(x$Ethnological.group)),
                                            e=paste0(unique(x$Ethnological.group),collapse = "|")))
  return(as.vector(cluster::daisy(D))) }

comparison_random<-rdply(nsim,function(x) baseline_comp(pan[,c("Ethnological.group",pan_traits)]))
comparison_random<-data.frame(d=as.vector(as.matrix(comparison_random[,c(2:ncol(comparison_random))])),
                             type="random",stringsAsFactors = F)

distances_empirical<-cluster::daisy(pan[,pan_traits])
comparison_empirical<-data.frame(d=as.vector(distances_empirical),type="empirical",stringsAsFactors = F)

distances<-rbind(comparison_random,comparison_empirical)
```

We plot the distribution of dissimilarities

```
ggplot(distances,aes(x=d,y=..density..,group=type,fill=type,color=type))+
  geom_histogram(bins=15)+
  scale_x_continuous(limits=c(0,0.6))+
```

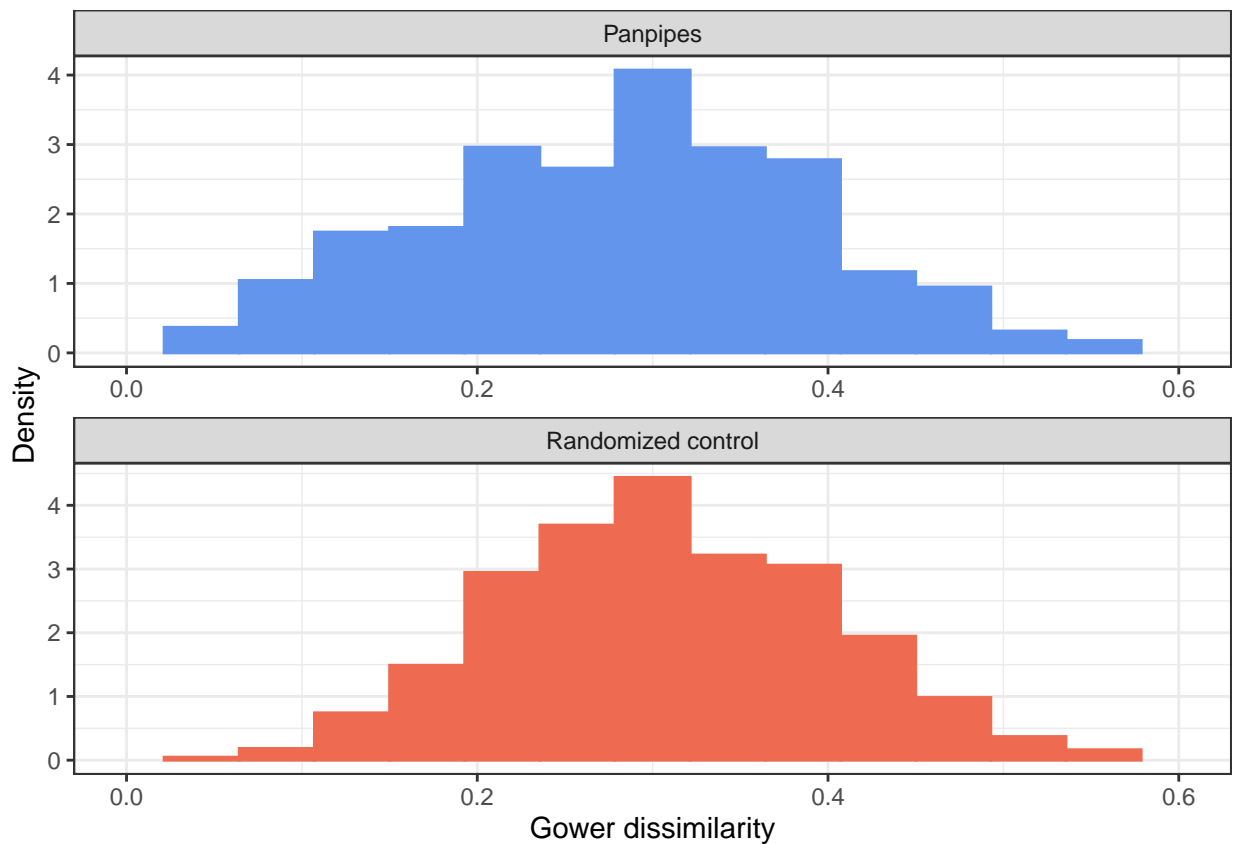
```

facet_wrap(~type,scales = "free",nrow=2,
           labeller = as_labeller(c("empirical"="Panpipes","random"="Randomized control")))+
labs(x="Gower dissimilarity",y="Density")+
theme(legend.position = "none")+
scale_color_manual(values=c("cornflowerblue","coral2"))+
scale_fill_manual(values=c("cornflowerblue","coral2"))

```

```
## Warning: Removed 53369 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 4 rows containing missing values (geom_bar).
```



```
ggsave("panpipes_distances.tiff",dpi=300)
```

```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 53369 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 4 rows containing missing values (geom_bar).
```

Now we evaluate how do panpipes cluster in the trait space by appealing to a t-SNE algorithm applied to the Gower dissimilarities between panpipes. Notice that we consider a range of perplexity values (a free parameter in the t-SNE algorithm that relates to the number of effective neighbors expected for each observation.)

```

set.seed(26111985)

perplexities<-c(2,5,10,25,50,100)
plots_tsne<-vector("list",length=length(perplexities))

for(ppx in 1:length(perplexities)) {
  tsne_p <- Rtsne(distances_empirical, dims = 2,
    perplexity=perplexities[ppx], verbose=FALSE, max_iter = 500,
    check_duplicates=F)
  if(ppx==1) tsne<-data.frame(Dim1=tsne_p$Y[,1],
    Dim2=tsne_p$Y[,2],
    Area=pan$Area_fine,
    Perplexity=perplexities[ppx])
  else{tsne<-rbind(tsne,data.frame(Dim1=tsne_p$Y[,1],
    Dim2=tsne_p$Y[,2],
    Area=pan$Area_fine,
    Perplexity=perplexities[ppx]))}

  tsne$Macro<-sapply(as.character(tsne$Area),
    function(x) ifelse(x %in% c("Africa","Europe","China","SE_Asia"),"Old World",
      ifelse(x %in% c("SA_notAndes","Andes"),"South America","Pacific")))

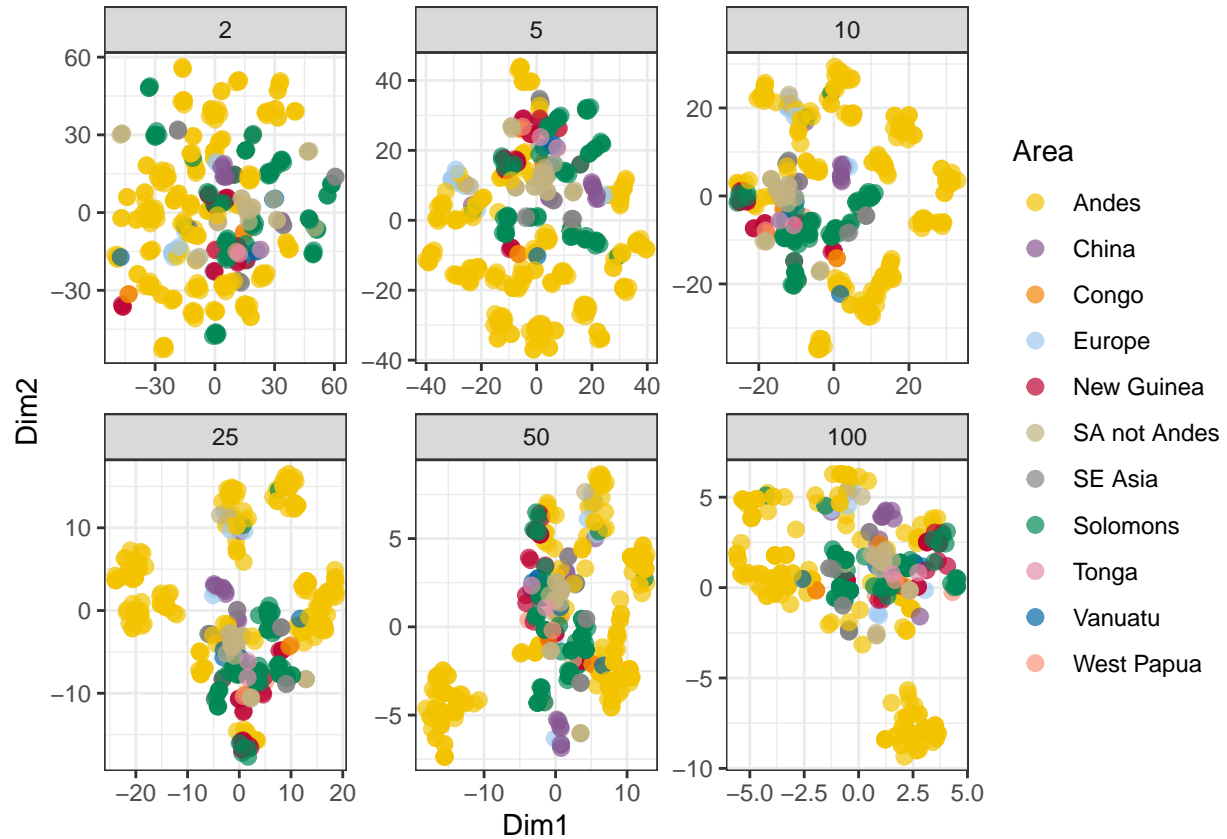
  tsne$Area<-sapply(as.character(tsne$Area),
    function(x) ifelse(x=="NewGuinea","New Guinea",
      ifelse(x=="Papuan","West Papua",
        ifelse(x=="SE_Asia","SE Asia",
          ifelse(x=="SA_notAndes",
            "SA not Andes",x))))))

  cvxhull <- tsne %>%
  group_by(Macro) %>%
  slice(chull(Dim1,Dim2))

  ## Plotting
  ggplot(tsne,aes(x=Dim1,y=Dim2,color=Area,label=Area))+
  scale_color_manual(values=as.vector(kelly(13)[c(3:13)]))+
  geom_point(alpha=0.7,size=2.5)+
  facet_wrap(~Perplexity,scales = "free")

```





```
ggsave("tsne_panpipes.tiff",width=7.5,dpi=300)
```

```
## Saving 7.5 x 4.5 in image
```

## Traceability of provenance given traits

Now we focus on potential indicators of cultural transmission. First we put together the Old World (for data size considerations)

```
pan$Region<-sapply(as.character(pan$Area_coarse),function(x)
  ifelse(x %in% c("Africa","Asia","Europe"),"Old World",x))
table(pan$Region)
```

```
##
##      Andes  Melanesia  Old World SA_notAndes
##      225      104      41      31
```

We remove trait levels that are present in a single region. We code NA for such levels.

```
pan_redux<-pan[,c(7:ncol(pan))]
for(i in 1:(ncol(pan_redux)-1)){
  tab<-table(pan_redux[,c("Region",colnames(pan_redux)[i])])
  check<-apply(tab,2,function(x) ifelse(sum(x!=0)==1,"fix","ok"))
```

```

pan_redux[,colnames(pan_redux)[i]]<-sapply(pan_redux[,colnames(pan_redux)[i]],
      function(x) ifelse(x %in% names(check)[check=="fix"],NA,as.c
pan_redux[,colnames(pan_redux)[i]]<-as.factor(pan_redux[,colnames(pan_redux)[i]])}
pan_redux<-pan_redux[,sapply(pan_redux, function(x) !all(is.na(x)))]
pan_redux$Region<-as.factor(pan_redux$Region)

```

We focus only on pan pipes produced out of vegetal sources, since those are the only ones present around the globe

```
print(summary(pan_redux$Region))
```

```
##      Andes  Melanesia  Old World SA_notAndes
##      225      104      41      31
```

```
pan_redux<-subset(pan_redux,Material==2)
print(summary(pan_redux$Region))
```

```
##      Andes  Melanesia  Old World SA_notAndes
##      137      104      40      31
```

```
pan_redux<-pan_redux[,colnames(pan_redux)!="Material"]
print(summary(pan_redux$Region))
```

```
##      Andes  Melanesia  Old World SA_notAndes
##      137      104      40      31
```

We train an efficient weighted random forest (or more precisely, a random conditional inference forest) to predict the region of origin of a pipe given its features

```

weights_pan<-sapply(pan_redux$Region,
      function(x) nrow(pan_redux)/nrow(pan_redux[pan_redux$Region==x,]))
rf_redux<-cforest(Region~.,
      controls=
        cforest_control(ntree = 500,
          mtry=5,
          mincriterion=qnorm(0.9),
          fraction = 0.632,
          testtype = "Teststatistic",
          teststat="max",
          replace=TRUE,
          trace=F,
          savesplitstats=F,
          minsplit=20,
          minbucket=8),
      data=pan_redux,
      weights = weights_pan)

```

Produce the confusion matrix

```

cmat_redux<-table(pan_redux$Region, predict(rf_redux))
print(cmat_redux)

```

```

##
##           Andes Melanesia Old World SA_notAndes
## Andes      128      3      5      1
## Melanesia   3      87      1     13
## Old World   0      1     39      0
## SA_notAndes 0      1      1     29

```

Statistics per region

```

stats_region<-ldply(c(1:nrow(cmat_redux)),
  function(x) data.frame(id=rownames(cmat_redux)[x],
    N=sum(cmat_redux[,x]),
    d=cmat_redux[x,x],
    A=sum(cmat_redux[x,]))) %>% transform(p=d/N,
  r=d/A)

```

```
stats_region
```

```

##           id  N  d  A      p      r
## 1      Andes 131 128 137 0.9770992 0.9343066
## 2  Melanesia  92  87 104 0.9456522 0.8365385
## 3  Old World  46  39  40 0.8478261 0.9750000
## 4 SA_notAndes 43  29  31 0.6744186 0.9354839

```

Obtain all the panpipes that are misclassified

```

pan_redux$predReg<-predict(rf_redux)
missclass<-cbind(pan[rownames(pan_redux[pan_redux$Region!=pan_redux$predReg,]),],
  data.frame(predReg=pan_redux$predReg[pan_redux$Region!=pan_redux$predReg]))
missclass

```

```

##           Collection.code Ethnological.group Area_fine Area_coarse
## 7           EMVA12138           Paracas      Andes      Andes
## 8           EMVA16097           Paracas      Andes      Andes
## 15          EMVA40298           Pachacamac      Andes      Andes
## 25          EMVIIId12a           Kwaio      Solomons  Melanesia
## 26          EMVIIId12b           Kwaio      Solomons  Melanesia
## 27          EMVIIId12c           Kwaio      Solomons  Melanesia
## 28          EMVIIId12d           Kwaio      Solomons  Melanesia
## 51          MAEB15381.01           Paracas      Andes      Andes
## 63          MAEB15985      Tihuanaco-Huari      Andes      Andes
## 76           MIM1855           Papua      NewGuinea  Melanesia
## 82          MIM1979.028-03           Peru      Andes      Andes
## 83          MIM1979.028-04           Yaguas SA_notAndes SA_notAndes
## 90          MIM1984.036-06           Peru      Andes      Andes
## 91          MIM1984.036-07           Peru      Andes      Andes
## 92          MIM1984.036-08           Peru      Andes      Andes
## 113          MIM2169           Luba      Congo      Africa

```

## 132	MQB71.1890.63.7	Solomons	Solomons	Melanesia			
## 143	MQB71.1930.29.439	Vanuatu	Vanuatu	Melanesia			
## 151	MQB71.1934.188.1271	Papua	NewGuinea	Melanesia			
## 153	MQB71.1934.188.1370	Bouganville	NewGuinea	Melanesia			
## 168	MQB71.1937.0.104X	Vanuatu	Vanuatu	Melanesia			
## 188	MQB71.1961.103.105	Solomons	Solomons	Melanesia			
## 189	MQB71.1963.57.36	Ache_Guayaki	SA_notAndes	SA_notAndes			
## 197	MQB71.1970.101.1	Areare	Solomons	Melanesia			
## 208	MQB71.1970.101.2	Areare	Solomons	Melanesia			
## 219	MQB71.1970.101.3	Areare	Solomons	Melanesia			
## 224	MQB71.1970.101.34	Areare	Solomons	Melanesia			
## 230	MQB71.1970.101.4	Areare	Solomons	Melanesia			
## 265	MQB72.56.750.1	Tongans	Tonga	Melanesia			
##	Area_coarse_time	Dated..	archaeological..	ethnological..	modern.	Size	
## 7	Andes precolonial	800 BC - 100 BC	(wikipedia)			1	
## 8	Andes precolonial	800 BC - 100 BC	(wikipedia)			1	
## 15	Andes precolonial	200-1500 AD	(wikipedia)			0	
## 25	Melanesia		Ethnological			1	
## 26	Melanesia		Ethnological			1	
## 27	Melanesia		Ethnological			1	
## 28	Melanesia		Ethnological			1	
## 51	Andes precolonial	800 BC - 100 BC	(wikipedia)			1	
## 63	Andes precolonial	500-1000 AD	(Wikipedia)			1	
## 76	Melanesia		Ethnological			1	
## 82	Andes postcolonial		Ethnological			1	
## 83	SA_notAndes		Ethnological			1	
## 90	Andes postcolonial		Ethnological			1	
## 91	Andes postcolonial		Ethnological			1	
## 92	Andes postcolonial		Ethnological			1	
## 113	Africa		Ethnological			1	
## 132	Melanesia		late 19th century			1	
## 143	Melanesia		Ethnological			1	
## 151	Melanesia		Ethnological			1	
## 153	Melanesia		Ethnological			1	
## 168	Melanesia		Ethnological			1	
## 188	Melanesia		Ethnological			1	
## 189	SA_notAndes		Ethnological			1	
## 197	Melanesia		Ethnological			2	
## 208	Melanesia		Ethnological			1	
## 219	Melanesia		Ethnological			1	
## 224	Melanesia		Ethnological			1	
## 230	Melanesia		Ethnological			1	
## 265	Melanesia		some centuries old			1	
##	Wider.than.high	Material	Raft.or.bundle	One.or.two.rows	Parts	No.pipes.S1	
## 7	0	2	0	1	0	1	
## 8	0	2	0	1	0	1	
## 15	0	2	0	1	0	1	
## 25	0	2	0	0	0	2	
## 26	0	2	0	0	0	2	
## 27	0	2	0	0	0	1	
## 28	0	2	0	0	0	1	
## 51	0	2	0	0	0	1	
## 63	0	2	0	0	0	0	
## 76	0	2	0	0	0	2	

## 82	1	2	0	0	0	0
## 83	1	2	0	0	0	0
## 90	0	2	0	2	0	2
## 91	1	2	0	0	0	1
## 92	0	2	0	0	0	1
## 113	0	2	0	0	0	3
## 132	0	2	0	0	0	0
## 143	0	2	0	0	0	1
## 151	0	2	0	0	0	0
## 153	0	2	0	1	0	0
## 168	0	2	0	0	0	2
## 188	0	2	0	1	0	3
## 189	0	2	0	0	0	1
## 197	0	2	0	0	0	1
## 208	0	2	0	0	0	1
## 219	0	2	0	0	0	1
## 224	0	2	0	0	0	2
## 230	0	2	0	0	0	1
## 265	0	2	0	0	0	2
##	Stopped.or.open	Serialiation.of.pipes	Ligature.material	Thread.ligature.knot		
## 7	0		0	0		4
## 8	0		0	0		4
## 15	0		0	0		2
## 25	0		0	0		3
## 26	0		0	0		<NA>
## 27	0		0	0		3
## 28	0		0	0		<NA>
## 51	0		0	0		0
## 63	0		0	3		0
## 76	0		0	0		3
## 82	0		0	1		0
## 83	0		0	1		0
## 90	0		0	2		6
## 91	0		2	1		0
## 92	0		0	3		0
## 113	0		0	0		0
## 132	0		0	1		0
## 143	0		<NA>	0		0
## 151	0		1	0		5
## 153	0		0	0		5
## 168	0		0	2		6
## 188	0		0	1		0
## 189	0		<NA>	2		0
## 197	0		0	0		3
## 208	0		0	0		3
## 219	0		0	0		3
## 224	0		4	0		0
## 230	0		0	0		3
## 265	0		0	0		<NA>
##	Splint.arrangement	Tubes.cut.below.node	Indentation.at.distal.end			
## 7	4		0			1
## 8	4		<NA>			1
## 15	4		0			0
## 25	4		0			0

## 26	4	0	0
## 27	4	0	0
## 28	4	0	0
## 51	4	0	0
## 63	4	0	0
## 76	4	0	0
## 82	1	0	0
## 83	1	0	0
## 90	4	1	0
## 91	1	0	0
## 92	4	0	0
## 113	4	1	0
## 132	0	0	0
## 143	4	0	2
## 151	4	1	0
## 153	4	0	0
## 168	4	0	2
## 188	0	0	1
## 189	4	0	0
## 197	4	0	0
## 208	4	0	0
## 219	4	0	0
## 224	4	0	0
## 230	4	0	0
## 265	4	<NA>	0
##	Indentation.proximal.end	Distal.profile	cubical.tubes painting
## 7	0	1	0 0
## 8	0	1	0 0
## 15	0	1	0 0
## 25	0	1	0 0
## 26	0	1	0 0
## 27	0	1	0 0
## 28	0	1	0 0
## 51	0	1	0 0
## 63	0	1	0 0
## 76	0	1	0 0
## 82	0	1	0 0
## 83	0	1	0 0
## 90	0	0	0 0
## 91	1	1	0 0
## 92	3	1	0 0
## 113	0	1	0 0
## 132	0	1	0 0
## 143	0	1	0 0
## 151	0	1	0 0
## 153	0	1	0 0
## 168	0	1	0 0
## 188	0	1	0 0
## 189	0	1	0 0
## 197	0	1	0 0
## 208	0	1	0 0
## 219	0	1	0 0
## 224	0	1	0 0
## 230	0	1	0 0

##	carving.model	textile	Region	predReg	0	1	0	0
## 265					0	1	0	0
##	carving.model	textile	Region	predReg				
## 7	0	2	Andes	Melanesia				
## 8	0	0	Andes	Melanesia				
## 15	0	0	Andes	Melanesia				
## 25	0	0	Melanesia	SA_notAndes				
## 26	0	0	Melanesia	SA_notAndes				
## 27	0	0	Melanesia	SA_notAndes				
## 28	0	0	Melanesia	SA_notAndes				
## 51	0	2	Andes	SA_notAndes				
## 63	0	2	Andes	Old World				
## 76	0	0	Melanesia	SA_notAndes				
## 82	0	0	Andes	Old World				
## 83	0	0	SA_notAndes	Old World				
## 90	0	0	Andes	Old World				
## 91	0	1	Andes	Old World				
## 92	0	0	Andes	Old World				
## 113	0	0	Old World	Melanesia				
## 132	0	0	Melanesia	SA_notAndes				
## 143	0	0	Melanesia	SA_notAndes				
## 151	0	0	Melanesia	Old World				
## 153	0	0	Melanesia	Andes				
## 168	0	0	Melanesia	Andes				
## 188	0	0	Melanesia	Andes				
## 189	0	0	SA_notAndes	Melanesia				
## 197	0	0	Melanesia	SA_notAndes				
## 208	0	0	Melanesia	SA_notAndes				
## 219	0	0	Melanesia	SA_notAndes				
## 224	0	0	Melanesia	SA_notAndes				
## 230	0	0	Melanesia	SA_notAndes				
## 265	0	0	Melanesia	SA_notAndes				