

perClass 5.1 cheat-sheet

help: [doc perclass](#)

<http://perclass.com/doc>

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Labels ↗

create labels by specifying individual sample labels

```
lab=sdlab({'apple','banana','apple','pear'})
```

create labels by giving class list and vector of class sizes

```
lab=sdlab({'apple','banana'},'sizes',[10 5])
```

create labels per-sample names and indices

```
lab=sdlab({'apple','banana','lemon'},[1 1 2 3])
```

create labels by giving class name and number of samples

```
lab=sdlab('apple',10,'banana',5)
```

find samples of a class

```
ind=find(lab=='apple')
```

find given class index

```
ind=find(lab==2)
```

get class index by name

```
lab.list('banana')
```

get class name by index

```
lab.list(2)
```

number of classes

```
length(lab.list)
```

number of entries (samples)

```
length(lab)
```

class/category sizes

```
lab.sizes
```

class/category fractions/priors

```
lab.fractions
```

subset of samples by index

```
lab(1:10)
```

test if class is present

```
isempty(lab.list('A'))
```

▶ lab.list contains only classes present in lab

display label details (classes, sizes and fractions): `lab'` or `info(lab)`

Data sets ↗

create data set

```
a=sddata(matrix,lab)
```

raw data matrix

```
+a ; double(a)
```

access class labels

```
a.lab
```

display data set details

```
a ; info(a)
```

subset of samples

```
a(1:10)
```

remove samples

```
a(1:10)=[]
```

subset of features by indices

```
a(:,[1 2 5])
```

subset of features by names

```
a(:,{'Skew','Entropy'})
```

select classes by names

```
a(:,:,{'apple','pear'})
```

select classes by indices

```
a(:,:,1:2)
```

set new data matrix in a data set (optionally provide new feature labels)

```
b=setdata(a,data)
```

```
b=setdata(a,data,featlab)
```

create new labels

```
a.patient=sdlab('Pat1',10,'Pat2',30)
```

create numerical property

```
a.pixel=1:1024
```

select samples by property

```
a(a.pixel<50)
```

test if property exists

```
isprop(a,'patient')
```

remove sample property

```
rmprop(a,'patient')
```

make patient labels current

```
a=setlab(a,'patient')
```

find current label set

```
name=setlab(a)
```

▶ a.lab now points to a.patient

label all samples in one class

```
a.lab='pear'
```

change label for a subset

```
a(1:10).lab='banana'
```

Subsets ↗

sample subset by values

```
b=subset(a,'lab','cancer','patient',1:3)
```

▶ get cancer samples from the first three patients

return also the rest of samples

```
[b,rest]=subset(a,'patient',5)
```

select classes matching regular expression

```
b=subset(a,'/substring')
```

iterate over classes

```
for i=1:length(a.lab.list), b=a(:, :, i); end
```

Random subsets ↗

100 samples per class

```
sub=randsubset(a,100)
```

select 30% per class

```
b=randsubset(a,0.3)
```

select 100 samples per patient

```
sub=randsubset(a,'patient',100)
```

select 100 samples from complete data set

```
[sub,rest]=randsubset(a,100,'all')
```

Bootstrap sampling (with replacement): `sub=randsubset(a)`

Classifiers ↗

train a classifier (returns decisions by default)

```
p=sdlinear(a)
```

```
p=a*sdlinear
```

▶ if trained on one class, all training samples are accepted

get decisions

```
dec=b*p
```

get data with decision labels

```
c=b.*p
```

display pipeline details

```
p ; info(p)
```

get type of pipeline output

```
p.output
```

remove decision step

```
-p
```

get soft outputs

```
out=b * -p
```

all classifier decisions

```
p.list
```

get output labels (soft outputs)

```
p.lab
```

▶ dec.list or c.lab.list contains all classes present in dec (may be less than in p.list)

▶ p.inlab gets input labels (features names of training data)

Relabeling ↗

relabel data set (what is not stone becomes fruit)

```
a2=sdrelabel(a,{'~stone','fruit'})
```

relabel first two classes into fruit and stone class in other

```
a=sdrelabel(a,{1:2,'fruit','stone','other'})
```

relabel by regular expression (apple or pear becomes fruit)

```
a=sdrelabel(a,{'/apple|pear','fruit'})
```

relabel label set, return label set (can be set as new in the data set)

```
a.gender=sdrelabel(a.patient,{'/male','male','~male','female'})
```

add prefix to class names

```
a2=sdrelabel(a,'add','new-')
```

add prefix to all class names in all sets of labels

```
a2=sdrelabel(a,'add to all','new data-')
```

relabel classifier decisions

```
p=sdrelabel(p,{'/apple|banana','fruit'})
```

Detection ↗

train on one class, accept all training samples (models marked d in table)

```
sdparzen(a(:, :,'class_name'))
```

train a detector (data, target class, model)

```
pd=sdetect(a,'banana',sdknn)
```

▶ change decision names with 'target' and 'non-target' opts.

train a one-class detector rejecting 10% of bananas

```
pd=sdetect(a,'banana',sdparzen,'reject',0.1)
```

train a detector on all samples (by default accept all)

```
pd=sdetect(a,'all',sdknn)
```

▶ use target name that is not present in a.lab.list

provide a set to estimate ROC (does not split tr)

```
pd=sdetect(tr,'banana',sdgauss,'test',val)
```

▶ use pd.roc to access ROC curve (empty for one-class detectors)

▶ specify ROC performance measures with measures option

Classifier combining and cascades ↗

Create classifier cascade

```
pc=sdcascade(pd1,'fruit',pd2)
```

▶ pd1 is fruit/non-fruit detector, pd2 apple/banana classifier

Combine classifiers: `p1=sdlinear(a); p2=sdgauss(a);`

soft-output fusion

```
pc=sdcombine([-p1 -p2])
```

crisp (decision) fusion

```
pc=sdcombine([p1 p2])
```

Available classifiers ↗

d ... can be used for detection

Nearest mean

d sdnmean

Fisher linear discriminant

sdfisher

Gaussian model (for detection)

d sdgauss

Linear discriminant

sdlinear

Quadratic discriminant

sdquadratic

Least mean square classifier (also regression)

sdlms

Logistic classifier

sdlogistic

Parzen

d sdparzen

Mixture of Gaussians

d sdmixture

k-NN

d sdknn

k-means prototype extraction

d sdkmeans

Support Vector Machine

d sdsvc

Neural network (feed-forward or RBF)

sdneural

Deep convolutional network

sddeepnet

Naïve Bayes

d sdnbayes

Decision tree

sdtree

Random forest

sdrandforest

Minimum distance classifier (on sdprox output)

d sdmindist

Look-up table (2D classifier approximation)

sdlut

Rejection ↗

Add reject option to a classifier (reject 5% of samples in a)

```
p=sdparzen(a); pr=sdreject(p,a,'reject',0.05)
```

▶ to reject low confidence, make normalized outputs with sdnorm

Reject specific number of samples

```
pr=sdreject(p,a,'reject',10)
```

Find samples that are not rejected: `dec=a*pr; a(dec~='reject')`

Evaluation ↗

find error on a test set (default mean error over classes)

```
err=sdtest(p,b)
```

compute **specific performance measures**

```
perf=sdtest(p,ts, 'measures',{ 'TPr','apple',  
'mean-error','precision','banana' })
```

confusion matrix (use `'norm'` option to normalize)

```
sdconfmat(a.lab,a*p)
```

specific order of classes (rows) or **decisions** (columns)

```
sdconfmat(a.lab,a*p,'classes',  
{ 'lemon','apple','decisions',{ 'lemon','apple' } })
```

confusion matrix **in a figure**

```
sdconfmat(a.lab,a*p,'figure')
```

get sample indices **in a specific entry** of confusion matrix

```
ind=sdconfmatind(a.lab,a*p,'apple','banana')
```

▶ `a(ind)` are *apple* samples, labeled as *banana*

cross-validate a classifier (10-fold rotation)

```
p=sdlinear; [s,res]=sdcrossval(p,a)
```

▶ `s` is a string summary, `res` struct with results

cross-validation by **randomization** (30-fold, 80% in training)

```
s=sdcrossval(p,a, 'method','random',0.8,...  
'folds',30,'seed',42)
```

retrieve training, test subsets and the classifier in fold 5

```
[s,res,e]=sdcrossval(p,a);  
tr=gettrdata(e,a,5); ts=gettsdata(e,a,5);  
p=e(5); dec=ts*p
```

leave-one-out over patients

```
res=sdcrossval(p,a,'method','loo','over','patient')
```

simple leave-one-out **loop over patients**

```
for i=1:length(a.patient.list)  
    [ts,tr]=subset(a,'patient',i);  
    p=sdlinear(tr);  
    err(i)=sdtest(ts,p);  
end
```

Performance measures ↗

		decisions		sum
		target	non-target	
true labels	target	TP	FN	Nt
	non-target	FP	TN	Nn

Accuracy

$FN/Nt+FP/Nn$

True positive ratio (recall,sensitivity)

$TPr=TP/Nt$

True negative rate (specificity)

$TNr=TN/Nn$

Precision (purity)

$TP/(TP+FP)$

Positive fraction (posfrac)

$(TP+FP)/N$

Detection rate (detrate)

$(TP+FP)/Nt$

measures: mean-error, class-errors, TP,TN,FP,FN, TPr,FPr,TNr,FPr, sensitivity, specificity, precision, posfrac, detrare

ROC analysis ↗

estimate ROC characteristic (two- or multi-class)

```
[tr,ts]=randsubset(a,0.5); p=sdlinear(tr);  
r=sdroc(ts,p)
```

estimate ROC from soft outputs (use `-p` to remove decision step)

```
out=ts*-p; r=sdroc(out)
```

draw interactive ROC plot

```
sddrawroc(r)
```

▶ select op.point by clicking; press 's' to save it back to workspace

▶ press 'c' in `sddrawroc` figure to show **interactive confusion matrix**

▶ press 'd' to view conf.mat. differences w.r.t. selected op.point

add ROC to classifier **access ROC** stored in the classifier

```
p=p*r r=roc
```

create ROC **with specific measures**

```
r=sdroc(out,'measures',  
{ 'FPr','apple','TPr','apple' })
```

get performances at op.point 10

```
r(10)
```

estimate ROC **for user-defined class weights**

```
pd=sddecide('w',rand(10000,3),a.lab.list)  
r=sdroc(pd,out)
```

constrain ROC to a subset with error on apple<0.3

```
r2=constrain(r,'err(apple)',0.3)
```

set curent operating point by index

```
r=setcurop(r,100); ind=getcurop(r);
```

set curent operating point by constraining TPr and minimizing FPr

```
r=setcurop(r,'constrain','TPr(apple)',0.99,...  
'min','FPr(apple)')
```

set operating point **minimizing the cost** (confmat is stored)

```
M=ones(3); M(1,2)=10; r=sdroc(out,'confmat');  
r=setcurop(r,'cost',M)
```

Dimensionality reduction ↗

Principal Component Analysis

```
sdpca
```

Fisher projection (class separation)

```
sdllda
```

Proximity representation (distance to prototypes)

```
sdprox
```

Scaling data

```
sdscale
```

Polynomial feature space expansion

```
sdexpand
```

Preprocessing/spectral indices

```
sdprep
```

Feature selection

```
sdfeatsel
```

Forward feature selection with 1-NN error as criterion

```
pf=sdfeatsel(data,'forward')
```

Backward selection **using error of a specific model:**

```
pf=sdfeatsel(data,'backward','model',sdfisher)
```

select fixed feature subset using regular expression

```
pf=sdfeatsel(a,[1 5 10]) sdfeatsel(a,'/substr')
```

▶ see `pf.lab` for output features and `pf.inlab` for input features

Select features with non-zero variance `sdfeatsel(a,'var>0')`

Interactive visualization ↗

interactive scatter plot: `sdscatter(a)` **keyboard commands:**

show all keyboard shortcuts	?
change feature	→/←/↑/↓
change z-order of classes	+/- or =
cycle through classes one at a time	</>
show/hide legend	l
rename class (also class merging)	r
hide current class	h
show only this class	o
invert filter on this label set	i
remove filter on this label set	R
tag sample under cursor (also via double-click)	t
label visible samples as...	L
switch to label set	1:9
switch between full data set and subset axes	a
switch axes limits between visible samples / space of total set	v
show/hide feature distributions	d
show/hide confusion matrix with visible/hidden samples	c
return to previous sample filter	f
show all samples (remove filter)	F

classifier decisions (also in multi-dimensional space)

```
p=sdlinear(a); sdscatter(a,p)
```

▶ change color of decision backdrop under cursor c

open also connected **ROC plot for scatter/image view**

```
sdscatter(a,p*r,'roc'); sdimage(im,p*r,'roc')
```

show feature distributions

```
sdfeatplot(a)
```

▶ right-click to control interactive threshold selection

Cluster analysis ↗

cluster data with k-means algorithm into 10 clusters

```
b=sdcluster(a,sdkmeans,10)
```

train k-means model returning cluster labels

```
p=sdkmeans(a,10,'cluster')
```

get labels

```
lab=a*p
```

protect clustering from outliers

```
pr=sdreject(p,a)
```

execute and set decisions as new labels `b=a.*p`

Execution out-of-Matlab ↗

Export classifier for execution: `sdexport(p,filename)`

▶ Classifier can be run from any application via `perclass.dll` runtime

▶ For details see: <http://perclass.com/doc/guide/deployment.html>

Export classifier as a **C header file for static linking:**

```
sdexport(p,filename,'header')
```