

Retrieve the AUC

Source: `R/models.R` (<https://github.com/h2oai/h2o-3/blob/master/R/models.R>)

Retrieves the AUC value from an `H2OBinomialMetrics`. If "train", "valid", and "xval" parameters are FALSE (default), then the training AUC value is returned. If more than one parameter is set to TRUE, then a named vector of AUCs are returned, where the names are "train", "valid" or "xval".

```
h2o.auc(object, train = FALSE, valid = FALSE, xval = FALSE)
```

Arguments

object An `H2OBinomialMetrics` or `H2OMultinomialMetrics` object.

train Retrieve the training AUC

valid Retrieve the validation AUC

xval Retrieve the cross-validation AUC

See also

`h2o.giniCoef` (<https://www.rdocumentation.org/packages/h2o/topics/h2o.giniCoef>) for the Gini coefficient, `h2o.mse` (<https://www.rdocumentation.org/packages/h2o/topics/h2o.mse>) for MSE, and `h2o.metric` (<https://www.rdocumentation.org/packages/h2o/topics/h2o.metric>) for the various threshold metrics. See `h2o.performance` (<https://www.rdocumentation.org/packages/h2o/topics/h2o.performance>) for creating `H2OModelMetrics` objects.

Examples

```
# NOT RUN {  
library (https://www.rdocumentation.org/packages/base/topics/library)(h2o)  
h2o.init (https://www.rdocumentation.org/packages/h2o/topics/h2o.init())  
  
prostate_path <- system.file (https://www.rdocumentation.org/packages/base/topics/system  
prostate <- h2o.uploadFile (https://www.rdocumentation.org/packages/h2o/topics/h2o.impor  
  
prostate[, 2] <- as.factor (https://www.rdocumentation.org/packages/h2o/topics/as.factor  
model <- h2o.gbm (https://www.rdocumentation.org/packages/h2o/topics/h2o.gbm)(x = 3:9, y  
perf <- h2o.performance (https://www.rdocumentation.org/packages/h2o/topics/h2o.performa  
h2o.auc (https://www.rdocumentation.org/packages/h2o/topics/h2o.auc)(perf)  
# }
```

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