How to calculate tpr

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How to calculate torque. How to calculate tpr and fpr in python. How to calculate tpr in kerala. How to calculate tpr rate. How to calculate tpr in rwanda. How to calculate tpr and fpr. How to calculate tpr and fpr in r. How to calculate tpr in covid.

Temperature, pulse and respiration (TPR) are the basic physiological parameters that every owner or health care professional needs to know if they want to take care of a horse. These three vital signs are very important and can help you and your veterinarian a lot when you think your horse might be sick. Knowing the normal values of these three vital signs can provide a great understanding of the physiological state of your horse. Normal TPR To know if your horse’s TPR values are abnormal, you must first know what is normal. Although the normal heart rate for most horses is 32-36 beats per minute, some horses have a lower heart rate, 24 beats per minute, or perhaps a slightly higher heart rate, 40 beats per minute. You will need a thermometer, a stethoscope and a clock with a second hand hand or one that counts seconds. You should use a digital thermometer because the time needed for a reading is much shorter and more flexible than a mercury glass thermometer. The thermometer should have a small hole at the end so you can attach a long piece of string or colored tape to help find the thermometer if it has fallen or lost in the barn. A small clip or clip can be placed at the end of the rope so you can attach it to the tail of the horse and leave it in place until you can read the temperature. This way, you don’t need to keep the thermometer in place. These thermometers can be purchased at any pharmacy. The stethoscope is used to clearly hear the heartbeat and the sounds of breathing. A cheap stethoscope can be purchased at a drug store or horse that will be enough to hear the heartbeat and determine the heart rate (pulsations) and respiratory rate. Temperature The rectal temperature is easily taken on most horses by putting a small amount of lubricant (petroleum jelly) on the thermometer. Approach the horse on one side; do not stand directly behind the horse in case they decide to kick. Raise or move the tail of the horse and insert the thermometer into the hull. Thermometers designed for use with livestock have a ring on top. This ring can be attached to a rope and a clip attached to the opposite end of the rope. The clip can be attached to the horse’s tail when measuring the horse’s temperature. The normal rectal temperature of a horse is 99.5 to 101.5 Â°F (37.5 to 38.6 Â°C). Foals less than 1 month of age have a normal temperature of 100.0-102.0 Â°F (37.7-38.8 Â°C). Newborn foals can easily suffer from hypothermia (low body temperature), so if the foal’s temperature drops below 98.0°F (36.6°C), call your veterinarian. In the meantime, the foal with towels or blankets to stimulate blood circulation and/or dry the coat. If the rectal temperature of the horse is above normal, he has a fever, not the temperature. All horses have a temperature above normal (fever), below normal (hypothermia), or normal. Pulse Heart rate can be detected without a stethoscope, but having a stethoscope makes the job work If a stethoscope is impractical, the wrist can be taken from the facial artery, which is on the lower side of the jaw in a superficial groove under the last cheek tooth. Count the number of beats for 15 seconds, then multiply by four to calculate the heart rate in beats per minute. Remember, any excitement of the horse will increase the pulse frequency. If a stethoscope is available, listen to the heart on the left side of the horse’s chest, just behind the elbow. Every sound of the heart is considered a beat. The normal heart rate for an adult horse is about 32 to 36 beats per minute. The heart rates of foal vary according to age. Newborn foals have a heart rate between 80 and 100 beats per minute. The foals that are a few weeks to a few months of age will have heart rates of 60 to 80 beats per minute. Respiration Respiration can be taken by watching the horse’s chest move in and out (an inhale and exhale is a breath) or feeling the air come out of the nostrils. The stethoscope can be used to hear the breaths as the air travels through the trachea as the horse inhales and exhales. Respiratory characteristics should also be noted. Is the sound clear? Are the breaths shallow or deep? Is there any abnormal creeping or cracking sounds associated with breathing? The normal breathing rate for adult horses is eight to 12 breaths per minute. Newborn foals have breathing rates ranging from 60 to 80 breaths per minute. Older foals have respiratory wings from 20 to 40 breaths per minute. Remember, if your horse or foal gets excited for any reason, your breathing rate can be temporarily elevated. Capillary recharge time Another indicator of health is the mucous membrane, or rubber, color. Healthy horses have beautiful pink gums that are moist to the touch. Capillary charging time is tested by firmly pressing the finger on the rubber over the front incisors and removing it quickly. The time needed for the area to turn from white back to pink is the capillary recharge time. The normal charging time is about 2 seconds. If the capillary filling time is longer than 2 seconds you should notice the color of the mucous membrane and contact your veterinarian. You greatly increase your horse’s chance of surviving a serious illness or accident by knowing your horse’s normal vital signs and being able to take his vital signs in an emergency. Help us to improve our website! Please take a moment to fill out our survey so that we can continue to improve our website. Full investigation now. Craig Wood, University of Kentucky I would recommend Hanley & McNeil’s 1982 paper ‘The Meaning and Use of Area Under a Receiver Functioning Feature (ROC) Example They have the following table of disease status and test result (corresponding for example to the risk estimated by a logistic model). The first number on the right is the number of patients with true “normal” disease and the second number is the number of patients with true “abnormal” disease: (1) (1) Normal: 33/3 (2) Probably Normal: 6/2 (3) So there are a total of 58 “normal” and “51” abnormal patients. We see that when the predictor is 1, â€œDefinitely normalâ€TM, the patient is usually normal (true for 33 of the 36 patients,) and when it is 5, â€Definitely abnormalâ€TM patients are usually abnormal (true for 33 of the 35 patients,) so the predictor makes sense. But how should we judge a patient with a score of 2, 3 or 4? What we set up our cutoff to judge a patient as abnormal or normal to determine the sensitivity and specificity of the resulting test. Sensitivity and Specificity We can calculate the estimated sensitivity and specificity for different cuts. (I will write “sensitivity” and “specificity” from now on, leaving the estimated nature of values to be implicit.) If we choose our cutoff to classify all patients as abnormal, no matter what test results it says (i.e., we choose the cutoff 1,+) we get a sensitivity of 51/51 = 1. The specificity would be 0/58 = 0. It doesn’t sound so good. OK, so let’s go for a lighter cut. We only classify patients as abnormal if they have a test result of 2 or higher. Then we are missing 3 abnormal patients, and they have a sensitivity of 48/51 = 0.94 But we have a much increased specificity, of 33/58 = 0.57 Now we can continue this, choosing various cuts (3, 4, 5, >5.) (In the latter case, we will not classify any patient as abnormal, even if they have the highest possible test score of 5.) The ROC Curve If we do this for all possible cuts, and the weft sensitivity versus 1 minus specificity, we get the ROC curve. We can use the following R code: # Data norm = rep (1:5, times=c (33,6,11,2) abnorm = rep (1:5, times=c (3,2,11,33) testres = c (abnorm,norm) truestat = c (rep (1,length (abnorm) rep (0,length (norm) # The output is: testres truestat 1 2 3 4 5 0 33 6 11 2 1 3 2 11 33 We can calculate various statistics: (tot=colSums (tab)) # Number of patients w/ each test result (truepos=unname (rev (rev (tab[2,)]) # Number of true positives (falsipos=unname (rev (rev (tab[1,)]) # Number of false positives # # The total number of positives (one number) (totneg=sum (tab[1,)]) # # The total number of negatives (one number) (sens=truepos/totpos) # Sensitivity (fraction true positives) (omspec=falsepos/totneg) # 1 âÀ specificity (false positives) sens=c (sens,0;) omspec=c (omspec,0) # Numbers when we classify all as normal and using this, we can plot= We can easily calculate the area under the ROC curve, using the formulathe area of a trapeze: height = (sens[-1]+sens[-length (sens)]) /2 width = -diff (omspec) # = diff (rev (omspec)) sum (height*width) The result is 0.8 931 711. A Concordance Measure LâAUC can also be seen as a concordance measure. If we take all possible pairs of patients in which one is normal and the other is abnormal, we can calculate how often the abnormal has the highest result (the most “abnormal-looking”) of the test (if they have the same value, consider this as “half win”): o = external (year normal, norm, Â”-Â”) medium ((o>0) + .5* (o==0)) The answer is still 0.8 931 711, the area under the ROC curve. It’ll always be like this. A graphical view of concordance As Harrell pointed out in his reply, this too has a graphical interpretation. Let’s draw the test score (risk estimate) on the y-axis and the actual disease state on the x-axis (here with some jittering, to show the overlapping points): plot (jitter (truestat,.2), jitter (testres,.8), las=1, xlab=Â”Real disease stateÂ”, ylab=Â”P We now draw a line draw a line draw a line drawing drawing drawing drawing drawing drawing drawing drawing drawing drawing drawing drawing drawing drawing drawing drawing drawing drawing drawing one each point to the left (a “normal” patient) and each point to the right (a “abnormal” patient). The proportion of lines with positive slope (i.e. the proportion of matching pairs) is the concordance index (flat lines count as “50% match”). It is a bit difficult to visualize the actual lines of this example, due to the number of links (the same risk score), but with some jittering and transparency we can get a reasonable graph: d = cbind (x_norm=0, x_abnorm=1, expand.grid (y_norm=norm, y_abnorm=abnorm)) library (ggplot) 2) ggplot (d, aes (x=x_norm, xend=x_abnorm, y=y_norm, yend=y_abnorm)) + geom_segment (colour=#ff000 006Â”, position=position_jitter (width=0, height=.1)) + xlab (True disease status) + ylab (Â”TestscoreÂ”) + theme_light () + theme (axis.title.y=element_text (angle=0)) We see that most of the lines slope upwards, so the concordance index will be high. We also see the contribution to the index of each type of observation pair. Most come from normal patients with a risk score of 1 paired with abnormal patients with a risk score of 5 (1Â”5 pairs), but much also comes from 1Â”4 pairs and 4Â”5 pairs. And it is very easy to calculate the actual concordance index based on the slope definition: d = transform (d, slope= (y_norm-y_abnorm) / (x_norm-x_abnorm)) mean ((d$slope > 0) + .5* (d$slope==0)) The answer is It’s still 0.8 931 711, i.e., the AUC. The Wilcoxon “Mann” test by Whitney There is a close connection between the measurement of concordance and the Wilcoxon “Mann” test by Whitney. In fact, the latter checks whether the probability of a match (i.e. the abnormal patient in a normal random pair to have the most “abnormal” result is exactly 0.5. And its statistical test is just a simple transformation of the estimated probability of concordance: > (wi = wilcox.test (abnorm,norm)) Wilcoxon rank sum test with continuity correction data: abnorm and norm W = 2642, 2642, = 1,44e-13 alternative hypothesis: the true shift of the position is not equal to 0 The statistical test (W = 2642) counts the number of concordant pairs. If we split it from the number of possible couples, we get a number familare: w = wi$statistic w/(blue(abnorm)*length(norm)) Yes, it is 0.8931711, the area under the ROC curve. Easier ways to calculate the AUC (in R) But we make life easier for ourselves. There are various packages that calculate the UAC for us automatically. The Epi Package The Epi package creates a beautiful ROC curve with various statistics (including the UAC) embedded: library (Epi) ROC (testre, verostato) # even try to add plot="sp" The pROC package also likes the pROC package, as it can adjust the ROC estimate (and calculate a smooth ROC based AUC estimate): (The red line is the original ROC, and the black line is the smoothed ROC. Also note the default appearance ratio 1:1. It makes sense to use it, since both sensitivity and specificity have a range 0-1.) The AUC estimated by the smoothed ROC is 0,9107, similar to, but slightly larger than, the AUC from the unsmoked ROC (if you look at the figure, you can easily see why it is bigger). (Although we really have too few possible distinct result values to calculate a smooth AUC). The rms package of Harrell can calculate various matching statistics using the rcorr.cens(). The index C in its output is the UAC: > library(rms) > rcorr.cens(testres,truestat) [1] Index C 0.8931711 Finally, we have the package caTools and its function colAUC(). It has some advantages over other packages (mainly speed and ability to work with multidimensional data – see ?colAUC) that can sometimes be useful. But of course it gives the same answer that we have calculated more and more times: library(caTools) colAUC (test, truestat, plotROC=TRUE) [1] 0 vs. 1 0.8931711 Final Words Many people seem to think that the AUC tells us how 'buon' is a test. And some people think that the AUC is the probability that the test correctly ranks a patient. It's not. As you can see from the above example and calculations, the AUC tells us something about a test family, a test for every possible cutoff. And the AUC is calculated according to the cuts that would never be used in practice. Why should we worry about the sensitivity and specificity of ‘nonsensical’ cutoff values? However, this is what the AUC is (in particular) based on. (Obviously, if the AUC is very close to 1, almost every possible test will have great discriminatory power, and we would all be very happy.) The “normal-normal” torque interpretation of the AUC is pleasant (and can be extended, for example to survival patterns, where we see if the person with the highest risk (relative) that dies before). But he would never use it in practice. It is a rare case where you know that you have a healthy person and a sick person, you do not know which person isYou have to decide which one of them to deal with. (Either way, the decision is easy; treat the one with the highest estimated risk.) So I think studying the real ROC curve will be more useful than just looking at the summary measurement AUC. And if you use the ROC along with (estimated of) the costs of false positives and false negatives, along with basic rates of what you are studying, you can get it somewhere. It should also be noted that the AUC measures only discrimination, not calibration. That is, it measures whether you can discriminate between two people (one sick and one healthy), based on the risk score. So, look only at the relative risk values (or rankings, if you like, see Wilcoxon’s interpretation of the “Mann”Whitney test), not the absolute ones, which you should be interested in. For example, if you divide each risk estimate from the logistics model by 2, you will get exactly the same AUC (and ROC). When evaluating a risk model, calibration is also very important. To examine it, you will look at all patients with a risk score of about, say, 0.7, and see if about 70% of these actually have been sick. Do this for any possible risk score (perhaps using some sort of smoothing/local regression). Plot the results and you’ll get a graphical calibration measurement. If you have a model with good calibration and good discrimination, then start having a good model. :) Model:)

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