Statistics III: Nonparametric tests

Stochastics

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We are going to discuss three non-parametric tests:

- *test for goodness of fit*: tests whether the distribution of a sample comes from a theoretical background distribution;
- *test for homogeneity*: tests whether two separate samples come have the same distribution;
- *test for independence*: tests whether two observed attributes on a given sample are independent or not.

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- *test for goodness of fit*: tests whether the distribution of a sample comes from a theoretical background distribution;
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- *test for independence*: tests whether two observed attributes on a given sample are independent or not.

The three tests are known collectively as *Pearson's* χ^2 -*tests* (because they all use the χ^2 distribution).

Assume we have a sample of size n where each element falls in one of r categories. We want to test on a significance level of $1-\varepsilon$ whether

- H₀: the distribution of the sample follows a theoretical distribution p₁,..., p_r on the categories, or
- H_1 : the distribution of the sample is different from p_1, \ldots, p_r .

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Denote the number of sample elements in each category by $\nu_i, i = 1, \ldots, r$. The statistic is

$$\chi^{2} = \sum_{i=1}^{r} \frac{(\nu_{i} - np_{i})^{2}}{np_{i}}$$

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Denote the number of sample elements in each category by $u_i, i = 1, \dots, r$. The statistic is

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If $\chi^2 < \chi^2_{arepsilon}$, we accept H_0 . Otherwise, H_0 is rejected.

A random generator is supposed to give random bits: 0 and 1, each with 50% random probability. We take 1000 samples, which result in 471 0's and 529 1's. Test on a 95% significance level that the probability of 0 is 50% against the hypothesis that the probability of 0 is not 50%.

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We test goodness of fit. There are r = 2 categories: 0 and 1. The theoretical background distribution according to H_0 is

$$p_1 = 0.5, \qquad p_2 = 0.5,$$

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and the sample is

$$u_1 = 529, \quad \nu_2 = 471$$

with sample size n = 1000.

The statistic is

$$\chi^{2} = \sum_{i=1}^{r} \frac{(\nu_{i} - np_{i})^{2}}{np_{i}}$$
$$= \frac{(471 - 1000 \cdot 0.5)^{2}}{1000 \cdot 0.5} + \frac{529 - 1000 \cdot 0.5)^{2}}{1000 \cdot 0.5} = 3.364.$$

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$$\chi^2_{arepsilon} = 3.84$$

from the table for the χ^2 distribution.

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holds, so we accept H_0 on a 95% significance level.

Now if the sample was 451 0's and 549 1's instead, then the statistic is $% \left(1-\frac{1}{2}\right) =0$

$$\chi^{2} = \sum_{i=1}^{r} \frac{(\nu_{i} - np_{i})^{2}}{np_{i}}$$
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Now if the sample was 451 0's and 549 1's instead, then the statistic is

$$\chi^{2} = \sum_{i=1}^{r} \frac{(\nu_{i} - n\rho_{i})^{2}}{n\rho_{i}}$$
$$= \frac{(451 - 1000 \cdot 0.5)^{2}}{1000 \cdot 0.5} + \frac{(549 - 1000 \cdot 0.5)^{2}}{1000 \cdot 0.5} = 10.404,$$

and

$$\chi^2 = 10.404 > 3.84 = \chi^2_{\varepsilon},$$

so we reject H_0 on a 95% significance level and conclude that the random bit generator does not give 0 with 50% probability.

The test for goodness of fit can be applied also when the background distribution is continuous. In this case, the continuous domain should be cut up into finitely many intervals before testing.

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As a rule of thumb, each interval should contain at least 5 sample elements. Otherwise, there is some freedom in the exact choice of intervals.

Once the intervals are fixed, they correspond to categories. The sample is grouped according to the intervals, and the p_i theoretical probabilities are equal to the probability of each interval according to the theoretical background distribution.

We have two samples of size n and m respectively. Each element falls into one of r categories. We want to test on a significance level of $1 - \varepsilon$ whether

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$$\chi^{2} = \sum_{i=1}^{r} nm \frac{(\nu_{i}/n - \mu_{i}/n)^{2}}{\nu_{i} + \mu_{i}}$$

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We have a sample of size n where each element has two attributes, the first property falling into one of r categories and the second attribute falling into one of s categories. We want to test on a significance level of $1 - \varepsilon$ whether

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- *H*₀: the two attributes are not independent.

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- H₀: the two attributes are independent, or
- *H*₀: the two attributes are not independent.

Let $\nu_{i,j}$ denote the number of sample elements with the first attribute falling into category *i* and the second attribute falling into category *j*. Also,

$$\nu_{i,.} = \sum_{j=1}^{s} \nu_{i,j} \quad \text{and} \quad \nu_{.,j} = \sum_{i=1}^{r} \nu_{i,j}.$$

The statistic is

$$\chi^{2} = \sum_{i=1}^{r} \sum_{j=1}^{s} n \frac{\left(\nu_{i,j} - \frac{\nu_{i,\nu,j}}{n}\right)^{2}}{\nu_{i,\nu,j}}.$$

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A lake contains 3 species of fish: carp, tilapia and catfish. Otto, the old fisherman tells us that the lake contains twice as much tilapia as either carp or catfish. Based on a sample of 60 fish caught, decide on a 95% confidence level whether we should believe Otto or not.

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11	35	14

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Solution. We do a goodness of fit test. We have r = 3 categories, and the theoretical background distribution according to Otto is

$$p_1 = 0.25, \qquad p_2 = 0.5, \qquad p_3 = 0.25.$$

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- H₀: the sample comes from this background distribution;
- *H*₁: the sample has a different distribution.

The sample size is n = 60 and the sample is

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$$\chi^{2} = \sum_{i=1}^{r} \frac{(\nu_{i} - np_{i})^{2}}{np_{i}} = \frac{(11 - 60 \cdot 0.25)^{2}}{60 \cdot 0.25} + \frac{(35 - 60 \cdot 0.5)^{2}}{60 \cdot 0.5} + \frac{(14 - 60 \cdot 0.25)^{2}}{60 \cdot 0.25} = 1.967.$$

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The comparison

$$\chi^2 = 1.967 < \chi^2_{arepsilon} = 5.99$$

holds, so we accept H_0 on a 95% significance level and conclude that we can believe Otto.

We are examining a certain type of crash helmets by color and level of protection. We have a sample of 1232 accidents where this type of helmet was involved.

	black	white	orange
no injury	501	367	31
minor injury	173	107	7
major injury	30	15	1

Accept or reject the hypothesis that the color of the helmet is independent from the level of protection provided on a 95% confidence level.

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- H₀: the color and protection level are independent;
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We have r = 3 color attributes and s = 3 injury attributes. $\nu_{i,j}$ are the elements inside the table, and we also need

$$\begin{split} \nu_{1,.} &= 501 + 367 + 31 = 905, \quad \nu_{.,1} = 501 + 173 + 30 = 704, \\ \nu_{2,.} &= 173 + 107 + 7 = 287, \quad \nu_{.,2} = 367 + 107 + 15 = 489, \\ \nu_{3,.} &= 30 + 15 + 1 = 46, \quad \nu_{.,3} = 31 + 7 + 1 = 39. \end{split}$$

The sample size is n = 1232.

The statistic is

$$\chi^{2} = \sum_{i=1}^{r} \sum_{j=1}^{s} n \frac{\left(\nu_{i,j} - \frac{\nu_{i,\nu,j}}{n}\right)^{2}}{\nu_{i,\nu,j}} = 1232 \cdot \left(\frac{\left(501 - \frac{905 \cdot 704}{1232}\right)^{2}}{905 \cdot 704} + \dots + \frac{\left(1 - \frac{46 \cdot 39}{1232}\right)^{2}}{46 \cdot 39}\right) = 3.875.$$

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The percentile is the 95% percentile of the χ^2 -distribution with degree of freedom (r-1)(s-1) = (3-1)(3-1) = 4:

$$\chi_{\varepsilon}^2 = 9.49.$$

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The comparison

$$\chi^2 = 3.875 < \chi^2_{arepsilon} = 9.49$$

holds, so we accept H_0 on a 95% confidence level and conclude that the color and protection level are independent.

Let's take N copies of a mini Markov chain. The mini Markov chain has state space of size K and its generator is $Q = (r_{ij})_{i,i=1}^{K}$.

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If the mini Markov chains are independent, then we haven't done much. We can make them dependent by letting the transition rates r_{ii} depend on other mini Markov chains.

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Let $X_k(t) = X_k^N(t)$ denote the number of mini Markov chains in state k at time t, and

$$x^{N}(t) = \frac{X^{N}(t)}{N}$$

are the ratio of the number of mini Markov chains in each state relative to the entire population.

A typical type of dependence is the so-called *density-dependent* Markov population process, where the r_{ij} rates can depend on the vector x(t). If the mini Markov chains are independent, then we haven't done much. We can make them dependent by letting the transition rates r_{ii} depend on other mini Markov chains.

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A typical type of dependence is the so-called *density-dependent* Markov population process, where the r_{ij} rates can depend on the vector x(t).

In this case, the mini Markov chains are no longer independent.

Example. SIR epidemic model. In a population, each individual is in state S, I or R, where:

- S: susceptible, that is, healthy, but may get infected;
- I: infected;
- R: recovered, can no longer get infected.

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- S: susceptible, that is, healthy, but may get infected;
- I: infected;
- R: recovered, can no longer get infected.

There are only two possible transitions:

- $S \rightarrow I$ is infection;
- $I \rightarrow R$ is recovery.

SIR model

Infection rate is proportional to the ratio of infected individuals within the entire population:

$$r_{S\to I}(x) = \beta x_I,$$

while recovery rate is constant:

$$r_{I\to R}(x)=\gamma,$$

where β és γ are constants for the given infection.

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(Parameters: $\beta = 5, \gamma = 1$, N = 100, initial state is x(0) = (0.9, 0.1, 0).)



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These look convergent to some smooth, deterministic curves. Is this the case?

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Yes! But first, preparations. For the SIR model, the mean-field system is:

$$\begin{split} \frac{\mathrm{d}}{\mathrm{d}t} v_{S}(t) &= -\beta v_{S}(t) v_{I}(t), \\ \frac{\mathrm{d}}{\mathrm{d}t} v_{I}(t) &= \beta v_{S}(t) v_{I}(t) - \gamma v_{I}(t), \\ \frac{\mathrm{d}}{\mathrm{d}t} v_{R}(t) &= \gamma v_{I}(t). \end{split}$$



(Parameters: $\beta = 5, \gamma = 1$, initial state is v(0) = (0.9, 0.1, 0).)

Theorem (Kurtz)

Assume that

- the r_{ij} rate functions are twice differentiable, and
- $x^N(0) \rightarrow v(0)$ in probability as $N \rightarrow \infty$.

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- the r_{ij} rate functions are twice differentiable, and
- $x^N(0) \rightarrow v(0)$ in probability as $N \rightarrow \infty$.

Then the solution of the mean-field system v(t) is unique, and for any finite T and $\varepsilon > 0$,

$$\lim_{N\to\infty} \Pr\left(\max_{0\leq t\leq T}\max_{1\leq k\leq K}|v_k(t)-x_k^N(t)|>\varepsilon\right)=0,$$

or in a more compact form,

$$\max_{0 \le t \le T} \max_{1 \le k \le K} |v_k(t) - x_k^N(t)| \xrightarrow{p} 0,$$

as $N o \infty$.

v(t) is the mean-field limit of the Markov population model.

Kurtz illustrated:



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v(t) is the solution of a system of ordinary differential equations, which are memoryless. This is due to the Markov property of the population process.

The fluctuations of x(t) around v(t) are of order $\frac{1}{\sqrt{N}}$ and converge to normal distribution as $N \to \infty$ (so effectively the CLT also holds).

Further remarks.

x(t) and v(t) denote the ratios of each class within the population. So this mean-field limit is applicable when every state has a number of individuals comparable to the entire population. Further remarks.

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For the SIR model, this means that the mean-field convergence holds in the region when the number of infected is comparable to the entire population. Further remarks.

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For the SIR model, this means that the mean-field convergence holds in the region when the number of infected is comparable to the entire population.

In the early parts of an epidemic, when there are very few infected individuals, other models may be better (like branching processes).