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STATISTICAL METHODS APPLIED TO PSD DATA: CHARACTERIZATION ON THE DETECTOR RESPONSE

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Abstract - Several procedures are considered for testing numerically the performances of some two-dimensional position sensitive gas detectors (PSD). The response of a PSD to a homogeneous flux of scattered neutrons is modelled by a two-dimensional Poisson process and specific statistical tests and techniques are developed in order to determine the PSD's characteristics. Two approaches are used: the first one employs a non-parametric probability scheme for recognizing the inhomogeneity in the experimental data. The second one extends the classical two-way analysis of variance to a more general Poisson scheme using the maximum likelihood principle. The temporal stability of PSD data is also tested by means of a new two-sample comparison test on Poisson data.

Numerical examples from simulated data are presented and the performances of the statistical algorithms are discussed.

I - INTRODUCTION

The present study is mainly devoted to the statistical analysis of the characteristics of two-dimensional position sensitive detectors' (2D-PSD), a first step towards data reduction of diffraction spectra.

Most of the algorithms given below are specifically designed for PSD's with coding discretization within the detecting medium and more precisely for gas neutron PSD's. In the latter the signal is recorded by a grid of parallel anodes orthogonal to a grid of parallel cathodes. Pixels are thus physically located at the crossing of anode and cathode wires.
Under standard experimental conditions the result of the measurements is a set of integers \( n_{i,j} \); \( 1 \leq i \leq n \) where \( n_{i,j} \) denotes the count recorded in the \( i,j \)th pixel of an \( n \times m \) detector. These accumulated counts can be reasonably considered as realizations of Poisson-distributed random variables (r.v.) \( N_{i,j} \) with parameter \( \lambda_{i,j} \). If the counting rate is not too high, dead-time effects are negligible and one can assume that the random variables \( N_{i,j} \) \( (i=1, \ldots , n; \ j=1, \ldots , m) \) are stochastically independent.

For a well designed gas PSD, an incoming neutron is equally likely to be detected anywhere on the sensitive area (ignoring edge effects) since the detecting medium (gas) is homogeneous. In other words, the detector counting efficiency is homogeneous. However, the individual pixel responses (effective cross-sections) are generally different due to imperfect wire spacing, unbalanced electronic tuning, etc...

Hence, for such PSD's, any lack in homogeneity in the overall response appears basically rowwise or columnwise.

II - DATA CORRECTION FOR RESPONSE HETEROGENEITY

In practice this correction is always necessary to obtain reasonably "flat" observed spectra from a homogeneous incoming background. The correction factors are estimated from "calibration" spectra with global mean count \( \bar{N} \) much larger than the maximum counts expected in diffraction spectra.

The classical correction is to multiply the counting variable \( N_{i,j} \) of each cell \((i,j)\) by a correction factor \( a_{i,j} \) estimated from calibration measurements as:

\[
a_{i,j} = \frac{n_{i,j}}{\bar{N}_{i,j}}, \quad N'_{i,j} = a_{i,j} N_{i,j}
\]

This approach destroys the Poisson nature of the recorded data since the mean and the variance of the \( N'_{i,j} \)'s are no longer equal, and this may affect the behaviour of future statistical tests.

To preserve as much as possible, the Poisson characteristics of the data we have developed an algorithm which transforms the original Poisson variates \( N_{i,j} \) into a new set of random variables \( N'_{i,j} = \beta_{i,j} N_{i,j} \), uncorrelated, with common variance and mean equal to the arithmetic average of the \( \lambda_{i,j} \).

Such a transformation relies on the following proposition, the proof of which can be found in /3/.

**Proposition:** Let \( X_1 \) and \( X_2 \) be two Poisson independently distributed random variables with parameters \( \lambda \) and \( \mu \) respectively. Then, the random variables \( Y_1 \) and \( Y_2 \) defined by

\[
Y_1 = \frac{(\sqrt{\lambda}+\sqrt{\mu})X_1+(\sqrt{\mu}-\sqrt{\lambda})X_2}{(2\sqrt{\lambda})} \\
Y_2 = \frac{(\sqrt{\lambda}-\sqrt{\mu})X_1+(\sqrt{\mu}+\sqrt{\lambda})X_2}{(2\sqrt{\mu})}
\]

are non-correlated and have the same mean and variance \((\lambda+\mu)/2\).

With four r.v. \((X_1,X_2,X_3,X_4)\) a two-step procedure is necessary. The formula (II) applied to couples \( X_1,X_3 \) and \( X_2,X_4 \) transforms them to couples \( Y_1,Y_3 \) and \( Z_2,Z_4 \) respectively and again transforms \( Y_1,Z_2 \) and \( Y_3,Z_4 \) to four non-correlated r.v. \((U_1,U_2,U_3,U_4)\) with the same mean and variance. Similarly a set of \( 2^P \) r.v. (with \( p \) an integer) requires \( p \) iterations.

To explain the practical use of this procedure to correct a diffraction spectrum for the detector response inhomogeneity let us come back to the case of a two-cell detector. If we assume that the unequal efficiency of the cells is due to unequal effective cross-sections, this means that one cell counts a part of the incident particles which, in the case of a homogeneous detector, would be counted by the
other, and reciprocally. In other words each of the corrected counts \((m_1^i, m_2^i)\) should be a mixture in proportions \(\beta_1^i\) of the raw counts \((m_1, m_2)\).

\[
m_1^i = \beta_1^i m_1 + \beta_2^i m_2
\]
\[
m_2^i = \beta_3^i m_1 + \beta_4^i m_2
\]

The counts \((n_1, n_2)\) of the calibration spectrum being large are good estimates of the parameters \((\lambda, \mu)\) of proportions \(\beta_1^i\) which, from (II) may be taken as:

\[
\beta_1 = (\sqrt{n_1} + \sqrt{n_2})/2\sqrt{n_1}
\]
\[
\beta_2 = (\sqrt{n_1} - \sqrt{n_2})/2\sqrt{n_1}
\]
\[
\beta_3 = (\sqrt{n_1} + \sqrt{n_2})/2\sqrt{n_1}
\]
\[
\beta_4 = (\sqrt{n_1} - \sqrt{n_2})/2\sqrt{n_1}
\]

Finally, one can remark that the \(\alpha\)-correction, when applied to the calibration spectra used for its determination leads to a non random spectrum while the \(\beta\)-correction as stated above preserves the randomness.

### III - TEMPORAL STABILITY OF THE DETECTOR RESPONSE.

Let us define the following experimental process:

(a) Calibration spectra recorded from a homogeneous background

(b) \(\alpha_{ij}\) or \(\beta_{ij}\) correction factors are estimated from (a)

(c) later (presumably after some diffraction experiments) new control spectra are recorded from homogeneous background.

In the case of relative temporal stability, the \(\alpha\) or \(\beta\)-correction applied to the control spectra would lead to homogeneous ones. Otherwise a row/column perturbation will be present. The absolute stability of response for any future experiment made under identical conditions to the calibration step can be tested by another procedure. Such a procedure is based on an approximate two sample test for Poisson processes, developed in [3] where the duration of the experiment needed to obtain a specified power is determined.

The subsequent tests are relevant to the relative stability case.

#### III.1 - Tests without assumption of row/column heterogeneity

As defined in the introduction the observed counts \(n_{ij}(i=1,n; j=1,m)\) are realisations of a family \(\{N_{ij}\}\) of independent Poisson random variables. If the detector was homogeneous, these random variables would be identically distributed and the observed data would be a sample drawn from a Poisson distribution with parameter \(\lambda\). Now if \(X\) is a Poisson r.v., the mean of \(X\), denoted by \(E(X)\), is equal to the variance of \(X\), \(V(X)\) and the ratio \(V\) is equal to 1. In our case the common mean and variance of the \(N_{ij}\)'s are unknown and have to be estimated by the sample mean and the sample variance of the observed counts, that is by:

\[
\hat{E} = \frac{1}{nm} \sum_{i=1}^{n} \sum_{j=1}^{m} N_{ij}
\]
\[
\hat{V} = \frac{1}{nm-1} \sum_{i=1}^{n} \sum_{j=1}^{m} (N_{ij} - \hat{E})^2
\]

which leads to the estimation statistic \(\frac{\hat{V}}{\hat{E}}\).

Fisher's theorem [5] states that if \(nm > 35\) and \(\lambda > 3\) then the distribution of the random variable

\[
T = (nm-1) \frac{\hat{V}}{\hat{E}}
\]

can be adequately approximated by a chi-square (\(\chi^2\)) distribution with \(nm-1\) degrees of freedom. These assumptions are satisfied in our case. Moreover, \(nm\) is usually big and the \(\chi^2\) distribution with \(nm-1\) degrees is approximated by a normal distribution with mean \((nm-1)\) and variance \(2(nm-1)\). Thus, we know that if the hypothesis of homogeneity \(H_0\) is true, the function \(T\) of the observations will be distributed...
according to a normal law whose parameters are known. Let \( \alpha \) be a level of significance, that is the maximum probability with which we are willing to reject homogeneity when actually there is homogeneity; one can find numbers \( c \) and \( d \) such that the probability that \( T < c \) when \( H_0 \) is true is less than \( \alpha/2 \) and the probability that \( T > d \) is less than \( \alpha/2 \). Since \( \alpha \) is small, it is reasoned that \( T \) has little chance of taking values outside \([c,d]\) when \( H_0 \) is true. Thus if one computes \( T \), if \( c < T < d \) then one would not wish to reject \( H_0 \). In our case the test we use at the \( \alpha \)-nominal level is,

\[
(\text{III}.1) \quad \text{if } \frac{|\mathbf{X}|}{E} > t_\alpha \left( \frac{2}{(nm-1)} \right)^{1/2}, \text{ reject homogeneity}
\]

where \( t_\alpha \) denotes the \( 1 - \frac{\alpha}{2} \) percentile of the standard normal distribution.

It is natural to require such a test to give the maximum probability of rejecting \( H_0 \) when \( H_0 \) is not true; this is generally not the case with the test (III.1), the set of alternatives being certainly too large.

Another non-parametric test which we use is the usual chi-square test of "goodness of fit". It is known that the limit distribution of the \( \chi^2 \) statistic depends generally on the bounds of the interval classes into which data are grouped. In practical applications these classes are chosen according to the data and are therefore random. For the PSD measurements we use a rule of grouping and the related limit distribution given in [44]. A discussion of the performances of these tests is given in the last section of this paper.

III.2 - Homogeneity tests for a row/column structure

Disorder tests

Suppose that an event occurs randomly in time and let \( X(I) \) be the number of occurrences of the event in an interval \( I \). A Poisson process with mean measure \( \mu \) is characterized by the property that for every finite collection of non overlapping intervals \( I_1, I_2, \ldots, I_k, X(I_1), X(I_2), \ldots, X(I_k) \) are independent Poisson distributed random variables with parameters \( \mu(I_1), \ldots, \mu(I_k) \). By convention a Poisson process on \([0, +\infty[\) is denoted by \((X_t, t>0)\) where \( X_t \) is the number of occurrences in the interval \([0,t] \). A Poisson process is homogeneous if \( N_t = \mu([0,t]) = \nu t \) where \( \nu \) is a positive constant.

The homogeneity test we are going to develop here is suggested by the following remark on homogeneous random Poisson processes. Let \( T \) be a fixed time and let us assume that \( N_T = k \), i.e., that the number of occurrences in the time interval \([0,T]\) is \( k \). If \( t_1, t_2, \ldots, t_k \) are the ones at which the events have occurred, \( \{t_1, t_2, \ldots, t_k\} \) can be considered as a set of independent observations of a random variable \( U_T \) uniformly distributed on \([0,T]\). It then follows that the random variable \( N_T/N_T \) provides an unbiased estimator of \( t/T \) for any \( t \) in \([0,T]\). A rephrasing of the above remark provides us with a method for testing the homogeneity of the control spectra corrected by the \( \alpha \)'s or \( \beta \)'s. For example in order to derive a test for a row homogeneity, we can consider the discretized Poisson process defined for \( 1 \leq i \leq n \) by

\[
N_i = \sum_{j=1}^{m} N'_{ij}.
\]

Let \( i_o \) be a fixed value of \( i \) corresponding to a homogeneous line. For each \( i_1 > i_o \) the rows with indices lying between \( i_o \) and \( i_1 \) will be homogeneous if the random variables \( U_i \) introduced above are uniformly distributed on \([i_o,i_1]\). Such a uniformity hypothesis can be tested by using the Kolmogorov-Smirnov statistic.

\[
KS = \sup_{i_o < i < i_1} \left| \frac{F_{U_i}(i) - F_{U_{i_1}}(i)}{N_i} \right| = \max_{i_o < i < i_1} \left| \frac{i - i_1}{N_i} \right|
\]

If the test rejects the homogeneity hypothesis (the disorder detected at the \( i_{th} \) location corresponds to a non homogeneous row) it is processed no further. By a similar technique we can construct a test for the column heterogeneity.
III.3 - Analysis of variance (ANOVA)

The term "analysis of variance" was introduced by Fischer who was responsible for its inception as a methodology. Much of its development in practice is due to Scheffe /8/.

As indicated earlier, the structure of a PSD allows us to consider the rows and the columns as two factors with \( n \) and \( m \) levels respectively. Under a homogeneous flux the observed counts can be arranged in a 2D array and are respectively distributed as Poisson random variables with mean \( \lambda_{ij} \). The statistical question is "can the observations represented by the nm counts be considered as having been drawn from the same Poisson population with mean \( \lambda \)"? The null hypothesis can be stated as \( H_0: \lambda_{ij} = \lambda \) for any \( (i,j) \). Hence we wish to determine whether the differences among the observations \( (N_{ij}; 1 \leq i \leq n, 1 \leq j \leq m) \) are too great to attribute to the chance errors of drawing the samples from the same population.

Before we discuss the procedures involved in our present application we will consider the general rationale underlying the ANOVA principle. If the null hypothesis that all the \( \lambda_{ij} \) are equal is true then both the variations among the row-means and the variations among the column-means reflect random errors of the sampling process and would be expected not to differ significantly from each other. On the other hand, if the null hypothesis is false and for example the column means are indeed different then the between-column variation would not reflect sample errors only and will be more important. Hence, a comparison of the between-column-variations and the between-row-variations yields information concerning differences among the column and the row means. This is the central insight provided by the ANOVA technique whose main characteristic is that the observations are assumed to be realizations of random variables normally distributed with the same variance \( \sigma^2 \).

In the model considered here such assumptions are not applicable since the variance of a Poisson variable is equal to the mean. Hence either the data has to be transformed in such a way that these assumptions are satisfied or we have to extend these ideas to the Poisson case. These two approaches are discussed in the following sections.

For data of the type considered here we assume the mathematical model

\[
\begin{align*}
\lambda_{ij} & = \mu + u_i + v_j & i=1,\ldots,n; & j=1,\ldots,m
\end{align*}
\]

where \( \mu \) is the general mean, \( u_i \) is the effect of the \( i^{th} \) row and \( v_j \) is the effect of the \( j^{th} \) column. The hypotheses of interest are:

- \( H_R \): row homogeneity \( u_i = u \) for all \( i \) in \( \{1,\ldots,n\} \)
- \( H_C \): column homogeneity \( v_j = v \) for all \( j \) in \( \{1,\ldots,m\} \)
- \( H \): \( H_R \) and \( H_C \) total homogeneity

III.3.1 - Square root transform of a Poisson variate

By the central limit theorem, if \( X \) is a Poisson variate with mean \( \mu \), then, as \( \mu \to \infty \), the random variable \( (X-\mu)/\sqrt{\mu} \) is distributed as a standard normal distribution \( N(0,1) \).

In /7/ it is shown that under the same conditions, \( \sqrt{X} \) is distributed as a normal random variable with mean \( \sqrt{\mu} \) and variance \( \frac{1}{4} \). It was found by ANSCOMBE /1/ that the transformation \( \sqrt{X+c} \), where \( c \) is a suitably determined constant, has some theoretical advantages. This transformation has been revisited by KIHLEBERG et al. /6/ who suggest \( c=31/80 \) as the best constant for normality and stabilisation of the variance. This is the transformation we used for the first ANOVA approach of our problem.

III.3.2 - Tests for transformed data

If the counts for each cell are large (\( \geq 25 \)) the statistical model obtained by applying the square root transformation is normal with the same variance but the additivity stated in (III.3) no longer holds. More precisely, the transformed variables are now

\( Z_{ij} = \sqrt{N_{ij}+0.386} \) and if \( m_{ij} \) denotes the mean of \( Z_{ij} \) we have, with no loss of generality:

\[
\begin{align*}
\text{H}_R & : \text{row homogeneity} \quad u_i = u \text{ for all } i \text{ in } \{1,\ldots,n\} \\
\text{H}_C & : \text{column homogeneity} \quad v_j = v \text{ for all } j \text{ in } \{1,\ldots,m\} \\
\text{H} & : \text{total homogeneity}
\end{align*}
\]
where, \( m_{ij} \) represents an interaction between the \( i \)th and \( j \)th level introduced by the square root transformation. However, by inspecting analytically the relations among \( \lambda_{ij} \) and \( m_{ij} \) we have, for the hypotheses \( H_r \) and \( H_c \) defined earlier:

\[
H_r : \text{for all } i \text{ and all } j \quad m_1(i) = 0 \quad \text{and} \quad m_{12}(i,j) = 0
\]

\[
H_c : \text{for all } i \text{ and all } j \quad m_2(j) = 0 \quad \text{and} \quad m_{12}(i,j) = 0
\]

Hence, if an additivity model is assumed for the initial data, the tests of \( H_r, H_c \) and \( H \) can be processed by the usual ANOVA techniques (see for example /8/). This approach while well suited to the relative stability test of the detector is not applicable if interactions (e.g. peaks in Bragg diffraction spectra) are present in the original data.

III.4. - ANOVA for Poisson data

Instead of transforming the original data, we now consider a statistical model that is a natural generalization of classical ANOVA. This generalization largely removes the normality assumptions and the additivity of systematic effects and therefore may also be extended to estimate the Bragg intensity in diffraction experiments as discussed later.

Let us assume that the detector has a stable response and that \( Y \) is the random integer valued vector whose \( p = nm \) components are obtained from the random variables \( N_{ij} \) by:

\[
Y_1 = N_{11}, \quad Y_2 = N_{12}, \ldots, \quad Y_n = N_{1m}, \quad Y_m+1 = N_{21}, \ldots, \quad Y_{nm} = N_{mm}
\]

Hence, the components \( Y_i \) of \( Y \) are independent Poisson variates with corresponding means \( \mu_i \). Let \( \mu \) be the \( p \)-dimensional vector with components \( \mu_i \) and let \( y \) be an observed value of \( Y \). Neglecting a constant that does not involve \( \mu \), the logarithm of the likelihood function of our model, given \( y \), is:

\[
(III.4.a) \quad L(y, \mu) = \sum_{r=1}^{p} \left[ y_r \ln(\mu_r) - \mu_r \right]
\]

If the row/column structure heterogeneity is additive one can show easily that the mean \( \mathbb{E}(N_{ij}) \) of \( N_{ij} \) may be written as:

\[
(III.4.b) \quad \mathbb{E}(N_{ij}) = m_0 + \alpha_i + \beta_j \quad \text{with} \quad \sum_{i=1}^{n} \alpha_i = m \quad \sum_{j=1}^{m} \beta_j = 0
\]

such a decomposition being unique. Hence, if \( \nu \) denotes the \((n+m-1)\)-dimensional vector defined by:

\[
\nu_1 = m_0, \quad \nu_2 = \alpha_1, \ldots, \quad \nu_n = \alpha_{n-1}, \quad \nu_{n+1} = \beta_1, \ldots, \quad \nu_{n+m-1} = \beta_{m-1}
\]

the mathematical expectation \( \mathbb{E}(Y) \) can be expressed as: \( \mathbb{E}(Y) = A\nu \) where \( A \) is a known matrix of rank \( n+m-1 \). To extend the analysis of variance, "good" estimates of \( \nu \) are needed. To this end, we will apply the maximum likelihood principle /7/.

The maximum-likelihood algorithm we present is derived as a modification of the Newton-Raphson algorithm and may be interpreted as an iterative weighted least-squares method. More precisely, the maximum-likelihood equations are obtained by differentiating (III.4.a) with respect to each of the components of \( \nu \), i.e.:

\[
(III.4.c) \quad S(\nu) = \frac{\partial L}{\partial \nu} = t^T A \begin{bmatrix} y_1/\mu_1^{-1} \\ y_2/\mu_2^{-1} \\ \vdots \\ y_p/\mu_p^{-1} \end{bmatrix}
\]

Since the maximum likelihood equations are not linear with respect to \( \nu \), the method of scoring (/7/ p. 305) has been used to develop an algorithm to find a root of (III.4.c). We obtain the following adjustment at the \( t \)th iteration:
\[ \hat{\nu}(t+1) = \hat{\nu}(t) + \varepsilon(t) \]
where
\[ \varepsilon(t) = \Gamma_\nu I(\hat{\nu}(t)) A^{-1} S(\hat{\nu}(t)) \]
and
\[ I(\hat{\nu}(t)) = \begin{bmatrix} 1/\nu_1 & 0 \\ 0 & \ddots & 1/\nu_p \end{bmatrix} \]
is the information matrix at the \( t \)th iteration.

To start the iterations we take \( \nu(0) = y \) and \( \hat{\nu}(0) = \hat{\nu}(0) \). The procedure is repeated until a stable solution is reached. For more details the reader is referred to 7/3/ where we have shown that the estimators obtained by this method have good asymptotic properties. Once the maximum-likelihood estimators of \( \nu \) and \( \mu \) are obtained we can develop likelihood ratio tests 7/ for homogeneity. Denoting the deviance of our model at \( \hat{\mu} \) by \( D(\hat{\mu}) = 2(L(y, \hat{\mu}) - L(y, \mu)) \) the various tests are based on the statistics:
\[ D(\hat{\mu}_0) - D(\hat{\mu}) \]
where \( \hat{\mu}_0 = (\hat{\mu}_0, \ldots, \hat{\mu}_p) \) with \( \hat{\mu}_0 = \frac{1}{p} \sum_{r=1}^{p} y_r \) and \( \hat{\mu} \) is the maximum-likelihood estimator of \( \mu \) under the appropriate homogeneity hypothesis. By a suitable large-sample argument we have that, asymptotically under the various testing hypotheses, the appropriate statistics are \( \chi^2 \) distributed. Moreover a slight extension of the \( S \)-method of H. Scheffe 8/ for contrasts among rows or columns provides us with a way to find which rows or columns are heterogeneous when the homogeneity hypothesis is rejected.

IV. Numerical results and conclusions

For any statistical decision rule it is natural to ask for the rejection of the homogeneity hypothesis as frequently as possible when there is a lack of homogeneity. This maximum probability of the right decision when there is heterogeneity is called the power of the decision rule. However the power of a test depends on its significance level and (e.g. for the ANOVA test) is not always obtainable analytically.

Application computer programs written in PASCAL have been developed for the algorithms presented here and the power of the tests have been estimated or checked by means of simulated experiments.

Two types of experimental design have been used for the simulations:
A: Total homogeneity, i.e., \( \lambda_{ij} = \lambda \) \( w_{i,j} \).
B: Column homogeneity, but row heterogeneity due to a perturbation at an arbitrary fixed row \( i_0 \), i.e.:
\[ w_{i,j} \lambda_{i_0,j} = \lambda + \alpha \] \( w_{i,j} \) \( i \neq i_0 \) \( \lambda_{ij} = \lambda \)

The power of the Poisson ANOVA test has been parametrized by the signal to noise ratio \( \text{SNR} \) given by:
\[ \text{SNR} = \frac{\alpha \sqrt{m} \sqrt{n}}{\sqrt{\lambda} \sqrt{n}} \]
where \( nr \) is the total number of simulated spectra for a nm PSD submitted to a uniform background whose mean rate is \( \lambda \) and with one row perturbed by an average amount \( \alpha \).

A hundred simulations have been performed for various values of \( \text{SNR} \), using a random generation procedure for Poisson distributions developed in 7/2/. For each experimental design the relative frequency of rejections in 100 trials provides an estimate of the power of the test. The nominal significance level of our test was fixed at 10%.

The results (figure 1) show that the estimated significance level of the ANOVA test agrees with the nominal one (set to 10%). The test has a good power with a detection limit of \( \text{SNR} = 0.75 \) (the value for which the decision rule is better than a fair-coin decision).
Similar simulations on the other tests in this paper, have shown that the ANOVA test is equal or superior in power especially when compared to the aggregation test and the chi-square goodness of fit test. The power of the disorder test is of the same magnitude but its significance level can only be estimated by simulations since it is a multiple decision rule.

Finally the ANOVA test has the following advantages over the others: it is more general (no Gaussian approximation), its significance level is known theoretically, its algorithm may be extended to the peak detection in our "inclined" background in the following way:

We model the $\lambda_{ij}$ by:

$$\lambda_{ij} = \lambda + \alpha_i + \beta_j + \gamma_{ij}$$

where the non linear terms $\gamma_{ij}$ are due to the peak and detect by ANOVA techniques the cells at which $\gamma_{ij} \neq 0$. This will be discussed in a subsequent paper.

Preliminary tests of the ANOVA algorithm on real calculations and control spectra from the neutron diffractometer D19A of the Institute Laue-Langevin have given promising results.

![Graph](image)

**Fig. 1** - Power of the ANOVA test as a function of SNR. The nominal significance level is set to 10%. The dashed lines bound the region in which fall the results obtained for a large spread of background (b) and repetition (nr) parameter values.

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