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1998 J. Phys. A: Math. Gen. 31 L671

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LETTER TO THE EDITOR

Convex probability domain of generalized quantum measurementsAsher Peres[†] and Daniel R Terno[‡]

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Received 9 June 1998, in final form 10 July 1998

Abstract. Generalized quantum measurements with N distinct outcomes are used for determining the density matrix, of order d , of an ensemble of quantum systems. The resulting probabilities are represented by a point in an N -dimensional space. It is shown that this point lies in a convex domain having at most $d^2 - 1$ dimensions.

In elementary quantum measurement theory, a test performed on a quantum system is represented by a complete set of orthogonal projection operators \mathbf{P}_m , where the label m takes at most d different values (d is the dimensionality of the Hilbert space, assumed finite). The probability of obtaining outcome m of that test, following the preparation of a quantum ensemble in a state ρ , is $p_m = \text{tr}(\rho\mathbf{P}_m)$. If ρ is arbitrary, the only constraint on these probabilities is $\sum_m p_m = 1$.

It is well known that this type of test is not optimal if only a finite number of quantum systems can be observed. (As a concrete example, we receive five photons from a distant source, and we want a good estimate of their polarization. What is the best strategy?) In such a case, more information may be derived from a *positive operator valued measure* (POVM) [1, 2] with $N > d$ different outcomes. Such a POVM is a set of N positive matrices \mathbf{A}_μ , which in general do not commute, but still satisfy $\sum_\mu \mathbf{A}_\mu = \mathbb{I}$, where \mathbb{I} is the unit matrix in d dimensions, and μ is an arbitrary label running from 1 to N . If the quantum system is prepared in state ρ , the probability to get outcome μ is

$$p_\mu(\rho) \equiv p(\mathbf{A}_\mu|\rho) = \text{tr}(\rho\mathbf{A}_\mu). \quad (1)$$

To each preparation ρ of the system, we thus associate N probabilities, p_1, p_2, \dots, p_N . We refer to this set of positive numbers as a point $P(\rho)$ in probability space. The set of all output points is labelled by P . Density matrices form a convex set whose extreme points are pure states [3]. The linear relation (1) between input states and output probabilities implies that the set of points P is also convex:

$$P(\rho) \equiv P(x\rho_1 + (1-x)\rho_2) = xP(\rho_1) + (1-x)P(\rho_2). \quad (2)$$

Thus the shape of the hypersurface that bounds the domain of the points $P(\rho)$, for all possible preparations of the system, is determined by the outputs for the pure states only.

Obviously $\sum_\mu p_\mu = 1$, so that the points $P(\rho)$ lie on a hyperplane of dimension $(N-1)$. However, the results of generalized measurements are subject to stronger constraints (which

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may be important for the statistical analysis of experimental results). Let D be the number of linearly independent parameters in ρ (for a generic density matrix in a d -dimensional complex Hilbert space, $D = d^2 - 1$). The following proposition will now be proved: *If $N > (D + 1)$, the output of any POVM is confined to a D -dimensional subspace.*

Indeed, let us write the elements of a generic density matrix in terms of real (symmetric) and imaginary (antisymmetric) parts,

$$\rho_{mn} = \xi_{mn} + i\eta_{mn}. \quad (3)$$

There are $d(d - 1)/2$ independent elements η_{mn} and $(d + 2)(d - 1)/2$ independent ξ_{mn} , because of the condition $\text{tr } \rho = 1$ which can be written

$$\xi_{dd} = 1 - \sum_{n=1}^{d-1} \xi_{nn}. \quad (4)$$

Likewise, the elements of each POVM matrix \mathbf{A}_μ , of order d , can be written as $x_{mn}^\mu + iy_{mn}^\mu$ in terms of d^2 real parameters. We thus obtain from equation (1),

$$p_\mu(\rho) = \sum_{m=1}^{d-1} (x_{mm}^\mu - x_{dd}^\mu) \xi_{mm} + 2 \sum_{m=1}^d \sum_{n>m}^d (x_{mn}^\mu \xi_{mn} + y_{mn}^\mu \eta_{mn}) + x_{dd}^\mu. \quad (5)$$

Thus $P(\rho)$ is obtained from ρ by an affine transformation [4]

$$\mathbf{p} = \mathbf{M}\mathbf{r} + \mathbf{c} \quad (6)$$

where \mathbf{p} is a ‘vector’ consisting of any $N - 1$ components p_μ (the remaining component is obtained from $\sum_\mu p_\mu = 1$). Likewise \mathbf{r} is a vector of D linearly independent parameters of ρ . The matrix \mathbf{M} , with $N - 1$ rows and D columns, depends only on the POVM used for the test; and \mathbf{c} is a vector whose $N - 1$ components are x_{dd}^μ , which also are parameters of the POVM. Explicitly, the μ th row of \mathbf{M} , which is

$$(x_{11}^\mu - x_{dd}^\mu) \dots (x_{d-1,d-1}^\mu - x_{dd}^\mu) \quad 2x_{12}^\mu \dots 2x_{d-1,d}^\mu \quad 2y_{12}^\mu \dots 2y_{d-1,d}^\mu \quad (7)$$

and

$$\mathbf{r}^T = (\xi_{11} \dots \xi_{d-1,d-1} \quad \xi_{12} \dots \xi_{d-1,d} \quad \eta_{12} \dots \eta_{d-1,d}) \quad (8)$$

have $D = d^2 - 1$ real components.

If $N - 1 > D$, the rank of \mathbf{M} is at most D , and any $D + 1$ vectors $\tilde{\mathbf{p}} = \mathbf{M}\mathbf{r}$ are linearly dependent. A translation by the constant vector \mathbf{c} in the $(N - 1)$ -dimensional vector space transforms a D -dimensional subspace into another D -dimensional subspace. Thus the output of any POVM on a system whose density matrix has D linearly independent parameters is confined to a D -dimensional subspace of the probability space.

Next, let us examine the shape of the surface that encloses the domain of $P(\rho)$. The set of density operators, and therefore the set of probabilities, are convex. The extreme points of these sets are the pure states, which are defined by $2(d - 1)$ real parameters, and the probabilities corresponding to these pure states, respectively. Thus any interior point of the D -dimensional set P is a convex combination of the extreme points of that set, which lie on a $2(d - 1)$ -dimensional hypercurve.

Note that any density matrix ρ of rank d can be written as a convex combination of no more than d pure density matrices, corresponding to the eigenvectors of ρ . As a result, any interior point of P can be obtained from at most d extreme points. This result ought to be compared with Caratheodory’s theorem [4], which states that any interior point of an arbitrary convex set of dimension D can be obtained as a convex combination of $D + 1$ (or fewer) extreme points of that set. Here, $D + 1 = d^2$. The smaller number of extreme

points needed in the present case is due to the fact that density matrices are not an *arbitrary* convex set (they are positive and have unit trace).

As a simple example, consider the case of spin- $\frac{1}{2}$ systems. Their states can be described by means of a Bloch sphere. The pure states correspond to points on the surface of the sphere, and mixed states lie in its interior. With our notations, we have

$$rho = \begin{pmatrix} x_{11} & x_{12} + iy_{12} \\ x_{12} - iy_{12} & 1 - x_{11} \end{pmatrix} \quad (9)$$

where the three parameters are subject to the positivity condition

$$x_{11}(1 - x_{11}) - x_{12}^2 - y_{12}^2 \geq 0. \quad (10)$$

The transformation (6) is linear. Therefore the Bloch sphere is transformed into another quadratic surface, usually an ellipsoid. Exceptionally, if a POVM element has unit norm (so that the corresponding p_μ can be equal to 1, and then all the other p_μ vanish), we have a straight segment.

In particular, consider a POVM with four elements, $\mathbf{A}_\mu = (\mathbb{I} + \mathbf{a}_\mu \cdot \boldsymbol{\sigma})/4$, where the four unit vectors \mathbf{a}_μ form a regular tetrahedron in a real three-dimensional Euclidean space, and $\boldsymbol{\sigma}$ denotes the three Pauli matrices. Likewise, any state ρ can be written as $\rho = (\mathbb{I} + \mathbf{n} \cdot \boldsymbol{\sigma})/2$. We thus have

$$p_\mu = \text{tr}(\rho \mathbf{A}_\mu) = (\mathbb{I} + \mathbf{a}_\mu \cdot \mathbf{n})/4 \quad (11)$$

whence

$$\sum_{\mu=1}^4 (p_\mu - \frac{1}{4})^2 = \mathbf{n}^2/12. \quad (12)$$

The Bloch sphere is thus mapped into a three-dimensional sphere of radius $1/\sqrt{12}$, centred at $p_\mu = \frac{1}{4}$, and lying in the hyperplane $\sum_\mu p_\mu = 1$. If we want to parametrize that hyperplane with three of the p_μ , we substitute in the above equation $p_4 = 1 - p_1 - p_2 - p_3$. We then obtain an ellipsoid in a three-dimensional space, as shown in figure 1. It is also possible to use as coordinates suitable linear combinations of the p_μ , such as

$$\begin{aligned} x &= p_1 + p_2 - p_3 - p_4 \\ y &= p_1 - p_2 + p_3 - p_4 \\ z &= p_1 - p_2 - p_3 + p_4. \end{aligned} \quad (13)$$

The Bloch sphere is then mapped into a sphere $x^2 + y^2 + z^2 \leq \frac{1}{3}$.

The case of spin-1 systems is more complicated. A generic density matrix can be written in terms of its eigenstates as

$$\rho = \sum_{j=1}^3 \lambda_j |v_j\rangle \langle v_j|. \quad (14)$$

This is as a convex combination of three extreme points. Any pure state, such as the above eigenstates, can be parametrized, with a suitable choice of its phase, as

$$|v\rangle = (\sin \theta \cos \phi e^{i\alpha}, \sin \theta \sin \phi e^{i\beta}, \cos \theta) \quad (15)$$

where

$$0 \leq \theta, \phi \leq \pi/2 \quad \text{and} \quad 0 \leq \alpha, \beta < 2\pi. \quad (16)$$

All the components of the corresponding pure ρ , which is a matrix of rank 1, are functions of the four parameters θ, ϕ, α , and β . Thus all the probabilities $p_\mu = \text{tr}(\rho \mathbf{A}_\mu)$ are also

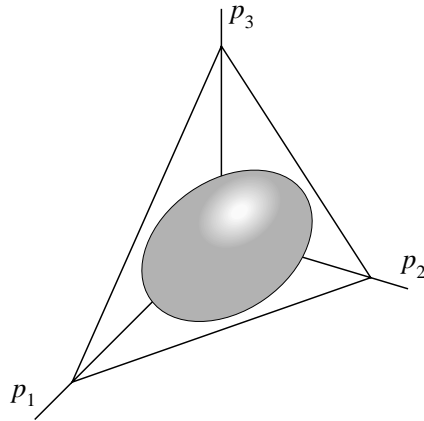


Figure 1. The probability ellipsoid that corresponds to the Bloch sphere is tangent to the plane $p_1 + p_2 + p_3 = 1$ (that is $p_4 = 0$) at the point $p_1 = p_2 = p_3 = \frac{1}{3}$ and likewise it is tangent to each coordinate plane at the point where the two coordinates in that plane are $\frac{1}{3}$.

functions of these four angles. This gives the extreme points of the set P : they form a four-parameter hypersurface in an eight-dimensional space S (which is itself embedded in the N -dimensional space of the p_μ). The rest of the boundary of S , corresponding to density matrices of rank two, lies on the segments between any pair of extreme points. The interior points of S can be obtained by a convex combination of three suitably chosen extreme points, as in equation (14). All these considerations are readily extended to quantum systems whose Hilbert spaces have more than three dimensions: there are $(d - 1)$ polar angles like θ and ϕ , and $(d - 1)$ phases like α and β .

Finally, let us consider potential applications of the above results to the analysis of experimental data. The probabilities p_μ cannot be measured exactly, as this would require testing an infinite number of quantum systems. If only n systems are available, and the μ th outcome is found to occur n_μ times (so that the experimenter records a set of N integers or zeros), then the N ratios $q_\mu = n_\mu/n$ are the only data available for evaluating the true p_μ . Obviously, $\sum_\mu q_\mu = 1$, just like $\sum_\mu p_\mu$, but the other constraints on p_μ may not be satisfied. In particular, if $N > D + 1$, the point $Q = \{q_\mu\}$ will not in general lie in the hyperplane of dimension D to which the point P is restricted.

How far can Q be from the true P ? Each one of the experimental data n_μ has an expected binomial distribution with dispersion

$$\Delta n_\mu = [n p_\mu (1 - p_\mu)]^{1/2} \simeq [n_\mu (n - n_\mu) / n]^{1/2} \quad (17)$$

where the last expression is valid if $n_\mu \gg 1$. We can imagine an error box with sides equal to Δq_μ , centred at the point Q , and we then have to examine where that error box overlaps with the hyperplane to which P is constrained.

Obviously, it is best to design the experiment so as to have $N = D + 1 = d^2$, and not more than that. A larger value of N leads to a less efficient use of the experimental data. This result is reminiscent of Davies's theorem [5] which deals with a related question, namely how to maximize the mutual information obtainable from a set of non-orthogonal signals. The theorem asserts that no more than d^2 outputs are needed.

If $N = D + 1$, the only question is whether Q lies in the convex domain of P , namely whether the resulting ρ , obtained by solving equation (1), is a positive matrix. If it is, then Q is the best estimate for the true P . In the opposite case, the experimenter should either test a larger number of samples, or use maximum likelihood or similar nonlinear methods [6] to analyse the existing data.

DRT was supported by a grant from the Technion Graduate School. Work by AP was supported by the Gerard Swope Fund, and the Fund for Encouragement of Research.

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