CHRONOSOMES AND QUANTITATIVE STRATIGRAPHY

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Abstract : The three-dimensional mapping of time-bounded bodies of rock (chronosomes, after Schultz, 1982) forms the basis of quantitative prediction of both rock properties and biostratigraphy in the subsurface.

High resolution seismic data can provide mappable reflection-bounded units (RBU's) with a vertical resolution of 10 to 20 ms two-way-time (approximately 10-20 m in Tertiary sediments). Lateral resolution varies from 10 m in a 3D survey, to 500 m plus in the case of a regional 2D survey. We can begin with the working hypothesis that seismic reflectors are isochrons and map RBU's to chronosomes. Each chromosome has a unique combination of geological time interval and paleogeographical location. They are composed, generally, of lesser chronosomes below the current observational resolution, and can be combined to form higher-order chronosomes. The chromosome concept is therefore both time, and scale independent. Seismic stratigraphy forms a genetic framework in which the vertical development of chronosomes at any given location can be related to regional and/or global processes. Current seismic stratigraphic concepts and terminologies are essentially two-dimensional, yet sediment distribution throughout a basin is, of course, three-dimensional. Only by mapping chromosome development in three-dimensions can one find the predictive relationships between shape, location and content that are needed both for practical application of quantitative stratigraphy and in the theoretical analysis of causative processes within the basin.

Key words : Chromosome, Quantitative stratigraphy, Geological time interval, paleogeography, Biostratigraphy

INTRODUCTION

We will start by defining a few terms and explaining some of the concepts that will be used in this paper.

1. Quantitative Stratigraphy

The literal meaning of stratigraphy is "description of layers", and Grabau (1913) defined the term as "The inorganic side of historical geology or the development through the successive geological ages of the Earth's rocky framework or lithosphere."

Use of the term "stratigraphy" has come to include both the organic content of rock layers (biostratigraphy) and indirect indications of layering (seismic sequence stratigraphy).

Quantitative stratigraphy has been defined in many ways, by many people. The aims of quantitative stratigraphy have been stated as:

- To quantify the definition and correlation of stratigraphic units
- To develop, improve, and promote the use of computer algorithms in stratigraphic definition and correlation
- To promote the formal use and testing of multiple working hypotheses in stratigraphy
- To develop formal geological process models for hypothesis testing

In general we can say that Quantitative Stratigraphy aims to

- Maximize predictive capacity with a minimum of data

In practice it is the combination of:

- stratigraphic principles
- mathematics
- computer science
- statistics

in an interrelated group of methods designed to assist in, and improve confidence in, stratigraphy.

The development of a quantitative predictive capacity based on stratigraphic principles is fundamental to the research being carried out in many areas under the name of quantitative stratigraphy.

Of the many problems that we look to stratigraphy to solve, one of the most important concerns that of the stratigraphic correlation surface (SCS) at a given moment in geological time. This surface is the diachronous surface across which all superposed strata are younger than all underlying strata. It would have been possible to walk (swim) anywhere over this preserved surface at a unique instant in time.

The stratigraphic correlation surface is important because it is the closest we can come to the paleogeographical surface, and on that depends our ability to model processes and thence make predictions.

Biostratigraphy has played a major historical role in identifying this surface, and quantitative biostratigraphy (Gradstein, Agterberg, Brower and Schwarzacher (1985), Agterberg (1990)) is playing an increasingly important role in helping us to understand the uncertainties involved in different environmental predictions at different ages.

The stratigraphic correlation surface may be

identified using techniques such as quantitative biostratigraphy, chemostratigraphy (Williams, 1988) and magnetostratigraphy (Johnson et al, 1988), but it is also possible to nail the relative position of these surfaces to an absolute time (see Harland et al, 1989, and Gradstein, 1990 for discussions). Radio-isotope stratigraphy has helped to place absolute dates on many lithologies overlying important surfaces, and the combination of isotopic dating, magnetic reversal stratigraphy, and probabilistic biostratigraphy or chemostratigraphy enables absolutely dated stratigraphic correlation surfaces to be mapped in many environments to a resolution of better than 1 Ma (at least in the Mesozoic and Cenozoic).

In non-exposed basins the need for SCS maps is even more important, both from a mineral exploitation and from an academic point of view. However none of the above techniques are of any use without samples or borehole measurements. In this case our understanding of surfaces must be based largely on seismic data. Vail et al. (1977) presented a working hypothesis that seismic reflection were in fact SCS's. Since this time the hypothesis has been tested extensively but is still not proven beyond doubt. We will assume in this paper that a seismic reflection (allowing for multiples, migration problems etc.) is a stratigraphic correlation surface.

Once the stratigraphic correlation surface has been identified throughout a basin then regional or local variation in the internal properties of the overlying chronosome are of interest.

2. The "chronosome"

Digitizing seismic reflections is equivalent to digitizing stratigraphic correlation surfaces if (and it is not yet proven) such horizons are indeed time planes as proposed by the "Exxon School". Schultz (1982) has proposed the term "chronosome" for the 3D space bounded by such planes. Schultz recognized the problems of equating seismic reflections with time-planes and at the present time we should accept the assumption as an un-proven working hypothesis. Given the above assumptions, the relationship between chronosomes is therefore the relationship between paleogeographic surfaces in 3D. It is not necessary to use seismic sections to derive chronosome maps. The surfaces defined during a "facies architecture" study (Miall, 1985) are also time planes and will define chronosome boundaries. Having defined the chronosome we are faced with the problem of quantifying its character. Some properties are immediately available. Volume is defined once a suitable time-depth conversion is available (in the case of seismic data). Shape, surface, and attitude pose problems that are more intractable. Defining and describing the shape of 3D bodies in a useful way is a problem that has been avoided by the geological community, which has been satisfied with terms such as "wedge-shaped", "elongate" etc.

There have been many recent developments in 3D

visualization Tipper (1977), Auerbach and Schaeben (1990), Klein et al. (1989), Marschallinger (1991), but such representations do not provide functional descriptions. By a functional description we mean a description that can be used directly to make predictions concerning the distribution of lithological properties within the chronosome. Connell and Brady (1985) discuss the problem of generalizing functional form descriptions using a declarative strategy. In a declarative strategy the description is complex and all-inclusive (at a given resolution) and can be either verbose or mathematical. The shape components may be listed as in a verbal description using syntactic symbols such as "straight" "long" "curved" etc. linked to operators such as "connected-to", "orthogonal-to" etc. The mathematical equivalent of this is the bicubic spline or the use of "Coon" patches as described by Tipper (1977). A formal 3D description of a body may be built up in this way and compared to other templates of generalized geological bodies. The representation is all-inclusive at the chosen resolution but does not itself indicate functionality. It is a convenient visualization tool that leaves traditional qualitative interpretation methods unaffected. Tipper has shown how such representations can be manipulated to show the effects of compaction or deformation, and they can of course be used to calculate volumes.

An alternative image analysis strategy is known as "procedural". In this case the body itself is defined using rather simple concepts and data structures but the knowledge concerning these structures is incorporated in complex heuristics. This is equivalent to mathematical formalization of the simple geological descriptions "wedge-shaped", "drape" etc. which are simple generalizations which only have contextual meanings.

A good discussion of the functional form problem is to be found in Thorn (1988) Chapter 8. Chorley (Chorley (1957), and Chorley and Morley (1959) in: Thorn (1988) p. 102) developed a functional form based on the "lemniscate" (Fig. 1) described in radial coordinates by

Fig.1. Chorley's lemniscate representation of a drainage system form.

where ϕ lies between $-\pi/2k$ and $+\pi/2k$, l is the longest diameter of the loop and $k > -1$ is a constant (when $k = 1$ the loop is a circle). This form description was developed for drainage basins but also has a role in fan form description. A modification of the lemniscate to describe different fan types is shown in Fig. 2. In Fig. 3 a simple skeletal shape function is developed that can handle one of the major problems of subsurface shape identification. The margins of subsurface bodies are often defined only by a lack of resolution, that is they may continue laterally in all directions below seismic resolution. The skeletal shape function identifies the salient characteristics that are incontrovertibly identifiable on seismic i.e. shallowest observed point, thickest observed point and extension both in maximum gradient direction and perpendicular to this.

Combinations of such simple shapes may be usefully applied to well-bounded chronosomes with a direct relationship to depositional processes, or they could be used to test whether or not a given form is related to an unmodified depositional process or has been influenced by erosion. More complex shapes are usual at the limit of seismic resolution because the chromosome usually represents an aggregate of many individual depositional events, the number of which will increase with the subsurface depth of the chromosome. In this case the shape of the chromosome will be more often related to preservation potential than individual depositional processes,

LITHOSOME PREDICTION

There have been many different approaches to this next step. The traditional qualitative estimates based on paleogeographical models have been supplemented recently by a host of quantitative techniques developed as a response to the needs of hydrocarbon-reservoir description. We will briefly examine below some of the techniques that have been published over the past few years in the field of one, two, and three-dimensional quantitative lithostratigraphic prediction, and see how they relate to the chromosome.

In current terminology we are largely concerned with predicting the contents of parasequences or parasequence sets (Van Wagoner et al., 1988, p. 39). A parasequence is defined as a "relatively conformable succession of genetically related beds or bed-sets bounded by marine-flooding surfaces". Note however that the concepts of being "relatively conformable" and "genetically related" are not defined.

Walter Schwarzacher in his 1975 book on "Sedimentation models and Quantitative Stratigraphy" and again in Schwarzacher (1985) discussed the principles of predictive lithostratigraphy. Dealing first with one-dimensional sections he extended the models to two dimensions basing the simulations on empirical observations of lithology occurrence and transition.

In its simplest form such a model consists of random occurrences of lithologies. In the one-dimen-

sional case this can be represented as

$$x_t = \varepsilon_t$$

where x_t is the new state which is a function only of the random number ε_t .

In the case of a palaeosequence influenced by cyclic events, such as orbital forcing, the model may appear as

$$x_t = A \sin \frac{2\pi t}{\omega} + \varepsilon_t$$

in which the lithology at x_t is a function of a single deterministic cycle of frequency ω and amplitude A , with an additional random function (Schwarzacher, 1985, p. 368).

A one-dimensional Milankovitch model would have at least the function

$$x_t = A \cos \frac{2\pi t}{23 ka} + B \cos \frac{2\pi t}{41 ka} + C \cos \frac{2\pi t}{100 ka} + \varepsilon_t$$

where A , B , and C are the amplitudes of dominant frequencies of the precession, obliquity and eccentricity cycles respectively. Note that the cycles are assumed to be in phase in this case. A good discussion of the relationship between the precession, obliquity and eccentricity (ETP after Imbrie (1985)) cycles and the sediment record, taking into consideration phase lag is to be found in Imbrie (1985) and Clemens et al. (1991).

Systems that can be considered to have a "memory", that is, to be partially dependent on the previous state are called Markov processes after Markov (1924). Such processes can be described by

$$x_t = a x_{t-1} + \varepsilon_t$$

where a is a constant less than unity.

Note that the Markov process concept as stated above is empirical in nature, it says nothing about the causative process that leads x_t to depend on x_{t-1} . the Milankovitch approach however is an attempt to link causative processes to the observed record. In a similar vein the global eustatic sea level curve of Haq et al. (1987) attempts to provide a causative model for sedimentation patterns. If we carry out a Fourier spectral analysis of the sea-level changes as recorded by the $\delta^{18}O$ record from DSDP and ODP legs we obtain spectra that contain slightly modified Milankovitch frequencies for the first 0.4 Ma years or so but then the spectra begin to deviate (Imbrie, 1985). Older than 1 Ma BP the resolution of dating usually drops below that necessary to identify orbital forcing components. In exceptional cases, where we have a combination of high continuous sedimentation rates, unusually good absolute dating, and where assumptions may be made concerning the differential sedimentation rates between isochrons (Griffiths, Bøe, and Hodkinson, 1992) it may be possible to translate depth to geological time at such high resolution that orbital forcing components may be recognized for at least some of the Neogene. However the uncertainty in dating the large scale changes in relative sea level as recorded by

Fig. 2. A functional 2D chromosome shape description.

Haq et al. (1987) means that in the Mesozoic the likely error in absolute age exceeds the longest eccentricity period. Since most actual sedimentation events are probably dominated by periodicities less than or equal to Milankovitch cycles (storm, flood, and monsoon frequencies for example) then these longer period relative sea level controls are influencing the relationships between chromosome sets or parasequences rather than the internal distribution of lithosomes.

Empirical Markov models may be applied in two and three dimensions (Schwarzacher, 1985, p.404). In the two-dimensional case we can express the relationship as

$$x_{s,t} = \alpha x_{s-1,t} + \beta x_{s,t-1} + \varepsilon_{s,t}$$

where s is the lateral direction and t is time (vertical). The lithology at $x_{s,t}$ is thus a function of both the underlying lithology at $x_{s,t-1}$, and the laterally preceding lithology at $x_{s-1,t}$. Note that in this case s is directional and the assumption is that s and t are orthogonal. If, however the s direction is both parallel to the direction of sedimentation, and parallel to an unconformity or chromosome lower boundary then the model begins to be sedimentologically more realistic. In the three-dimensional case

$$x_{a,b,t} = \alpha x_{a-1,b,t} + \beta x_{a,b-1,t} + \gamma x_{a,b,t-1} + \varepsilon_{a,b,t}$$

the two spatial coordinates a and b would be related to chromosome boundaries. The scale of the chromosome is now important. If the time period involved is so great that the x_{t-1} to x_t relationship crosses a break in sedimentation then we cannot reasonably expect the underlying assumptions to hold, and predictions based on this model will not be successful. Within a parasequence then we can build a lot of our knowledge concerning cyclicity and sedimentary processes into this simple equation by making the constants into time and space-dependent functions and changing

the coordinate relationships. Given empirical or theoretical knowledge concerning the cumulative probabilities of transitions between likely lithologies within the chromosome then a Monte Carlo simulation can produce a probabilistic or stochastic model of the lithosome-to-chromosome mapping.

This latter approach to the mapping of lithosomes to the chromosome in two or three dimensions has been well described by Haldorsen and Damsleth (1990), and Damsleth et al. (1990, 1992). Damsleth et al.'s 3D facies units within which the predictive modelling is to take place are lithosomes such as "mouth-bar sands", "calcite", "delta plain fines", rather than chromosomes, but there is no reason why the same approach should not be used at the chromosome level.

Several people have built heuristic models of intra-chromosome variation. The modelling of alluvial systems provides an interesting example. Bridge and Leeder (1979), and Mackey and Bridge (1992) among others, have proposed models of meandering and avulsing river channels set in fine-grained overbank deposits. Their models are not empirical "stochastic" models such as described above, but based on a simplification of the physical controls on alluvial sedimentation. Because of the complexity of modelling a hydraulic system over many thousands of years many short-cuts are taken which involve simplification of the physical processes and their scaling in time.

The variables considered include channel-belt dimensions, floodplain width, variation in depositional rate, differential compaction, and tectonic tilting. There are no hydraulic parameters input to the model, and the model is not capable of deciding itself whether, or where, to deposit sand given an input grain-size distribution. The modelling concerns the distribution of sand channels treated as bounded, discrete, plastic bodies set in a fine-grained matrix. This is typical of the type of quantitative model that the present state of mathematics and computing pow

er enables. The model explicitly includes more understanding of the way river channels behave than a purely empirical stochastic model such as those of Jacod and Joathon (1971, 1972). Begg and King (1985), Haldorsen and Macdonald (1987), but the models are not constrained by chronostratigraphic position or chromosome shape, they exist in a sort of stratigraphic limbo.

Geostatistics

Another approach is that of so-called "geostatistics" (Matheron (1962, 1963)). The underlying assumption here is that the variance of a desired property is itself a function of the distance between, and orientation of observations. In other words the uncertainty in prediction of a value at a given point in space has a functional relationship to the distance to (and orientation in relation to) measured neighboring points.

There has been an increase in interest in the topic over the past few years (Agterberg and Griffiths, 1991). Using geostatistical techniques in our present case, the successful prediction of properties within the chromosome is based either on the identification of a suitable analog on which the variogram structure can be based, or on measured one-, or two-dimensional data sets from the actual chromosome. In the case of subsurface data, for example from hydrocarbon reservoirs or aquifers, the identification of suitable analogues is not a trivial matter. Often neither the analogues themselves nor the observed facies are defined in such a way as to enable the uncertainty in selection to be quantified. Vertical lithosome structure within the chromosome is often available from wells drilled through the chromosome but this must be translated to lateral structure to be of practical use. Information from dipmeter and chromosome attitude and orientation are useful in this context.

Fractals

The use of fractals in lithosome prediction (Hewett (1986) and Hewett and Behrens (1990)) closely parallels the use of geostatistics, and the same problems arise in practice.

Quantitative Dynamic Stratigraphy

The use of sediment process modelling (Harbaugh (1970)), or quantitative dynamic stratigraphy (QDS) as it has come to be called (Cross (1990)) also has a role to play in lithosome prediction within the chromosome. The two basic factors; preserved chromosome shape (at all scales), and the underlying (depositional) surface, provide the necessary constraints for three-dimensional QDS. If this type of study is carried out at the limit of resolution then the problems of running 3D models over large time intervals can be avoided, and the results tightly constrained. Quantitative information concerning 3D chromosome orientation in relation to the underlying surface (see Nordlund and Griffiths, this volume) can

provide gradient, minimum sedimentation rate, depositional slope and other input parameters for the model.

There are obviously problems with the application of QDS as the chromosome time interval increases. Thus a Jurassic chromosome of 1 Ma duration will be the preserved record of many different sedimentation and erosion processes. Nevertheless we can still generate a series of sufficient models each of which meet the constraints of the preserved chromosome. We must also, however have the possibility of an independent test of the range of possible solutions. This may be ultimately provided by stratigraphic inversion.

Seismic Inversion

Several workers have looked at the link between stratigraphic forward models (in this case within the chromosome) and the seismic record. The potential with this type of analysis is that we can constrain the lithosome model derived using one or several of the above-mentioned techniques within the chromosome by producing a synthetic acoustic (in the case of subsurface seismic), or visual reflectance (in the case of surface outcrop) section that can be compared quantitatively with the observed section. An acoustic reflectance (seismic) section is a function of reflectance (acoustic impedance contrast) between superimposed layers within the chromosome, whereas the visual light reflectance is a function of mineralogy, porosity and water saturation. In the seismic case therefore it is relatively simple to prepare a forward model but difficult to produce a necessary inverse model (in the sense that many sufficient inverse models can be produced).

A major problem here is that of mapping lithosome properties such as mineralogy, grain-size distribution, state of compaction and diagenesis to velocity and density (see papers by Samec et al (1989), Blangy (1992)). This is problematical because the mapping from mineralogy, grain size and sorting, porosity and cementation state, to log-scale petrophysics, let alone to low frequency acoustic reflection, is not straightforward. This problem, that of scaling, has engaged several workers over the past few years and is still not fully resolved.

The integration of forward and inverse modelling would seem to offer the best hope of quantitative lithosome prediction in the long term, and the present state-of-the-art is that we can produce forward models of chromosome fill from several different starting models but have difficulty quantitatively verifying the results. On the inverse side we are able to produce either high frequency acoustic impedance contrast sections or low frequency absolute velocity sections but not both, and without both together we cannot produce a unique solution. We need therefore substantial improvements in both forward modelling and inversion before we can unambiguously predict lithosome distribution with the chromosome.

Fig.3. a. Examples of a skeletal shape description applied to different geological bodies.

Fig.3. b. A simplified example of a series of consecutive bodies representing shallowing conditions. Nos. 1 - 5 are prograding chronosomes, 7 - 9 are delta lobes. Arrows indicate transport direction.

QUANTITATIVE BIOSTRATIGRAPHY AND THE CHRONOSOME

Several workers have shown the dependence of paleontologic assemblages on lithology (Armentraut, (1986), McDougal (1980), Poag (1976), and Poag and Valentine (1976) etc.). This dependence may be a function of unimodal specific preference (ter Braak, 1987, p. 1) during life, or preservation potential. Whatever the cause we should anticipate both lateral and vertical variation in paleontological assemblage within a chronosome at all scales. Quantitative mapping, and indeed prediction, of this variation in three dimensions can be assisted by the use of software such as ter Braak's CANOCO program (canonical community ordination by partial de-trended canonical correspondence analysis, ter Braak, 1987). Quantifying the lithostratigraphic control on biostratigraphy in three dimensions is necessary in order help tie down the duration of the chronosome, as different vertical sections within the chronosome will yield different assemblages. the use of a probabilistic "scaled optimum sequence" (Agterterg (1990), p. 250) may help to identify those species which are potentially lithologically influenced.

STRATIGRAPHIC LAWS AND THE CHRONOSOME

Although we live in a three-dimensional world, most of our stratigraphic concepts are at most two-dimensional. The law of superposition relates a vertical sequence to relative age (in an undisturbed sequence the younger formation is spatially superimposed on the older). Although this concept is valid at each individual point throughout a basin it does not help in relating neighboring sequences, hence the need for the concept of stratigraphic correlation (the identification of coeval parts of a sequence). The Law of Superposition is thus a one-dimensional law which says nothing about three-dimensional relative time. Walther's Law concerns two-dimensional relationships (the lateral sequence of lithologies is the same as the vertical sequence in an undisturbed succession). In sedimentary sequences this law is true only for limited distances in the direction of deposition, and only for certain environments. The definition of "lateral" is also incomplete, do we mean along the paleoslope. or do we mean parallel to the geoid or spheroid ("horizontal"). The three-dimensional world is more complex, with many different environments interacting at all scales. Sediments are transported and deposited as a function of the local variations in physical or chemical gradients. Only a few meters away from a channel sand is an embayment, whereas the channel sand is overlain by a coal deposit. For Walther's law to be of use in this case we need three-dimensional information concerning the distribution of gradients and fluid energy.

The chronosome and sequence stratigraphy
Sequence stratigraphy (Vail et al. (1977), van

Wagoner (1988)) depends absolutely on the mapping of chromosome relationships. Current published practice uses the type of termination to determine the relationship. Groups of related chromosomes are assigned to "system tracts" and these system tracts are qualitatively associated with lithosome prediction. The scale independence has been neatly illustrated by Posamentier et al. (1992) by studying a number of sequences developed in a road-side ditch.

Quantifying lithosome prediction within the various system tracts is not possible without information concerning the three-dimensional chromosome shape, orientation and underlying surface.

CONCLUSION

A lot of effort is being currently expended throughout the world in the field of lithosome prediction. Most of this effort is being directed towards porosity and permeability prediction in aquifers and hydrocarbon reservoirs. The field of three-dimensional visualization has also expanded dramatically as a function of access to computing power and color graphics technology, and there seems to be some confusion in the role of such representation in lithosome prediction. The three-dimensional representation of geological bodies can only be of quantitative use in lithosome prediction if we can achieve a) a stratigraphic framework for the body, b) a functional shape description, and c) a quantitative relationship between preserved shape, depositional surface, and depositional process.

A formalized three-dimensional chromosome concept is the first step towards this goal. The chromosome surface is the diachronous stratigraphic correlation surface at all scales, and is the nearest we can approach to a paleotopography. The time duration of a chromosome will vary according to the resolution of the observational technique, but at the limit of resolution the chromosome will always provide the optimum predictive unit. Any technique that improves the resolution will also improve the predictive potential. To put this another way, one should adjust the expected resolution of prediction to the expected time duration (temporal resolution) of the chromosome. Thus, given a 1 Ma temporal resolution in the Mesozoic, one should not expect to model sand distribution to the same accuracy as in a 10 ka Tertiary chromosome even though the thickness may be the same. The same process model or statistical model may be applied in both cases but the uncertainty increases with chromosome duration. This principle may be stated in the following way:

The probability of successful prediction of lithologic properties throughout a chromosome is generally inversely proportional to its duration

The physical thickness of a chromosome is of less importance, thick sands can be deposited by a single process in very short periods of time.

We must ask the following questions of our three-dimensional mapping systems therefore if we are to

have any success in lithosome prediction. The questions are;

- What is the 3D form of the chronosome ?
- What is its sequence stratigraphic position ?
- What is its duration ?
- What is its orientation and attitude ?
- What is the nature of its underlying surface ?
- What is its spatial relationship to neighboring chronosomes ?

Once we have quantitative answers to these questions we can begin to choose an appropriate statistical or process model to predict lithosome distribution within the chronosome. Our expectation of success can be estimated in advance by considering the duration of the chronosome involved.

We can conclude that any lithosome prediction model that does not take the chronosome into consideration has very little chance of success.

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