SUPPORTING INFORMATION

Stochastic Models of Octamer Loss – For stochastic models of octamer loss, the frequency of such loss from a mononucleosome would constitute the frequency of octamer loss from any (and every) nucleosome site in an array (case 1), or would constitute the average frequency of loss of a single octamer per array (case 2). In both cases one would predict that an array with fewer nucleosomes would reach a state of free DNA more readily than those with more nucleosomes, as is observed. However, both cases also would predict a different distribution of array saturations than occurs experimentally.

For case 1, the independence of each nucleosomal site toward octamer loss would mean that the distribution of array saturations would be described by a binomial distribution, with the most frequent array saturations being at or near the average array saturation (frequency of octamer loss of the mononucleosome times the number of nucleosomes initially present in the array). Since the observed frequency of mononucleosome loss can be up to 50%, for arrays that start with two octamers (both the dinucleosome, and the trinucleosome with two nucleosome sites saturated), the most common octamer loss product should be arrays with a single octamer (Supplemental Figure *S2*). This array saturation is not observed, and instead, species containing either two octamers or no octamer predominate. For longer arrays, intermediate saturation states predicted by the case 1 model are also absent, with tetranuclosomal arrays showing no octamer loss at all.

For case 2, each array has the same average frequency of losing one of its nucleosomes, e.g. if a mononucleosome has an average occupancy of 0.5, a tetranucleosomal array will have an average of 3.5 octamers. Under these circumstances, the distribution of array saturation species would still be described by a binomial distribution. However, the frequency of octamer loss from each site would be the frequency of mononucleosome loss divided by the number of nucleosomes in an array. For example, for the observed frequency of octamer loss of approximately 0.5 for the monomer, in a dinucleosome the frequency of loss from each site would be 0.5/2=0.25. This would mean that the average occupancy of each site would be 0.75; the saturation frequency distribution would be 6.25% no octamers, 37.5% one octamer, and 56.25% two octamers; and the average array saturation would be 1.5 nucleosomes (Supplemental Figure *S3*). In general, under conditions where the mononucleosome is significantly disassembled, for longer arrays some subsaturated array species should occur and be most frequent near the average array saturation. However, this again contradicts our observed distribution. The dinucleosomal array has a significant amount of free DNA, representing loss of two octamers, with no observable arrays containing only a single octamer. Further, tetranucleosomal array do not show evidence of subsaturated species.

FIGURE S1. **Restriction digestion analysis of undersaturated trinucleosomal arrays.** Tetranucleosomes, dinucleosomes, and three different subsaturated trinucleosomal arrays were digested with *BglI*. *A*, schematic of arrays and expected digestion products. *B*, uncut (U) and cut (C) arrays were run on a 4% native polyacrylamide gel and stained with ethidium bromide. Numbered lanes correspond to numbered arrays in *A*.

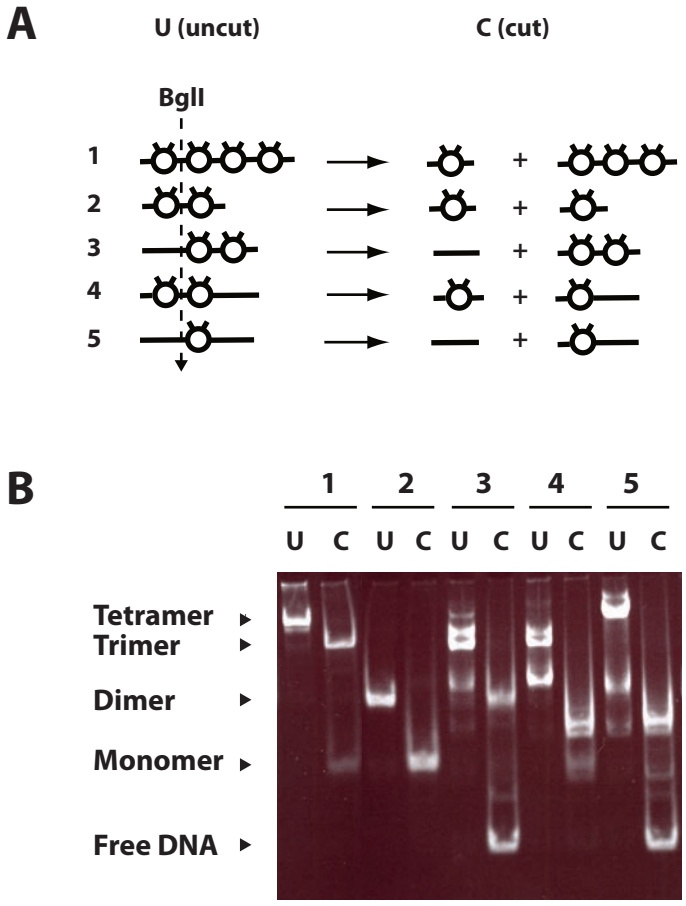
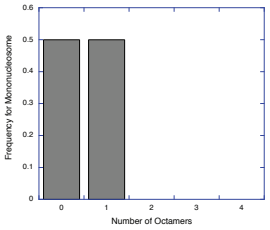


FIGURE S2. **Modeling of independent octamer loss from each site of a nucleosomal array, where the probability of octamer loss from any given site is 0.5.** Saturation distributions and statistics for various arrays in which a 50% chance of octamer loss occurs at every site in *A,* a mononucleosome, *B,* a dinucleosomal array, *C,* a trinucleosomal array, and *D,* a tetranucleosomal array. Distributions assume equal probability of octamer loss from each site, and are described by a binomial distribution. To explicitly demonstrate the source of the distributions, all possible saturation states of an array are enumerated with their associated probability. The summing of the probability of similar saturation states results in the associated binomial distribution. X represents an occupied nucleosomal site, O an unoccupied one. P_O represents the probability of loss of an octamer from a given nucleosomal site. P_X represents the probability of retention of an octamer from a given nucleosomal site.

A Mono: $P_O = 0.50$, $P_X = 1 - P_O = 0.50$

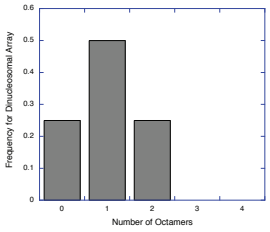
Mean: 0.5 Oct/Mono
Mode: 0 and 1 Oct/Mono



O – 0 Oct: $1xP_O = 0.5$
X – 1 Oct: $1xP_X = 0.5$

B Di: $P_O = 0.50$, $P_X = 1 - P_O = 0.50$

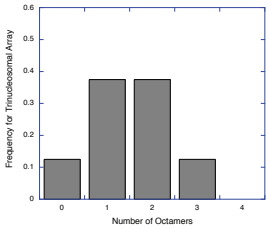
Mean: 1 Oct/Array
Mode: 1 Oct/Array



OO – 0 Oct: $1xP_OxP_O = 1x(0.50)^2 = 0.25$
OX – 1 Oct: $2xP_OxP_X = 2x(0.50)(0.50) = 0.50$
XO
XX – 2 Oct: $1xP_XxP_X = 1x(0.50)^2 = 0.25$

C Tri: $P_O = 0.50$, $P_X = 1 - P_O = 0.50$

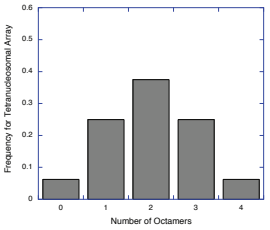
Mean: 1.5 Oct/Array
Mode: 1 and 2 Oct/Array



OOO – 0 Oct: $1xP_O^3 = 1x(0.50)^3 = 0.125$
OOX – 1 Oct: $3xP_O^2xP_X = 3x(0.50)^2(0.50) = 0.375$
OXO
XOO
OXX – 2 Oct: $3xP_OxP_X^2 = 3x(0.50)(0.50)^2 = 0.375$
XOX
XXO
XXX – 3 Oct: $1xP_x^3 = 1x(0.50)^3 = 0.125$

D Tetra: $P_O = 0.50$, $P_X = 1 - P_O = 0.50$

Mean: 2 Oct/Array
Mode: 2 Oct/Array



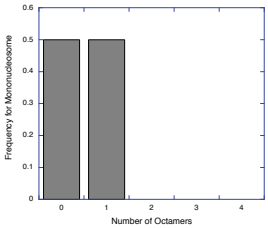
OOOO – 0 Oct: $1xP_O^4 = 1x(0.50)^4 = 0.0625$
OOOX – 1 Oct: $4xP_O^3xP_X = 4x(0.50)^3(0.50) = 0.250$
OOXO
OXOO
XOOO
OOXX – 2 Oct: $6xP_O^2xP_X^2 = 6x(0.50)^2(0.50)^2 = 0.375$
OXOX
XOOX
XOXO
XXOO
OXXO
XXXO – 3 Oct: $4xP_OxP_X^3 = 4x(0.50)(0.50)^3 = 0.250$
XXOX
XOXX
OXXX
XXXX – 4 Oct: $1xP_x^4 = 1x(0.50)^4 = 0.0625$

FIGURE S3. **Modeling of stochastic loss of 0.5 octamers per nucleosomal array.** Saturation distributions and statistics for various arrays in which a 50% chance of octamer loss is spread over *A,* a mononucleosome, *B,* a dinucleosomal array, *C,* a trinucleosomal array, and *D,* a tetranucleosomal array. Distributions assume equal probability of octamer loss from each site, and are described by a binomial distribution. To explicitly demonstrate the source of the distributions, all possible saturation states of an array are enumerated with their associated probability. The summing of the probability of similar saturation states results in the associated binomial distribution. X represents an occupied nucleosomal site, O an unoccupied one. P_O represents the probability of loss of an octamer from a given nucleosomal site. P_X represents the probability of retention of an octamer from a given nucleosomal site.

A

Mono: $P_O = 0.5/1 = 0.50$
$P_X = 1 - P_O = 0.50$

Mean: 0.5 Oct/Mono
Mode: 0 and 1 Oct/Mono

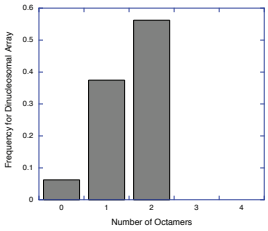


O – 0 Oct: $1xP_O = 0.5$
X – 1 Oct: $1xP_X = 0.5$

B

Di: $P_O = 0.5/2 = 0.25$
$P_X = 1 - P_O = 0.75$

Mean: 1.5 Oct/Array
Mode: 1 Oct/Array

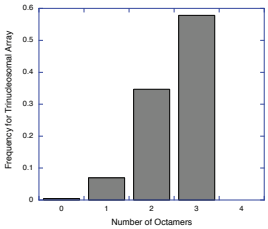


OO – 0 Oct: $1xP_OxP_O = 1x(0.25)^2 = 0.063$
OX – 1 Oct: $2xP_OxP_X = 2x(0.25)(0.75) = 0.375$
XO
XX – 2 Oct: $1xP_XxP_X = 1x(0.75)^2 = 0.563$

C

Tri: $P_O = 0.5/3 = 0.167$
$P_X = 1 - P_O = 0.833$

Mean: 2.5 Oct/Array
Mode: 1 Oct/Array

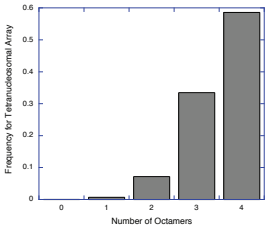


OOO – 0 Oct: $1xP_O^3 = 1x(0.167)^3 = 0.005$
OOX – 1 Oct: $3xP_O^2xP_X = 3x(0.167)^2(0.833) = 0.069$
OXO
XOO
OXX – 2 Oct: $3xP_OxP_X^2 = 3x(0.167)(0.833)^2 = 0.347$
XOX
XXO
XXX – 3 Oct: $1xP_x^3 = 1x(0.833)^3 = 0.578$

D

Tetra: $P_O = 0.5/4 = 0.125$
$P_X = 1 - P_O = 0.875$

Mean: 3.5 Oct/Array
Mode: 1 Oct/Array



OOOO – 0 Oct: $1xP_O^4 = 1x(0.125)^4 = 0.0002$
OOOX – 1 Oct: $4xP_O^3xP_X = 4x(0.125)^3(0.875) = 0.007$
OOXO
OXOO
XOOO
OOXX – 2 Oct: $6xP_O^2xP_X^2 = 6x(0.125)^2(0.875)^2 = 0.072$
OXOX
XOOX
XOXO
XXOO
OXXO
XXXO – 3 Oct: $4xP_OxP_X^3 = 4x(0.125)(0.875)^3 = 0.335$
XXOX
XOXX
OXXX
XXXX – 4 Oct: $1xP_x^4 = 1x(0.875)^4 = 0.586$