SINGULARITIES ON FIXED CYCLE UNDIRECTED ANIMALS

A FEW ADDITIONAL ANALYSES

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ABSTRACT — The cycle animal values on the triangular and square site problems (extended by one more term) and the honeycomb bond cycle 1 animals are studied for their leading and confluent singularities as well as their multiplicities.

INTRODUCTION AND SUMMARY

In this presentation we aim at a consistent revision of results on the singularity location and exponent values for fixed cycle undirected animals. A classification of such undirected site animals according to their cyclomatic index for two-dimensional lattices was published by Duarte in 1981 [1]. Trees — or zero cycle animals — were much debated around the period following the field theoretic predictions of Lubensky and coworkers [2]. Duarte and Ruskin [3] proved that the leading singularity estimates for trees overlapped with those for the complete animals, as predicted in [2], and a significant advance followed in ref. [4], where 2 and 3-dimensional data for most usual lattices were found to back a graph-theoretical prediction for bond animals (i.e. pertaining to weak embeddings) that the singularity alteration for c-cycle animals is reduced to a change in the exponent (leading exponent here) according to the law

$$\Theta_c = \Theta_o - c \tag{1}$$

As can be seen, singularities get progressively stronger. Also, the multiplicity for trees remains unaltered for all c-cycle values. This requires a shift of multiplicity on summing all cycle values to obtain the complete number of undirected animals: a significant difference in structure from the percolation perimeter partition, which is well known to be characterized by a variable multiplicity [1]. The data in Whittington, Torrie and Gaunt [3] for cycle values 2,1 in 2 dimensions are complemented in Duarte [1] to the order presently available for trees (and also for the honeycomb site animals). We have added here the 1-cycle honeycomb bond animals (for trees, see [3]) in table I and repeat the analyses for the additional evidence.

TABLE I

s	g_{s1}
6	1.
7	6.
8	27.
9	110.
10	432.
11	1,626.
12	5,956.
13	21,450.
14	76,296.
15	268,634.
16	938,667.
17	3,260,496.

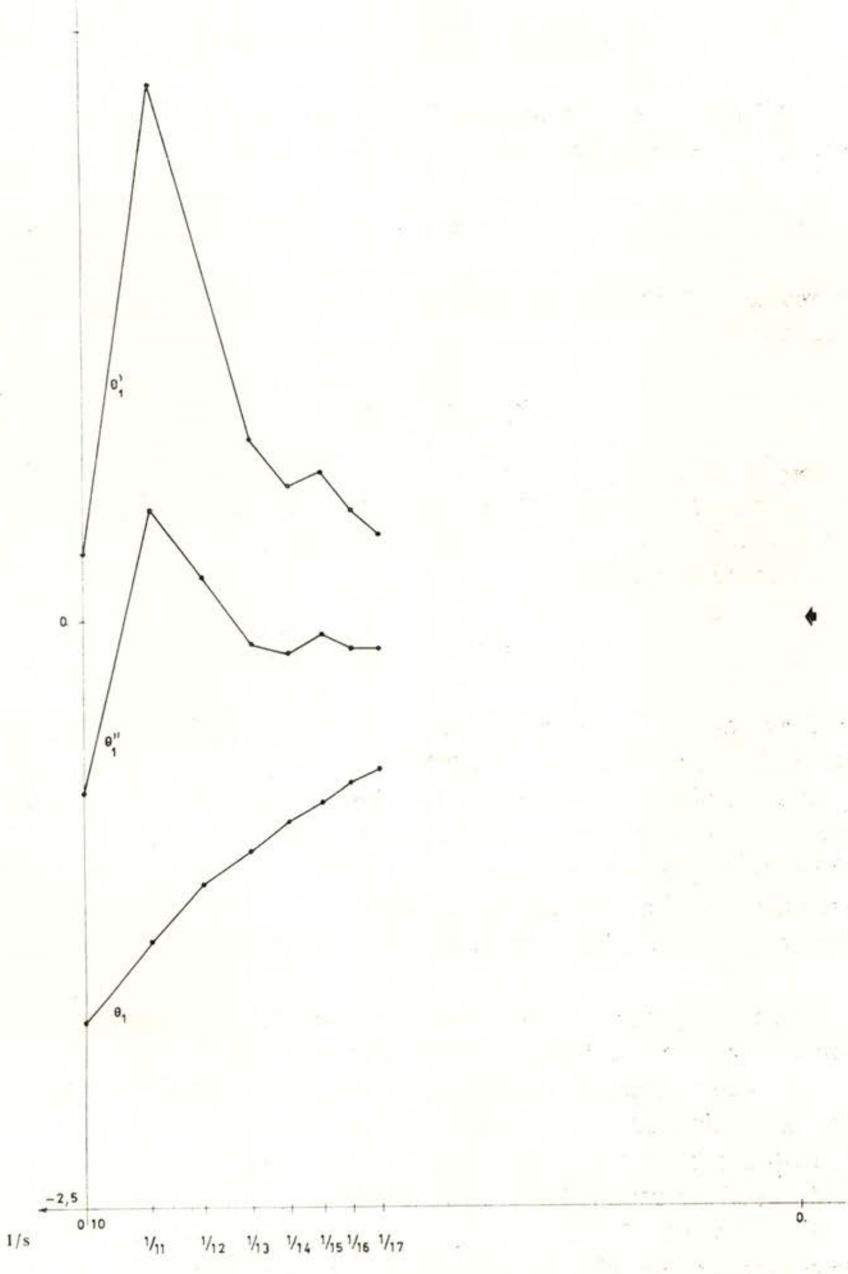

Fig. 1 — Θ_1 sequences for the honeycomb bond 1-cycle animals: Θ_1, biassed estimates, Θ_1' linear intercepts on them, Θ_1'', averages of the Θ_1 and Θ_1' sequences.

ANALYSES AND CONCLUSIONS

All sequences are for two-dimensional lattices. According to eq. 1, the leading singularity is therefore known to vary as

$$\Theta_c = 1 - c \tag{2}$$

a result that should be approached by the usual extrapolating sequences

$$\Theta_c(s) = s \ (1 - R_s/\lambda_o) \tag{3}$$

where $R_s = g_{s,\,c}/g_{s-1,\,c}$ is the ratio of successive c-cycle number of animals, λ_0 a good estimate of the multiplicity (in the present case, usually the central estimate for trees).

Linear extrapolants

$$\Theta_c'(s) = s \ \Theta_c(s) - (s\text{-}1) \ \Theta_c(s\text{-}1) \tag{4}$$

and averages of $\Theta_c(s)$ and $\Theta_c'(s)$ (here called $\Theta_c''(s)$) may also be used for assessing the evolution of the exponent sequences (Fig. 2): while the extra terms for the triangular site and square site sequences bring no great alteration in the pattern for Θ_1 or Θ_2, the new sequences according to eq. 3 for the honeycomb bond animals are of a comparable quality (Fig. 1), hovering somewhat below the $\Theta_1 = 0$ limit, as found for the other two lattices [4].

We also present graphical evidence on the λ_0 value estimates for the honeycomb bond problem (Fig. 3).

1 — cycle animals and trees are the most useful cycle values for estimation of the multiplicity. The combination $\Theta_1 = 0$ and $\Theta_0 = +1$ means that the ratios R_s and their linear intercepts under- and overestimate the λ_0 value, respectively. Their averages evolve closer to the multiplicity limit (cf. Fig. 3) and one expects to compare them with the tree estimates biassed with $\Theta_0 = 1$

$$\lambda_b(s) = s \ R_s/(s\text{-}\Theta_0) \tag{5}$$

This comparison helped halving the uncertainty for λ_0 in triangular site animals in [4] and trim it slightly here

$$\lambda_0 = \underset{[3]}{4.19 \pm 0.015} \; ; \; \underset{[4]}{4.196 \pm 0.007} \; ; \; \underset{\text{this work}}{4.195 \pm 0.005} \tag{6}$$

while the extra term for the square site animals warrants no alteration of the value in ref. [4]

$$\lambda_0 = 3.795 \pm 0.007 \tag{7}$$

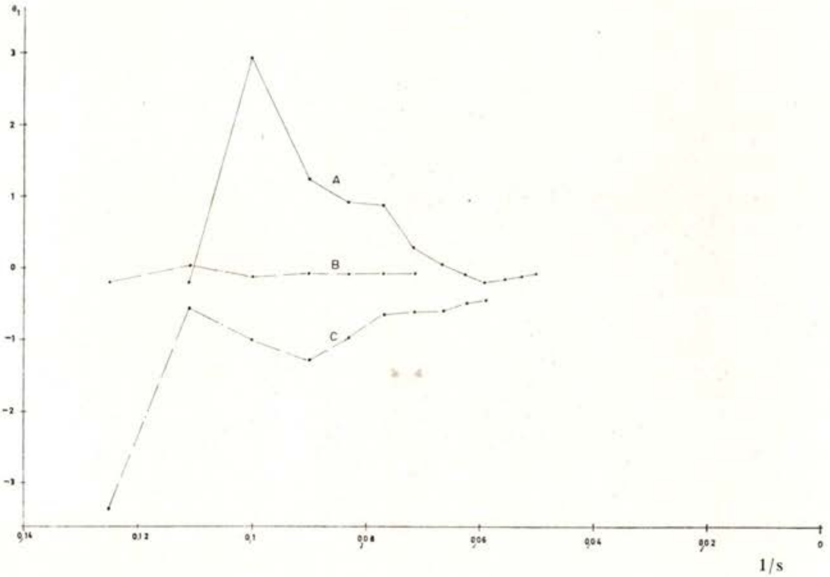

Fig. 2 — Comparison of site 1-cycle animal exponents for the triangular (B), square (C) and honeycomb site (A) cases. The overall estimate is $\Theta_1 = -0.1 \pm 0.2$.

The results for λ_0 relative to fixed cycle honeycomb bond animals given in Fig. 3 bring no revision of the estimate given in [3]

$$\lambda_0 = 3.35 \pm 0.01 \tag{8}$$

An interesting question arises with the possibility of a direct evaluation of the confluent singularities for fixed cycle animals.

Confluent singularities of an algebraic type have been referred by a number of authors and analysed for the total numbers of animals [5]. The asymptotic form of the tree values, for example, is then given by

$$g_{s,0} \sim \lambda_0^s \, s^{-1} \, (1 + E \, s^{-w} + \dots) \tag{9}$$

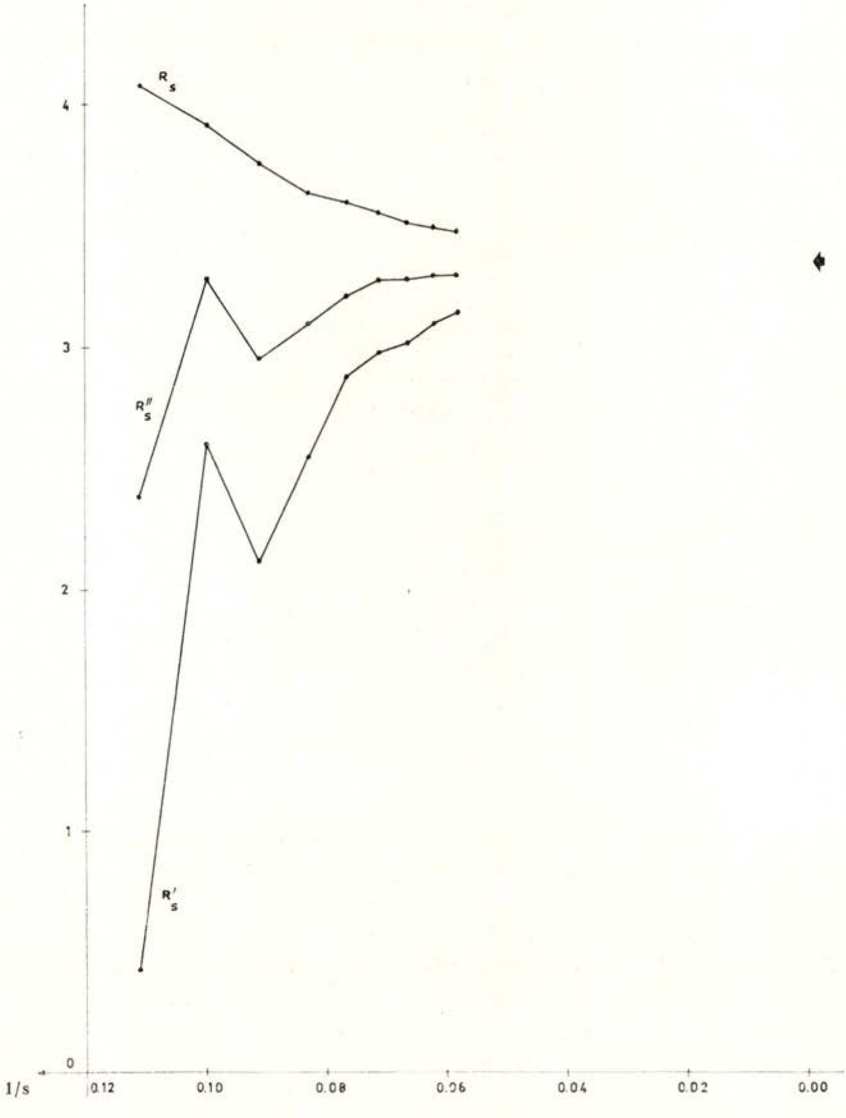

Fig. 3 — Multiplicity estimates for the honeycomb bond 1-cycle animals: R_s ratios, R'_s, linear intercepts on them, R''_s, averages of the previous sequences.

with w the confluent correction. An independent estimate of w, not sensitive to the λ_0 variation, can be obtained from the second log difference

$$\mathrm{Log}\ [\,(s^2-1)/s^2 \cdot g_{s+1,0}\, g_{s-1,0}/(g_{s,0})^2\,] \sim s^{-(w+2)} \qquad (10)$$

and the best results were obtained for the triangular bond trees (to $s < 11$ in [4]) and square matching trees (to $s < 11$ in [3]). All the others, including square site and bond trees, triangular site and both honeycomb trees were virtually of no pratical use. Even for the two best examples mentioned above, it is impossible to go beyond saying that the data are not incompatible with the w estimate for lattice animals [5]

$$w = 0.86 \pm 0.05 \qquad (11)$$

but an independent estimate is out of question for such comparatively short series.

In conclusion, the extended evidence confirms and marginally improves the multiplicity estimates, whereas the rather incipient evidence on the confluent singularity is not in disagreement with the animal value (11).

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